Package ‘chevreulPlot’

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Type Package

Title Plots used in the chevreulPlot package

Version 1.3.0

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`

Depends R (>= 4.5.0), SingleCellExperiment, chevreulProcess

Imports base, cluster, clustree, ComplexHeatmap (>= 2.5.4), circlize, dplyr, EnsDb.Hsapiens.v86, forcats, fs, ggplot2, grid, plotly, purrr, S4Vectors, scales, scater, scran, scuttle, stats, stringr, tibble, tidyr, utils, wiggleplotr (>= 1.13.1), tidyselect, patchwork

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Contents

`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()

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