Package 'chevreulPlot'

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Type Package

Title Plots used in the chevreulPlot package

Version 1.5.0

Description Tools for plotting SingleCellExperiment objects in the chevreulPlot package. Includes functions for analysis and visualization of single-cell data. Supported by NIH grants R01CA137124 and R01EY026661 to David Cobrinik.

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URL https://github.com/whtns/chevreulPlot, https://whtns.github.io/chevreulPlot/

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BugReports https://github.com/cobriniklab/chevreulPlot/issues

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Contents

chevreulPlot-package . . . 2
cc.genes.cyclone . . . 3
enframe_markers . . . 3
ensembl_version . . . 4
grch38 . . . 4
grch38_tx2gene . . . 5
human_to_mouse_homologs . . . 6
make_complex_heatmap . . . 6
plotly_settings . . . 7
plot_all_transcripts . . . 8
plot_colData_histogram . . . 8
plot_colData_on_embedding . . . 9
plot_feature_on_embedding . . . 10
plot_gene_coverage_by_var . . . 11
plot_marker_features . . . 12
plot_transcript_composition . . . 13
plot_violin . . . 13
small_example_dataset . . . 14
tiny_sce . . . 15

Index **16**

`chevreulPlot-package` *chevreulPlot: Plots used in the chevreulPlot package*

Description

Tools for plotting SingleCellExperiment objects in the chevreulPlot package. Includes functions for analysis and visualization of single-cell data. Supported by NIH grants R01CA137124 and R01EY026661 to David Cobrinik.

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See Also

Useful links:

- https://github.com/whtns/chevreulPlot
- https://whtns.github.io/chevreulPlot/
- Report bugs at https://github.com/cobriniklab/chevreulPlot/issues

---

`cc.genes.cyclone` *Cyclone cell cycle pairs by symbol*

Description

cell cycle genes with paired expression represented by HGNC symbol

Usage

```
cc.genes.cyclone
```

Format

a list of dataframes with G1, G2, and S gene expression

G1 G1 gene symbols

G2 G2 gene symbols

S S gene symbols ...

Source

cyclone

`enframe_markers` *Enframe Cluster Markers*

Description

Enframe Cluster Markers

Usage

```
enframe_markers(tbl)
```

Arguments

`tbl`	a tibble of marker genes

Value

a pivoted tibble of marker genes

ensembl_version *Ensembl version used for build*

Description

Ensembl version used for build

Usage

```
ensembl_version
```

Format

An object of class `character` of length 1.

Source

http://www.ensembl.org/

Examples

```
# ensembl_version
```

grch38 *Human annotation data*

Description

Human (*Homo sapiens*) annotations based on genome assembly GRCH38 from Ensembl.

Usage

```
grch38
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 76062 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

http://ensembl.org/homo_sapiens

Examples

```
data("grch38")
head(grch38)
```

`grch38_tx2gene` *Human transcripts to genes*

Description

Lookup table for converting Human (*Homo sapiens*) Ensembl transcript IDs to gene IDs based on genome assembly GRCH38 from Ensembl.

Usage

```
grch38_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 277081 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/homo_sapiens

Examples

```
data(grch38_tx2gene)
head(grch38_tx2gene)
```

human_to_mouse_homologs *Gene Homologs Between Human and Mouse*

Description

Homologs drawn from Biomart

Usage

```
human_to_mouse_homologs
```

Format

A data frame with 23188 rows and 2 columns

HGNC.symbol human gene symbols

MGI.symbol mouse gene symbols ...

Source

bioMart

make_complex_heatmap *Plot Annotated Complexheatmap from SingleCellExperiment object*

Description

Plot Annotated Complexheatmap from SingleCellExperiment object

Usage

```
make_complex_heatmap(
  object,
  features = NULL,
  group.by = "ident",
  cells = NULL,
  assayName = "logcounts",
  experiment = NULL,
  group.bar.height = 0.01,
  column_split = NULL,
  col_arrangement = "ward.D2",
  mm_col_dend = 30,
  ...
)
```

Arguments

object	A SingleCellExperiment object
features	Vector of features to plot. Features can come
group.by	Name of one or more metadata columns to annotate columns by (for example, orig.ident)
cells	Cells to retain
assayName	"counts" for raw data "scale.data" for log-normalized data
experiment	experiment to display
group.bar.height	height for group bars
column_split	whether to split columns by metadata value
col_arrangement	how to arrange columns whether with a dendrogram (Ward.D2, average, etc.) or exclusively by metadata category
mm_col_dend	height of column dendrogram
...	additional arguments passed to Heatmap

Value

a complexheatmap

Examples

```
data("tiny_sce")
make_complex_heatmap(tiny_sce)
```

---

plotly_settings *Plotly settings*

Description

Change settings of a plotly plot

Usage

```
plotly_settings(plotly_plot, width = 600, height = 700)
```

Arguments

plotly_plot	A plotly plot
width	Default set to '600'
height	Default set to '700'

Value

a plotly plot with altered settings

plot_all_transcripts *Plot All Transcripts*

Description

plot expression all transcripts for an input gene superimposed on embedding

Usage

```
plot_all_transcripts(
  object,
  features,
  embedding = "UMAP",
  from_gene = TRUE,
  ...
)
```

Arguments

object	A object
features	gene or vector of transcripts
embedding	umap
from_gene	whether to look up transcripts for an input gene
...	additional arguments passed to plot_feature_on_embedding

Value

a list of embedding plots colored by a feature of interest

Examples

```
data("tiny_sce")
plot_all_transcripts(tiny_sce, "NRL", from_gene = TRUE)
```

plot_colData_histogram *Plot Read Count*

Description

Draw a box plot for read count data of a metadata variable

Usage

```
plot_colData_histogram(
  object,
  group_by = NULL,
  fill_by = NULL,
  yscale = "linear",
  return_plotly = FALSE
)
```

Arguments

object	A object
group_by	Metadata variable to plot. Default set to "nCount_RNA"
fill_by	Variable to color bins by. Default set to "batch"
yscale	Scale of y axis. Default set to "linear"
return_plotly	whether to return an interactive plotly plot

Value

a histogram of read counts

Examples

```
data(small_example_dataset)
small_example_dataset <- sce_calcn(small_example_dataset)
# static plot
plot_colData_histogram((small_example_dataset), return_plotly = FALSE)
```

---

plot_colData_on_embedding

Plot Metadata Variables

Description

Plots static or interactive plot where each point represents a cell metadata variable whose position on the map depends on cell embeddings determined by the reduction technique used

Usage

```
plot_colData_on_embedding(
  object,
  group = "batch",
  embedding = "UMAP",
  dims = c(1, 2),
  highlight = NULL,
  return_plotly = FALSE,
  ...
)
```

Arguments

object	A SingleCellExperiment object
group	Name of one or more metadata columns to group (color) cells by
embedding	The dimensional reduction technique to be used
dims	Dimensions to plot, must be a two-length numeric vector
highlight	A list of vectors of cells to highlight
return_plotly	Convert plot to interactive web-based graph
...	extra parameters passed to ggplot

Value

a ggplot

Examples

```
data(small_example_dataset)

# static mode
plot_colData_on_embedding(small_example_dataset, "Mutation_Status", return_plotly = FALSE)
```

`plot_feature_on_embedding` *Plot Feature*

Description

Plots gene or transcript expression overlaid on a given embedding.

Usage

```
plot_feature_on_embedding(
  object,
  embedding = c("UMAP", "PCA", "TSNE"),
  features,
  dims = c(1, 2),
  return_plotly = FALSE,
  ...
)
```

Arguments

`object`	A SingleCellExperiment object
`embedding`	Dimensional reduction technique to be used
`features`	Feature to plot
`dims`	Dimensions to plot, must be a two-length numeric vector
`return_plotly`	return plotly object
`...`	additional arguments passed to plotReduceDim

Value

an embedding colored by a feature of interest

Examples

```
data(small_example_dataset)
plot_feature_on_embedding(small_example_dataset, embedding = "UMAP",
features = "Gene_0001")
```

plot_gene_coverage_by_var *Plot BigWig Coverage for Genes of Interest by a Given Variable*

Description

Plot BigWig coverage for genes of interest colored by a given variable

Usage

```
plot_gene_coverage_by_var(
  genes_of_interest = "NRL",
  cell_metadata,
  bigwig_tbl,
  group_by = "batch",
  values_of_interest = NULL,
  organism = c("human", "mouse"),
  edb = NULL,
  heights = c(3, 1),
  scale_y = "log10",
  reverse_x = FALSE,
  start = NULL,
  end = NULL,
  summarize_transcripts = FALSE,
  ...
)
```

Arguments

genes_of_interest	Gene of interest
cell_metadata	a dataframe with cell metadata from object
bigwig_tbl	a tibble with colnames "name", "bigWig", and "sample_id" matching the filename, absolute path, and sample name of each cell in the cell_metadata
group_by	Variable to color by
values_of_interest	values of interest
organism	human (default) or mouse
edb	ensembldb object
heights	The heights of each row in the grid of plot
scale_y	whether to scale coverage
reverse_x	whether to reverse x axis
start	start coordinates
end	end coordinates
summarize_transcripts	whether to summarize transcript counts
...	extra arguments passed to plotCoverageFromEnsembldb

Value

a ggplot with coverage faceted by group_by

`plot_marker_features` *Plot Cluster Marker Genes*

Description

Plot a dot plot of n marker features grouped by cell metadata available methods are wilcoxon rank-sum test

Usage

```
plot_marker_features(
  object,
  group_by = "batch",
  num_markers = 5,
  selected_values = NULL,
  return_plotly = FALSE,
  marker_method = "wilcox",
  experiment = "gene",
  hide_technical = NULL,
  unique_markers = FALSE,
  p_val_cutoff = 1,
  ...
)
```

Arguments

`object`	a object
`group_by`	the metadata variable from which to pick clusters
`num_markers`	default is 5
`selected_values`	selected values to display
`return_plotly`	whether to return an interactive plotly plot
`marker_method`	"wilcox"
`experiment`	experiment to plot default gene
`hide_technical`	whether to exclude mitochondrial or ribosomal genes
`unique_markers`	whether to plot only unique marker genes for group
`p_val_cutoff`	cutoff for p value display
`...`	extra parameters passed to ggplot2

Value

a ggplot with marker genes from group_by

Examples

```
data(small_example_dataset)
plot_marker_features(small_example_dataset, group_by = "gene_snn_res.1")
```

plot_transcript_composition *Plot Transcript Composition*

Description

plot the proportion of reads of a given gene map to each transcript

Usage

```
plot_transcript_composition(
  object,
  gene_symbol,
  group.by = "batch",
  standardize = FALSE,
  drop_zero = FALSE
)
```

Arguments

object	A object
gene_symbol	Gene symbol of gene of interest
group.by	Name of one or more metadata columns to annotate columns by (for example, orig.ident)
standardize	whether to standardize values
drop_zero	Drop zero values

Value

a stacked barplot of transcript counts

Examples

```
data(tiny_sce)
plot_transcript_composition(tiny_sce, "NRL")
```

plot_violin *Plot Violin plot*

Description

Plots a Violin plot of a single data (gene expression, metrics, etc.) grouped by a metadata variable

Usage

```
plot_violin(
  object,
  group_by = "batch",
  plot_vals = NULL,
  features = "NRL",
  experiment = "gene",
  ...
)
```

Arguments

object	A SingleCellExperiment object
group_by	Variable to group (color) cells by
plot_vals	plot values
features	Features to plot
experiment	Name of experiment to use, defaults to active experiment
...	extra parameters passed to ggplot2

Value

a violin plot

Examples

```
data("tiny_sce")
plot_violin(tiny_sce, "Prep.Method", features = "NRL")
```

---

small_example_dataset *Small example SingleCellExperiment*

Description

created with scuttle::mockSCE

Usage

```
small_example_dataset
```

Format

An SCE with 200 cells and 1000 genes

Source

scuttle::mockSCE

`tiny_sce` *Tiny example SingleCellExperiment*

Description

subset to only NRL from chevreuldata::human_gene_transcript_sce()

Usage

```
tiny_sce
```

Format

An SCE with only expression of NRL gene and NRL transripts

Source

chevreuldata::human_gene_transcript_sce()

Index

∗ **datasets**
cc.genes.cyclone, 3
ensembl_version, 4
grch38, 4
grch38_tx2gene, 5
human_to_mouse_homologs, 6
small_example_dataset, 14
tiny_sce, 15
∗ **internal**
chevreulPlot-package, 2

cc.genes.cyclone, 3
chevreulPlot *(*chevreulPlot-package*)*, 2
chevreulPlot-package, 2

enframe_markers, 3
ensembl_version, 4

grch38, 4
grch38_tx2gene, 5

human_to_mouse_homologs, 6

make_complex_heatmap, 6

plot_all_transcripts, 8
plot_colData_histogram, 8
plot_colData_on_embedding, 9
plot_feature_on_embedding, 10
plot_gene_coverage_by_var, 11
plot_marker_features, 12
plot_transcript_composition, 13
plot_violin, 13
plotly_settings, 7

small_example_dataset, 14

tiny_sce, 15