

Package: ggseurat (via r-universe)

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Type Package

Title ggplot2 Bindings for Seurat Objects

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Description Provides methods to allow Seurat objects to be utilized directly in the ggplot2 ecosystem.

URL <https://mojaveazure.github.io/ggseurat>,
<https://github.com/mojaveazure/ggseurat>

BugReports <https://github.com/mojaveazure/ggseurat/issues>

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Depends ggplot2 (>= 3.3.5), R (>= 4.0.0), SeuratObject (>= 4.1.0)

Imports Matrix (>= 1.4.1), methods, rlang (>= 0.4.12), stats, utils

Suggests cowplot (>= 1.1.1), knitr (>= 1.36), patchwork (>= 1.1.1),
rmarkdown (>= 2.11)

Enhances Seurat (>= 4.0.0)

VignetteBuilder knitr

Collate 'zzz.R' 'assay.R' 'centroids.R' 'dimreduc.R' 'fov.R'
'ggplot.R' 'ggplot2_utils.R' 'molecules.R' 'roxygen.R'
'segmentation.R' 'seurat.R'

Repository <https://mojaveazure.r-universe.dev>

RemoteUrl <https://github.com/mojaveazure/ggseurat>

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ggseurat-package	<i>ggseurat: ggplot2 Bindings for Seurat Objects</i>
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Description

Provides methods to allow Seurat objects to be utilized directly in the ggplot2 ecosystem.

Author(s)

Maintainer: Paul Hoffman <phoffman@nygenome.org> ([ORCID](#))

See Also

Useful links:

- <https://mojaveazure.github.io/ggseurat>
- <https://github.com/mojaveazure/ggseurat>
- Report bugs at <https://github.com/mojaveazure/ggseurat/issues>

autolayer.Assay	<i>Create a Layer to Add to ggplot Objects</i>
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Description

Generate a `geom_violin` layer to add to existing ggplot objects. The new plot data and aesthetics are stored at the geom level

Usage

```
## S3 method for class 'Assay'  
autolayer(  
  object,  
  data = missing_arg(),  
  features = NULL,  
  layer = c("data", "scale.data", "counts"),  
  na.rm = TRUE,  
  show.legend = NA,  
  ...  
)
```

Arguments

object	An Assay object
data	A <code>data.frame</code> (eg. from FetchData) with extra data for visualization
features	A vector of features to include in the fortified data; defaults to the variable features
layer	Name of layer to pull expression data for
na.rm	Remove values with NAs
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
...	Arguments passed to geom_violin

Details

The following aesthetics are mapped automatically and overwrite said aesthetics at the plot level if set:

- "x"
- "y"
- "fill"

Value

A [geom_violin](#) layer to add to `ggplot` objects

See Also

[ggplot2::autolayer\(\)](#), [ggplot2::geom_violin\(\)](#)

Visualize Assay Expression Data: [autoplot.Assay\(\)](#), [fortify.Assay\(\)](#)

Examples

```

data("pbmc_small")
rna <- pbmc_small[["RNA"]]
md <- FetchData(pbmc_small, vars = "ident")

# Generate a plot using `autolayer()`

```

autolayer.DimReduc *Create a Layer to Add to ggplot Objects*

Description

Generate a [geom_point](#) layer to add to existing ggplot objects. The new plot data and aesthetics are stored at the geom level

Usage

```

## S3 method for class 'DimReduc'
autolayer(
  object,
  data = missing_arg(),
  dims = c(1L, 2L),
  na.rm = TRUE,
  show.legend = NA,
  ...
)

```

Arguments

object	A DimReduc object
data	A data.frame (eg. from FetchData) with extra data for visualization
dims	Dimensions for visualization
na.rm	Remove values with NAs
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
...	Arguments passed to geom_point

Details

The following aesthetics are mapped automatically and overwrite said aesthetics at the plot level if set:

- “x”
- “y”
- “color”

Value

A [geom_point](#) layer to add to ggplot objects

See Also

[ggplot2::autolayer\(\)](#), [ggplot2::geom_point\(\)](#)

Visualize Dimensional Reductions: [autoplot.DimReduc\(\)](#), [fortify.DimReduc\(\)](#)

Examples

```
data("pbmc_small")
tsne <- pbmc_small[["tsne"]]
md <- FetchData(pbmc_small, vars = c("ident", "MS4A1"))

# Generate a plot using `autolayer()`
ggplot() + autolayer(tsne)
ggplot() + autolayer(tsne, data = md)
```

 autoplot.Assay

Create a Plot for Assay Objects

Description

Generate a ggplot plot for [Assay](#) objects

Usage

```
## S3 method for class 'Assay'
autoplot(
  object,
  data = missing_arg(),
  features = NULL,
  layer = c("data", "scale.data", "counts"),
  na.rm = TRUE,
  show.legend = NA,
  ...
)
```

Arguments

object	An Assay object
data	A data.frame (eg. from FetchData) with extra data for visualization
features	A vector of features to include in the fortified data; defaults to the variable features
layer	Name of layer to pull expression data for

na.rm	Remove values with NAs
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
...	Arguments passed to geom_violin

Details

The following aesthetics are mapped automatically:

- “x”
- “y”
- “fill”

Value

A [ggplot](#) object

See Also

[ggplot2::autoplot\(\)](#)

Visualize Assay Expression Data: [autolayer.Assay\(\)](#), [fortify.Assay\(\)](#)

Examples

```
data("pbmc_small")
rna <- pbmc_small[["RNA"]]
md <- FetchData(pbmc_small, vars = "ident")

# Generate a plot using `autoplot()``
```

autoplot.DimReduc

Create a Plot for DimReduc Objects

Description

Generate a ggplot plot for [DimReduc](#) objects

Usage

```
## S3 method for class 'DimReduc'
autoplot(
  object,
  data = missing_arg(),
  dims = c(1L, 2L),
  na.rm = TRUE,
```

```
  show.legend = NA,  
  ...  
)
```

Arguments

object	A DimReduc object
data	A data.frame (eg. from FetchData) with extra data for visualization
dims	Dimensions for visualization
na.rm	Remove values with NAs
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
...	Arguments passed to geom_point

Details

The following aesthetics are mapped automatically:

- “x”
- “y”
- “color”

Value

A [ggplot](#) object

See Also

[ggplot2::autoplot\(\)](#)

Visualize Dimensional Reductions: [autolayer.DimReduc\(\)](#), [fortify.DimReduc\(\)](#)

Examples

```
data("pbmc_small")  
tsne <- pbmc_small[["tsne"]]  
md <- FetchData(pbmc_small, vars = c("ident", "MS4A1"))  
  
# Generate a plot using `autoplot()`  
autoplot(tsne)  
autoplot(tsne, data = md)
```

fortify.Assay *Create a Data Frame Suitable for ggplot()*

Description

Generate a long-format data frame for ease of use with `ggplot()`; as a bonus, this method enables direct calling of `Assay` objects in `ggplot()` (see examples)

Usage

```
## S3 method for class 'Assay'  
fortify(  
  model,  
  data,  
  features = NULL,  
  layer = c("data", "scale.data", "counts"),  
  na.rm = FALSE,  
  ...  
)
```

Arguments

<code>model</code>	An <code>Assay</code> object
<code>data</code>	A <code>data.frame</code> (eg. from <code>FetchData</code>) with extra data for visualization
<code>features</code>	A vector of features to include in the fortified data; defaults to the variable features
<code>layer</code>	Name of layer to pull expression data for
<code>na.rm</code>	Remove values with NAs
<code>...</code>	Ignored

Details

`fortify.Assay()` generates a data frame based on the expression data stored in `layer`; automatically creates a column for cell names (“cell”). Also creates a column for identity classes (“ident”) if not present in `data`; the default identity class is “SeuratProject”; final column output order is:

- “cell”
- “ident”
- expression data for features
- additional meta data provided by `data`

Value

A long-format data frame for use with `ggplot()`

See Also

`ggplot2::ggplot()`, `ggplot2::fortify()`

Visualize Assay Expression Data: `autolayer.Assay()`, `autoplot.Assay()`

Examples

```
data("pbmc_small")
rna <- pbmc_small[["RNA"]]
md <- FetchData(pbmc_small, vars = "ident")

# Create a data frame for `ggplot()`
df <- fortify(rna, data = md)
head(df)
ggplot(df, mapping = aes(x = ident, y = PPBP, fill = ident)) +
  geom_violin()

# Use an `Assay` directly in `ggplot()`
ggplot(rna, mapping = aes(x = ident, y = GNLY, fill = ident), md) +
  geom_violin()
```

fortify.DimReduc

Create a Data Frame Suitable for ggplot()

Description

Generate a long-format data frame for ease of use with `ggplot()`; as a bonus, this method enables direct calling of `DimReduc` objects in `ggplot()` (see examples)

Usage

```
## S3 method for class 'DimReduc'
fortify(model, data, na.rm = FALSE, ...)
```

Arguments

<code>model</code>	A <code>DimReduc</code> object
<code>data</code>	A <code>data.frame</code> (eg. from <code>FetchData</code>) with extra data for visualization
<code>na.rm</code>	Remove values with NAs
<code>...</code>	Ignored

Details

`fortify.DimReduc()` generates a data frame based on the [cell embeddings](#). Automatically creates a column for cell names (“cell”). Also creates a column for identity classes (“ident”) if not present in data; the default identity class is “SeuratProject”; final column output order is:

- “cell”
- “ident”
- cell embeddings
- additional meta data provided by data

Value

A long-format data frame for use with `ggplot()`

See Also

`ggplot2::ggplot()`, `ggplot2::fortify()`

Visualize Dimensional Reductions: `autolayer.DimReduc()`, `autoplot.DimReduc()`

Examples

```
data("pbmc_small")
tsne <- pbmc_small[["tsne"]]
md <- FetchData(pbmc_small, vars = c("ident", "MS4A1"))

# Create a data frame for `ggplot()`
df <- fortify(tsne, data = md)
head(df)
ggplot(df, mapping = aes(x = tSNE_1, y = tSNE_2, color = ident)) +
  geom_point()

# Use a `DimReduc` directly in `ggplot()`
ggplot(tsne, mapping = aes(x = tSNE_1, y = tSNE_2, color = MS4A1), md) +
  geom_point()
```

ggplot.Seurat

Visualize Seurat objects

Description

Visualize Seurat objects

Usage

```
## S3 method for class 'Seurat'
ggplot(data = NULL, mapping = aes(), ..., environment = parent.frame())
```

Arguments

<code>data</code>	A Seurat object
<code>mapping</code>	Default list of aesthetic mappings to use for plot. If not specified, must be supplied in each layer added to the plot.
<code>...</code>	Other arguments passed on to methods. Not currently used.
<code>environment</code>	DEPRECATED. Used prior to tidy evaluation.

Value

A ggplot object

See Also

[ggplot](#)

`ggplot_build.ggseurat` [ggplot_build.Seurat](#)

Description

`ggplot_build.Seurat`

Usage

```
## S3 method for class 'ggseurat'  
ggplot_build(plot)
```

Arguments

`plot` ggplot object

Value

A built ggplot ready for viewing

See Also

[ggplot_build](#)

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