Package 'Giotto'

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Title Spatial Single-Cell Transcriptomics Toolbox

Version 2.0.0.9000

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Description Toolbox to process, analyze and visualize spatial single-cell expression data.

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Encoding UTF-8

LazyData true

URL https://rubd.github.io/Giotto/, https://github.com/RubD/Giotto

BugReports https://github.com/RubD/Giotto/issues

RoxygenNote 7.1.1

Depends base (>= 3.5.0),
utils (>= 3.5.0),
R (>= 3.5.0)

Imports ClusterR,
ComplexHeatmap (>= 1.20.0),
cowplot (>= 0.9.4),
data.table (>= 1.12.2),
dbscan (>= 1.1-3),
deldir,
dendextend (>= 1.13.0),
devtools,
farver (>= 2.0.3),
fitdistrplus,
ggalluvial (>= 0.9.1),
ggplot2 (>= 3.1.1),
ggdendro,
ggraph,
grDevices,
graphics,
igraph (>= 1.2.4.1),
irlba,
lfa (>= 1.12.0),
limma,
Matrix,
magick,
magrittr,

matrixStats (>= 0.55.0),
methods,
plotly,
parallel,
qvalue (>= 2.14.1),
RColorBrewer (>= 1.1-2),
Rcpp,
reshape2,
reticulate (>= 1.14),
Rfast,
Rtsne (>= 0.15),
rlang (>= 0.4.3),
R.utils,
scales (>= 1.0.0),
uwot (>= 0.0.0.9010)

Suggests Biobase,
biomaRt,
circlize,
FactoMineR,
factoextra,
geometry,
ggforce,
ggrepel,
htmlwidgets,
jackstraw,
knitr,
MAST,
multinet (>= 3.0.2),
png,
quadprog,
rmarkdown,
RTriangle (>= 1.6-0.10),
scran (>= 1.10.1),
SingleCellExperiment,
smfishHmrf,
SPARK,
tiff,
trendsceek

biocViews

VignetteBuilder knitr

R topics documented:

`addCellMetadata` *addCellMetadata*

Description

adds cell metadata to the giotto object

Usage

```
addCellMetadata(
  gobject,
  feat_type = NULL,
  new_metadata,
  vector_name = NULL,
  by_column = FALSE,
  column_cell_ID = NULL
)
```

Arguments

`gobject`	giotto object
`feat_type`	feature type
`new_metadata`	new cell metadata to use (data.table, data.frame, ...)
`vector_name`	(optional) custom name if you provide a single vector
`by_column`	merge metadata based on cell_ID column in pDataDT (default = FALSE)
`column_cell_ID`	column name of new metadata to use if by_column = TRUE

Details

You can add additional cell metadata in two manners:

- 1. Provide a data.table or data.frame with cell annotations in the same order as the cell_ID column in pDataDT(gobject)
- 2. Provide a data.table or data.frame with cell annotations and specificy which column contains the cell IDs, these cell IDs need to match with the cell_ID column in pDataDT(gobject)

Value

giotto object

addCellStatistics *addCellStatistics*

Description

adds cells statistics to the giotto object

Usage

```
addCellStatistics(
  gobject,
  feat_type = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  detection_threshold = 0,
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
feat_type	feature type
expression_values	expression values to use
detection_threshold	detection threshold to consider a gene detected
return_gobject	boolean: return giotto object (default = TRUE)

Details

This function will add the following statistics to cell metadata:

- nr_feats: Denotes in how many features are detected per cell
- perc_feats: Denotes what percentage of features is detected per cell
- total_expr: Shows the total sum of feature expression per cell

Value

giotto object if return_gobject = TRUE

Examples

```
data(mini_giotto_single_cell)

updated_giotto_object = addCellStatistics(mini_giotto_single_cell)
```

addGeneMetadata *addGeneMetadata*

Description

adds gene metadata to the giotto object

Usage

```
addGeneMetadata(gobject, new_metadata, by_column = F, column_gene_ID = NULL)
```

Arguments

gobject	giotto object
new_metadata	new metadata to use
by_column	merge metadata based on gene_ID column in fDataDT
column_gene_ID	column name of new metadata to use if by_column = TRUE

Details

You can add additional gene metadata in two manners: 1. Provide a data.table or data.frame with gene annotations in the same order as the gene_ID column in fDataDT(gobject) 2. Provide a data.table or data.frame with gene annotations and specificy which column contains the gene IDs, these gene IDs need to match with the gene_ID column in fDataDT(gobject)

Value

giotto object

addGenesPerc *addGenesPerc*

Description

calculates the total percentage of (normalized) counts for a subset of selected genes

Usage

```
addGenesPerc(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = NULL,
  vector_name = "gene_perc",
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
genes	vector of selected genes
vector_name	column name as seen in pDataDT()
return_gobject	boolean: return giotto object (default = TRUE)

Value

giotto object if return_gobject = TRUE, else a vector with

Examples

```
data(mini_giotto_single_cell)

# select genes (e.g. Rpl or mitochondrial)
random_genes = sample(slot(mini_giotto_single_cell, 'gene_ID'), 5)

# calculate percentage of those selected genes per cells/spot
updated_giotto_object = addGenesPerc(mini_giotto_single_cell,
                                      genes = random_genes,
                                      vector_name = 'random_gene_perc')

# visualize result in data.table format
pDataDT(updated_giotto_object)
```

---

addGiottoImage *addGiottoImage*

Description

Adds giotto image objects to your giotto object

Usage

```
addGiottoImage(gobject, images)
```

Arguments

gobject	giotto object
images	list of giotto image objects, see createGiottoImage

Value

an updated Giotto object with access to the list of images

addGiottoImageToSpatPlot *addGiottoImageToSpatPlot*

Description

Add a giotto image to a spatial ggplot object post creation

Usage

```
addGiottoImageToSpatPlot(spatpl = NULL, gimage = NULL)
```

Arguments

spatpl	a spatial ggplot object
gimage	a giotto image, see createGiottoImage

Value

an updated spatial ggplot object

addHMRF *addHMRF*

Description

Add selected results from doHMRF to the giotto object

Usage

```
addHMRF(gobject, HMRFoutput, k = NULL, betas_to_add = NULL, hmrf_name = NULL)
```

Arguments

gobject	giotto object
HMRFoutput	HMRF output from doHMRF()
k	number of domains
betas_to_add	results from different betas that you want to add
hmrf_name	specify a custom name

Value

giotto object

addNetworkLayout *addNetworkLayout*

Description

Add a network layout for a selected nearest neighbor network

Usage

```
addNetworkLayout(
  gobject,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  layout_type = c("drl"),
  options_list = NULL,
  layout_name = "layout",
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
nn_network_to_use	kNN or sNN
network_name	name of NN network to be used
layout_type	layout algorithm to use
options_list	list of options for selected layout
layout_name	name for layout
return_gobject	boolean: return giotto object (default = TRUE)

Details

This function creates layout coordinates based on the provided kNN or sNN. Currently only the force-directed graph layout "drl", see layout_with_drl, is implemented. This provides an alternative to tSNE or UMAP based visualizations.

Value

giotto object with updated layout for selected NN network

addStatistics *addStatistics*

Description

adds genes and cells statistics to the giotto object

Usage

```
addStatistics(
  gobject,
  feat_type = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  detection_threshold = 0,
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
feat_type	feature type
expression_values	expression values to use
detection_threshold	detection threshold to consider a feature detected
return_gobject	boolean: return giotto object (default = TRUE)

Details

See addFeatStatistics and addCellStatistics

Value

giotto object if return_gobject = TRUE, else a list with results

Examples

```
data(mini_giotto_single_cell)

updated_giotto_object = addStatistics(mini_giotto_single_cell)
```

anndataToGiotto *anndataToGiotto*

Description

Converts a spatial anndata (e.g. scanpy) .h5ad file into a Giotto object

Usage

```
anndataToGiotto(
  anndata_path,
  metadata_cols = c("total_counts", "pct_counts_mt"),
  instructions = NULL,
  ...
)
```

Arguments

anndata_path	path to the .h5ad file
metadata_cols	metadata columns to include
instructions	giotto instructions
...	additional parameters to createGiottoObject

Details

Function in beta. Converts a .h5ad file into a Giotto object.

Value

Giotto object

annotateGiotto *annotateGiotto*

Description

Converts cluster results into a user provided annotation.

Usage

```
annotateGiotto(
  gobject,
  feat_type = NULL,
  annotation_vector = NULL,
  cluster_column = NULL,
  name = "cell_types"
)
```

Arguments

gobject	giotto object
feat_type	feature type
annotation_vector	named annotation vector (names = cluster ids)
cluster_column	cluster column to convert to annotation names
name	new name for annotation column

Details

You need to specifify which (cluster) column you want to annotate and you need to provide an annotation vector like this:

- 1. identify the cell type of each cluster
- 2. create a vector of these cell types, e.g. cell_types = c('T-cell', 'B-cell', 'Stromal')
- 3. provide original cluster names to previous vector, e.g. names(cell_types) = c(2, 1, 3)

Value

giotto object

Examples

```
data(mini_giotto_single_cell)

# show leiden clustering results
cell_metadata = pDataDT(mini_giotto_single_cell)
cell_metadata[['leiden_clus']]

# create vector with cell type names as names of the vector
clusters_cell_types = c('cell_type_1', 'cell_type_2', 'cell_type_3')
names(clusters_cell_types) = 1:3

# convert cluster results into annotations and add to cell metadata
mini_giotto_single_cell = annotateGiotto(gobject = mini_giotto_single_cell,
                                         annotation_vector = clusters_cell_types,
                                    cluster_column = 'leiden_clus', name = 'cell_types2')

# visualize annotation results
spatDimPlot(gobject = mini_giotto_single_cell,
            cell_color = 'cell_types2',
            spat_point_size = 3, dim_point_size = 3)
```

annotateSpatialGrid *annotateSpatialGrid*

Description

annotate spatial grid with cell ID and cell metadata (optional)

Usage

```
annotateSpatialGrid(
  gobject,
  spatial_grid_name = "spatial_grid",
  cluster_columns = NULL
)
```

Arguments

gobject	Giotto object
spatial_grid_name	name of spatial grid, see showGrids
cluster_columns	names of cell metadata, see pDataDT

Value

annotated spatial grid data.table

annotateSpatialNetwork *annotateSpatialNetwork*

Description

Annotate spatial network with cell metadata information.

Usage

```
annotateSpatialNetwork(
  gobject,
  feat_type = NULL,
  spatial_network_name = "Delaunay_network",
  cluster_column,
  create_full_network = FALSE
)
```

Arguments

gobject	giotto object
feat_type	feature type
spatial_network_name	name of spatial network to use
cluster_column	name of column to use for clusters
create_full_network	convert from reduced to full network representation

Value

annotated network in data.table format

---

binSpect *binSpect*

Description

Previously: binGetSpatialGenes. BinSpect (Binary Spatial Extraction of genes) is a fast computational method that identifies genes with a spatially coherent expression pattern.

Usage

```
binSpect(
  gobject,
  feat_type = NULL,
  bin_method = c("kmeans", "rank"),
  expression_values = c("normalized", "scaled", "custom"),
  subset_feats = NULL,
  subset_genes = NULL,
  spatial_network_name = "Delaunay_network",
  spatial_network_k = NULL,
  reduce_network = FALSE,
  kmeans_algo = c("kmeans", "kmeans_arma", "kmeans_arma_subset"),
  nstart = 3,
  iter_max = 10,
  extreme_nr = 50,
  sample_nr = 50,
  percentage_rank = 30,
  do_fisher_test = TRUE,
  adjust_method = "fdr",
  calc_hub = FALSE,
  hub_min_int = 3,
  get_av_expr = TRUE,
  get_high_expr = TRUE,
  implementation = c("data.table", "simple", "matrix"),
  group_size = "automatic",
  do_parallel = TRUE,
  cores = NA,
  verbose = T,
```

```
  knn_params = NULL,
  set.seed = NULL,
  bin_matrix = NULL,
  summarize = c("p.value", "adj.p.value")
)
```

Arguments

gobject	giotto object
feat_type	feature type
bin_method	method to binarize gene expression
expression_values	expression values to use
subset_feats	only select a subset of features to test
subset_genes	deprecated, use subset_feats
spatial_network_name	name of spatial network to use (default = 'spatial_network')
spatial_network_k	different k's for a spatial kNN to evaluate
reduce_network	default uses the full network
kmeans_algo	kmeans algorithm to use (kmeans, kmeans_arma, kmeans_arma_subset)
nstart	kmeans: nstart parameter
iter_max	kmeans: iter.max parameter
extreme_nr	number of top and bottom cells (see details)
sample_nr	total number of cells to sample (see details)
percentage_rank	percentage of top cells for binarization
do_fisher_test	perform fisher test
adjust_method	p-value adjusted method to use (see p.adjust)
calc_hub	calculate the number of hub cells
hub_min_int	minimum number of cell-cell interactions for a hub cell
get_av_expr	calculate the average expression per gene of the high expressing cells
get_high_expr	calculate the number of high expressing cells per gene
implementation	enrichment implementation (data.table, simple, matrix)
group_size	number of genes to process together with data.table implementation (default = automatic)
do_parallel	run calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
verbose	be verbose
knn_params	list of parameters to create spatial kNN network
set.seed	set a seed before kmeans binarization
bin_matrix	a binarized matrix, when provided it will skip the binarization process
summarize	summarize the p-values or adjusted p-values

Details

We provide two ways to identify spatial genes based on gene expression binarization. Both methods are identicial except for how binarization is performed.

- 1. binarize: Each gene is binarized (0 or 1) in each cell with **kmeans** (k = 2) or based on **rank** percentile
- 2. network: Alll cells are connected through a spatial network based on the physical coordinates
- 3. contingency table: A contingency table is calculated based on all edges of neighboring cells and the binarized expression (0-0, 0-1, 1-0 or 1-1)
- 4. For each gene an odds-ratio (OR) and fisher.test (optional) is calculated

Three different kmeans algorithmes have been implemented:

- 1. kmeans: default, see `kmeans`
- 2. kmeans_arma: from ClusterR, see `KMeans_arma`
- 3. kmeans_arma_subst: from ClusterR, see `KMeans_arma`, but random subsetting the vector for each gene to increase speed. Change extreme_nr and sample_nr for control.

Other statistics are provided (optional):

- Number of cells with high expression (binary = 1)
- Average expression of each gene within high expressing cells
- Number of hub cells, these are high expressing cells that have a user defined number of high expressing neighbors

By selecting a subset of likely spatial genes (e.g. soft thresholding highly variable genes) can accelerate the speed. The simple implementation is usually faster, but lacks the possibility to run in parallel and to calculate hub cells. The data.table implementation might be more appropriate for large datasets by setting the group_size (number of genes) parameter to divide the workload.

Value

data.table with results (see details)

`binSpectMulti` *binSpectMulti*

Description

binSpect for multiple spatial kNN networks

Usage

```
binSpectMulti(
  gobject,
  feat_type = NULL,
  bin_method = c("kmeans", "rank"),
  expression_values = c("normalized", "scaled", "custom"),
  subset_feats = NULL,
  spatial_network_k = c(5, 10, 20),
```

```
  reduce_network = FALSE,
  kmeans_algo = c("kmeans", "kmeans_arma", "kmeans_arma_subset"),
  nstart = 3,
  iter_max = 10,
  extreme_nr = 50,
  sample_nr = 50,
  percentage_rank = c(10, 30),
  do_fisher_test = TRUE,
  adjust_method = "fdr",
  calc_hub = FALSE,
  hub_min_int = 3,
  get_av_expr = TRUE,
  get_high_expr = TRUE,
  implementation = c("data.table", "simple", "matrix"),
  group_size = "automatic",
  do_parallel = TRUE,
  cores = NA,
  verbose = T,
  knn_params = NULL,
  set.seed = NULL,
  summarize = c("adj.p.value", "p.value")
)
```

Arguments

gobject	giotto object
feat_type	feature type
bin_method	method to binarize gene expression
expression_values	expression values to use
subset_feats	only select a subset of features to test
spatial_network_k	different k's for a spatial kNN to evaluate
reduce_network	default uses the full network
kmeans_algo	kmeans algorithm to use (kmeans, kmeans_arma, kmeans_arma_subset)
nstart	kmeans: nstart parameter
iter_max	kmeans: iter.max parameter
extreme_nr	number of top and bottom cells (see details)
sample_nr	total number of cells to sample (see details)
percentage_rank	percentage of top cells for binarization
do_fisher_test	perform fisher test
adjust_method	p-value adjusted method to use (see p.adjust)
calc_hub	calculate the number of hub cells
hub_min_int	minimum number of cell-cell interactions for a hub cell
get_av_expr	calculate the average expression per gene of the high expressing cells
get_high_expr	calculate the number of high expressing cells per gene

implementation	enrichment implementation (data.table, simple, matrix)
group_size	number of genes to process together with data.table implementation (default = automatic)
do_parallel	run calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
verbose	be verbose
knn_params	list of parameters to create spatial kNN network
set.seed	set a seed before kmeans binarization
summarize	summarize the p-values or adjusted p-values
subset_genes	deprecated, use subset_feats

Details

We provide two ways to identify spatial genes based on gene expression binarization. Both methods are identicial except for how binarization is performed.

- 1. binarize: Each gene is binarized (0 or 1) in each cell with **kmeans** (k = 2) or based on **rank** percentile
- 2. network: Alll cells are connected through a spatial network based on the physical coordinates
- 3. contingency table: A contingency table is calculated based on all edges of neighboring cells and the binarized expression (0-0, 0-1, 1-0 or 1-1)
- 4. For each gene an odds-ratio (OR) and fisher.test (optional) is calculated

Three different kmeans algorithmes have been implemented:

- 1. kmeans: default, see `kmeans`
- 2. kmeans_arma: from ClusterR, see `KMeans_arma`
- 3. kmeans_arma_subst: from ClusterR, see `KMeans_arma`, but random subsetting the vector for each gene to increase speed. Change extreme_nr and sample_nr for control.

Other statistics are provided (optional):

- Number of cells with high expression (binary = 1)
- Average expression of each gene within high expressing cells
- Number of hub cells, these are high expressing cells that have a user defined number of high expressing neighbors

By selecting a subset of likely spatial genes (e.g. soft thresholding highly variable genes) can accelerate the speed. The simple implementation is usually faster, but lacks the possibility to run in parallel and to calculate hub cells. The data.table implementation might be more appropriate for large datasets by setting the group_size (number of genes) parameter to divide the workload.

Value

data.table with results (see details)

binSpectSingle *binSpectSingle*

Description

binSpect for a single spatial network

Usage

```
binSpectSingle(
  gobject,
  feat_type = NULL,
  bin_method = c("kmeans", "rank"),
  expression_values = c("normalized", "scaled", "custom"),
  subset_feats = NULL,
  subset_genes = NULL,
  spatial_network_name = "Delaunay_network",
  reduce_network = FALSE,
  kmeans_algo = c("kmeans", "kmeans_arma", "kmeans_arma_subset"),
  nstart = 3,
  iter_max = 10,
  extreme_nr = 50,
  sample_nr = 50,
  percentage_rank = 30,
  do_fisher_test = TRUE,
  adjust_method = "fdr",
  calc_hub = FALSE,
  hub_min_int = 3,
  get_av_expr = TRUE,
  get_high_expr = TRUE,
  implementation = c("data.table", "simple", "matrix"),
  group_size = "automatic",
  do_parallel = TRUE,
  cores = NA,
  verbose = T,
  set.seed = NULL,
  bin_matrix = NULL
)
```

Arguments

gobject	giotto object
feat_type	feature type
bin_method	method to binarize gene expression
expression_values	expression values to use
subset_feats	only select a subset of features to test
subset_genes	deprecated, use subset_feats
spatial_network_name	name of spatial network to use (default = 'spatial_network')

reduce_network	default uses the full network
kmeans_algo	kmeans algorithm to use (kmeans, kmeans_arma, kmeans_arma_subset)
nstart	kmeans: nstart parameter
iter_max	kmeans: iter.max parameter
extreme_nr	number of top and bottom cells (see details)
sample_nr	total number of cells to sample (see details)
percentage_rank	percentage of top cells for binarization
do_fisher_test	perform fisher test
adjust_method	p-value adjusted method to use (see p.adjust)
calc_hub	calculate the number of hub cells
hub_min_int	minimum number of cell-cell interactions for a hub cell
get_av_expr	calculate the average expression per gene of the high expressing cells
get_high_expr	calculate the number of high expressing cells per gene
implementation	enrichment implementation (data.table, simple, matrix)
group_size	number of genes to process together with data.table implementation (default = automatic)
do_parallel	run calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
verbose	be verbose
set.seed	set a seed before kmeans binarization
bin_matrix	a binarized matrix, when provided it will skip the binarization process

Details

We provide two ways to identify spatial genes based on gene expression binarization. Both methods are identicial except for how binarization is performed.

- 1. binarize: Each gene is binarized (0 or 1) in each cell with **kmeans** (k = 2) or based on **rank** percentile
- 2. network: Alll cells are connected through a spatial network based on the physical coordinates
- 3. contingency table: A contingency table is calculated based on all edges of neighboring cells and the binarized expression (0-0, 0-1, 1-0 or 1-1)
- 4. For each gene an odds-ratio (OR) and fisher.test (optional) is calculated

Three different kmeans algorithmes have been implemented:

- 1. kmeans: default, see kmeans
- 2. kmeans_arma: from ClusterR, see KMeans_arma
- 3. kmeans_arma_subst: from ClusterR, see KMeans_arma, but random subsetting the vector for each gene to increase speed. Change extreme_nr and sample_nr for control.

Other statistics are provided (optional):

- Number of cells with high expression (binary = 1)
- Average expression of each gene within high expressing cells

- Number of hub cells, these are high expressing cells that have a user defined number of high expressing neighbors

By selecting a subset of likely spatial genes (e.g. soft thresholding highly variable genes) can accelerate the speed. The simple implementation is usually faster, but lacks the possibility to run in parallel and to calculate hub cells. The data.table implementation might be more appropriate for large datasets by setting the group_size (number of genes) parameter to divide the workload.

Value

data.table with results (see details)

`calculateHVF` *calculateHVF*

Description

compute highly variable features

Usage

```
calculateHVF(
  gobject,
  feat_type = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  method = c("cov_groups", "cov_loess"),
  reverse_log_scale = FALSE,
  logbase = 2,
  expression_threshold = 0,
  nr_expression_groups = 20,
  zscore_threshold = 1.5,
  HVFname = "hvg",
  difference_in_cov = 0.1,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "HVFplot",
  return_gobject = TRUE
)
```

Arguments

`gobject`	giotto object
`feat_type`	feature type
`expression_values`	expression values to use
`method`	method to calculate highly variable features
`reverse_log_scale`	reverse log-scale of expression values (default = FALSE)
`logbase`	if reverse_log_scale is TRUE, which log base was used?

`expression_threshold`
: expression threshold to consider a gene detected

`nr_expression_groups`
: number of expression groups for cov_groups

`zscore_threshold`
: zscore to select hvg for cov_groups

`HVFname`
: name for highly variable features in cell metadata

`difference_in_cov`
: minimum difference in coefficient of variance required

`show_plot`
: show plot

`return_plot`
: return ggplot object

`save_plot`
: directly save the plot [boolean]

`save_param`
: list of saving parameters from `all_plots_save_function`

`default_save_name`
: default save name for saving, don't change, change save_name in save_param

`return_gobject`
: boolean: return giotto object (default = TRUE)

Details

Currently we provide 2 ways to calculate highly variable genes:

1. high coeff of variance (COV) within groups:
First genes are binned (*nr_expression_groups*) into average expression groups and the COV for each feature is converted into a z-score within each bin. Features with a z-score higher than the threshold (*zscore_threshold*) are considered highly variable.

2. high COV based on loess regression prediction:
A predicted COV is calculated for each feature using loess regression (COV~log(mean expression)) Features that show a higher than predicted COV (*difference_in_cov*) are considered highly variable.

Value

giotto object highly variable features appended to feature metadata (fDataDT)

Examples

```
data(mini_giotto_single_cell) # loads existing Giotto object

# update a giotto object
mini_giotto_single_cell <- calculateHVF(gobject = mini_giotto_single_cell,
                                        zscore_threshold = 0.1,
                                        nr_expression_groups = 3)

# return a data.table with the high variable genes annotated
hvg_dt <- calculateHVF(gobject = mini_giotto_single_cell,
                       zscore_threshold = 0.1, nr_expression_groups = 3,
                       return_plot = FALSE, return_gobject = FALSE)

# return the ggplot object
hvg_plot <- calculateHVF(gobject = mini_giotto_single_cell,
                       zscore_threshold = 0.1, nr_expression_groups = 3,
                       return_plot = TRUE, return_gobject = FALSE)
```

calculateHVG *calculateHVG*

Description

compute highly variable genes

Usage

```
calculateHVG(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  method = c("cov_groups", "cov_loess"),
  reverse_log_scale = FALSE,
  logbase = 2,
  expression_threshold = 0,
  nr_expression_groups = 20,
  zscore_threshold = 1.5,
  HVGname = "hvg",
  difference_in_cov = 0.1,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "HVGplot",
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
method	method to calculate highly variable genes
reverse_log_scale	reverse log-scale of expression values (default = FALSE)
logbase	if reverse_log_scale is TRUE, which log base was used?
expression_threshold	expression threshold to consider a gene detected
nr_expression_groups	number of expression groups for cov_groups
zscore_threshold	zscore to select hvg for cov_groups
HVGname	name for highly variable genes in cell metadata
difference_in_cov	minimum difference in coefficient of variance required
show_plot	show plot
return_plot	return ggplot object

save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param
return_gobject	boolean: return giotto object (default = TRUE)

Details

Currently we provide 2 ways to calculate highly variable genes:

1. high coeff of variance (COV) within groups:
First genes are binned (*nr_expression_groups*) into average expression groups and the COV for each gene is converted into a z-score within each bin. Genes with a z-score higher than the threshold (*zscore_threshold*) are considered highly variable.

2. high COV based on loess regression prediction:
A predicted COV is calculated for each gene using loess regression (COV~log(mean expression)) Genes that show a higher than predicted COV (*difference_in_cov*) are considered highly variable.

Value

giotto object highly variable genes appended to gene metadata (fDataDT)

Examples

```
data(mini_giotto_single_cell) # loads existing Giotto object

# update a giotto object
mini_giotto_single_cell <- calculateHVG(gobject = mini_giotto_single_cell,
                                        zscore_threshold = 0.1,
                                        nr_expression_groups = 3)

# return a data.table with the high variable genes annotated
hvg_dt <- calculateHVG(gobject = mini_giotto_single_cell,
                       zscore_threshold = 0.1, nr_expression_groups = 3,
                       return_plot = FALSE, return_gobject = FALSE)

# return the ggplot object
hvg_plot <- calculateHVG(gobject = mini_giotto_single_cell,
                       zscore_threshold = 0.1, nr_expression_groups = 3,
                       return_plot = TRUE, return_gobject = FALSE)
```

---

calculateMetaTable *calculateMetaTable*

Description

calculates the average gene expression for one or more (combined) annotation columns.

Usage

```
calculateMetaTable(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  metadata_cols = NULL,
  selected_genes = NULL
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
metadata_cols	annotation columns found in pDataDT(gobject)
selected_genes	subset of genes to use

Value

data.table with average expression values for each gene per (combined) annotation

Examples

```
data(mini_giotto_single_cell)

# show cell metadata
pDataDT(mini_giotto_single_cell)

# show average gene expression per annotated cell type
calculateMetaTable(mini_giotto_single_cell,
                   metadata_cols = 'cell_types')
```

---

calculateMetaTableCells

calculateMetaTableCells

Description

calculates the average metadata values for one or more (combined) annotation columns.

Usage

```
calculateMetaTableCells(
  gobject,
  value_cols = NULL,
  metadata_cols = NULL,
  spat_enr_names = NULL
)
```

Arguments

gobject	giotto object
value_cols	metadata or enrichment value columns to use
metadata_cols	annotation columns found in pDataDT(gobject)
spat_enr_names	which spatial enrichment results to include

Value

data.table with average metadata values per (combined) annotation

---

cellProximityBarplot *cellProximityBarplot*

Description

Create barplot from cell-cell proximity scores

Usage

```
cellProximityBarplot(
  gobject,
  CPscore,
  min_orig_ints = 5,
  min_sim_ints = 5,
  p_val = 0.05,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "cellProximityBarplot"
)
```

Arguments

gobject	giotto object
CPscore	CPscore, output from cellProximityEnrichment()
min_orig_ints	filter on minimum original cell-cell interactions
min_sim_ints	filter on minimum simulated cell-cell interactions
p_val	p-value
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

This function creates a barplot that shows the spatial proximity enrichment or depletion of cell type pairs.

Value

ggplot barplot

`cellProximityEnrichment` *cellProximityEnrichment*

Description

Compute cell-cell interaction enrichment (observed vs expected)

Usage

```
cellProximityEnrichment(
  gobject,
  feat_type = NULL,
  spatial_network_name = "Delaunay_network",
  cluster_column,
  number_of_simulations = 1000,
 adjust_method = c("none", "fdr", "bonferroni", "BH", "holm", "hochberg", "hommel",
    "BY"),
  set_seed = TRUE,
  seed_number = 1234
)
```

Arguments

`gobject`	giotto object
`feat_type`	feature type
`spatial_network_name`	name of spatial network to use
`cluster_column`	name of column to use for clusters
`number_of_simulations`	number of simulations to create expected observations
`adjust_method`	method to adjust p.values
`set_seed`	use of seed
`seed_number`	seed number to use

Details

Spatial proximity enrichment or depletion between pairs of cell types is calculated by calculating the observed over the expected frequency of cell-cell proximity interactions. The expected frequency is the average frequency calculated from a number of spatial network simulations. Each individual simulation is obtained by reshuffling the cell type labels of each node (cell) in the spatial network.

Value

List of cell Proximity scores (CPscores) in data.table format. The first data.table (raw_sim_table) shows the raw observations of both the original and simulated networks. The second data.table (enrichm_res) shows the enrichment results.

`cellProximityHeatmap` *cellProximityHeatmap*

Description

Create heatmap from cell-cell proximity scores

Usage

```
cellProximityHeatmap(
  gobject,
  CPscore,
  scale = T,
  order_cell_types = T,
  color_breaks = NULL,
  color_names = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "cellProximityHeatmap"
)
```

Arguments

`gobject`	giotto object
`CPscore`	CPscore, output from cellProximityEnrichment()
`scale`	scale cell-cell proximity interaction scores
`order_cell_types`	order cell types based on enrichment correlation
`color_breaks`	numerical vector of length 3 to represent min, mean and maximum
`color_names`	character color vector of length 3
`show_plot`	show plot
`return_plot`	return ggplot object
`save_plot`	directly save the plot [boolean]
`save_param`	list of saving parameters from `all_plots_save_function`
`default_save_name`	default save name for saving, don't change, change save_name in save_param

Details

This function creates a heatmap that shows the spatial proximity enrichment or depletion of cell type pairs.

Value

ggplot heatmap

`cellProximityNetwork` *cellProximityNetwork*

Description

Create network from cell-cell proximity scores

Usage

```
cellProximityNetwork(
  gobject,
  CPscore,
  remove_self_edges = FALSE,
  self_loop_strength = 0.1,
  color_depletion = "lightgreen",
  color_enrichment = "red",
  rescale_edge_weights = TRUE,
  edge_weight_range_depletion = c(0.1, 1),
  edge_weight_range_enrichment = c(1, 5),
  layout = c("Fruchterman", "DrL", "Kamada-Kawai"),
  only_show_enrichment_edges = F,
  edge_width_range = c(0.1, 2),
  node_size = 4,
  node_text_size = 6,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "cellProximityNetwork"
)
```

Arguments

`gobject`	giotto object
`CPscore`	CPscore, output from cellProximityEnrichment()
`remove_self_edges`	remove enrichment/depletion edges with itself
`self_loop_strength`	size of self-loops
`color_depletion`	color for depleted cell-cell interactions
`color_enrichment`	color for enriched cell-cell interactions
`rescale_edge_weights`	rescale edge weights (boolean)
`edge_weight_range_depletion`	numerical vector of length 2 to rescale depleted edge weights

edge_weight_range_enrichment
: numerical vector of length 2 to rescale enriched edge weights

layout
: layout algorithm to use to draw nodes and edges

only_show_enrichment_edges
: show only the enriched pairwise scores

edge_width_range
: range of edge width

node_size
: size of nodes

node_text_size
: size of node labels

show_plot
: show plot

return_plot
: return ggplot object

save_plot
: directly save the plot [boolean]

save_param
: list of saving parameters from all_plots_save_function

default_save_name
: default save name for saving, don't change, change save_name in save_param

Details

This function creates a network that shows the spatial proximity enrichment or depletion of cell type pairs.

Value

igraph plot

---

cellProximitySpatPlot *cellProximitySpatPlot*

Description

Visualize 2D cell-cell interactions according to spatial coordinates in ggplot mode

Usage

```
cellProximitySpatPlot(gobject, ...)
```

Arguments

gobject
: giotto object

...
: Arguments passed on to cellProximitySpatPlot2D

  feat_type feature type

  interaction_name cell-cell interaction name

  cluster_column cluster column with cell clusters

  sdimx x-axis dimension name (default = 'sdimx')

  sdimy y-axis dimension name (default = 'sdimy')

  cell_color color for cells (see details)

  cell_color_code named vector with colors

color_as_factor convert color column to factor
show_other_cells decide if show cells not in network
show_network show spatial network of selected cells
show_other_network show spatial network of not selected cells
network_color color of spatial network
spatial_network_name name of spatial network to use
show_grid show spatial grid
grid_color color of spatial grid
spatial_grid_name name of spatial grid to use
coord_fix_ratio fix ratio between x and y-axis
show_legend show legend
point_size_select size of selected points
point_select_border_col border color of selected points
point_select_border_stroke stroke size of selected points
point_size_other size of other points
point_alpha_other opacity of other points
point_other_border_col border color of other points
point_other_border_stroke stroke size of other points
show_plot show plots
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters from all_plots_save_function
default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

cellProximitySpatPlot2D and cellProximitySpatPlot3D for 3D

---

cellProximitySpatPlot3D *cellProximitySpatPlot2D*

Description

Visualize 3D cell-cell interactions according to spatial coordinates in plotly mode

Usage

```
cellProximitySpatPlot3D(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = "sdimx",
  sdimy = "sdimy",
  sdimz = "sdimz",
  cell_color = NULL,
  cell_color_code = NULL,
  color_as_factor = T,
  show_other_cells = T,
  show_network = T,
  show_other_network = F,
  network_color = NULL,
  spatial_network_name = "Delaunay_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  show_legend = T,
  point_size_select = 4,
  point_size_other = 2,
  point_alpha_other = 0.5,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "cellProximitySpatPlot3D",
  ...
)
```

Arguments

gobject	giotto object
interaction_name	cell-cell interaction name
cluster_column	cluster column with cell clusters
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimz')
cell_color	color for cells (see details)
cell_color_code	named vector with colors
color_as_factor	convert color column to factor

show_other_cells
: decide if show cells not in network

show_network
: show spatial network of selected cells

show_other_network
: show spatial network of not selected cells

network_color
: color of spatial network

spatial_network_name
: name of spatial network to use

show_grid
: show spatial grid

grid_color
: color of spatial grid

spatial_grid_name
: name of spatial grid to use

show_legend
: show legend

point_size_select
: size of selected points

point_size_other
: size of other points

point_alpha_other
: opacity of other points

axis_scale
: scale of axis

custom_ratio
: custom ratio of axes

x_ticks
: ticks on x-axis

y_ticks
: ticks on y-axis

z_ticks
: ticks on z-axis

show_plot
: show plots

return_plot
: return plotly object

save_plot
: directly save the plot [boolean]

save_param
: list of saving parameters from all_plots_save_function

default_save_name
: default save name for saving, don't change, change save_name in save_param

...
: additional parameters

Details

Description of parameters.

Value

plotly

`cellProximityVisPlot` *cellProximityVisPlot*

Description

Visualize cell-cell interactions according to spatial coordinates

Usage

```
cellProximityVisPlot(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  cell_color = NULL,
  cell_color_code = NULL,
  color_as_factor = T,
  show_other_cells = F,
  show_network = F,
  show_other_network = F,
  network_color = NULL,
  spatial_network_name = "Delaunay_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  coord_fix_ratio = 1,
  show_legend = T,
  point_size_select = 2,
  point_select_border_col = "black",
  point_select_border_stroke = 0.05,
  point_size_other = 1,
  point_alpha_other = 0.3,
  point_other_border_col = "lightgrey",
  point_other_border_stroke = 0.01,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  plot_method = c("ggplot", "plotly"),
  ...
)
```

Arguments

`gobject`	giotto object
`interaction_name`	cell-cell interaction name
`cluster_column`	cluster column with cell clusters

sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimz')
cell_color	color for cells (see details)
cell_color_code	named vector with colors
color_as_factor	convert color column to factor
show_other_cells	show not selected cells
show_network	show underlying spatial network
show_other_network	show underlying spatial network of other cells
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
coord_fix_ratio	fix ratio between x and y-axis
show_legend	show legend
point_size_select	size of selected points
point_select_border_col	border color of selected points
point_select_border_stroke	stroke size of selected points
point_size_other	size of other points
point_alpha_other	alpha of other points
point_other_border_col	border color of other points
point_other_border_stroke	stroke size of other points
axis_scale	scale of axis
custom_ratio	custom ratio of scales
x_ticks	x ticks
y_ticks	y ticks
z_ticks	z ticks
plot_method	method to plot
...	additional parameters

Details

Description of parameters.

Value

ggplot or plotly

`changeGiottoInstructions` *changeGiottoInstructions*

Description

Function to change one or more instructions from giotto object

Usage

```
changeGiottoInstructions(
  gobject,
  params = NULL,
  new_values = NULL,
  return_gobject = TRUE
)
```

Arguments

`gobject`	giotto object
`params`	parameter(s) to change
`new_values`	new value(s) for parameter(s)
`return_gobject`	(boolean) return giotto object

Value

giotto object with one or more changed instructions

`changeImageBg` *changeImageBg*

Description

Function to change the background color of a magick image plot to another color

Usage

```
changeImageBg(
  mg_object,
  bg_color,
  perc_range = 10,
  new_color = "#FFFFFF",
  new_name = NULL
)
```

Arguments

mg_object	magick image or giotto image object
bg_color	estimated current background color
perc_range	range around estimated background color to include (percentage)
new_color	new background color
new_name	change name of Giotto image

Value

magick image or giotto image object with updated background color

---

checkGiottoEnvironment *checkGiottoEnvironment*

Description

checkGiottoEnvironment

Usage

```
checkGiottoEnvironment(verbose = TRUE)
```

Arguments

verbose	be verbose

Details

Checks if a miniconda giotto environment can be found. Can be installed with installGiottoEnvironment.

---

clusterCells *clusterCells*

Description

cluster cells using a variety of different methods

Usage

```
clusterCells(
  gobject,
  cluster_method = c("leiden", "louvain_community", "louvain_multinet", "randomwalk",
    "sNNclust", "kmeans", "hierarchical"),
  name = "cluster_name",
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  pyth_leid_resolution = 1,
  pyth_leid_weight_col = "weight",
  pyth_leid_part_type = c("RBConfigurationVertexPartition",
    "ModularityVertexPartition"),
  pyth_leid_init_memb = NULL,
  pyth_leid_iterations = 1000,
  pyth_louv_resolution = 1,
  pyth_louv_weight_col = NULL,
  python_louv_random = F,
  python_path = NULL,
  louvain_gamma = 1,
  louvain_omega = 1,
  walk_steps = 4,
  walk_clusters = 10,
  walk_weights = NA,
  sNNclust_k = 20,
  sNNclust_eps = 4,
  sNNclust_minPts = 16,
  borderPoints = TRUE,
  expression_values = c("normalized", "scaled", "custom"),
  genes_to_use = NULL,
  dim_reduction_to_use = c("cells", "pca", "umap", "tsne"),
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  distance_method = c("original", "pearson", "spearman", "euclidean", "maximum",
    "manhattan", "canberra", "binary", "minkowski"),
  km_centers = 10,
  km_iter_max = 100,
  km_nstart = 1000,
  km_algorithm = "Hartigan-Wong",
  hc_agglomeration_method = c("ward.D2", "ward.D", "single", "complete", "average",
    "mcquitty", "median", "centroid"),
  hc_k = 10,
  hc_h = NULL,
  return_gobject = TRUE,
  set_seed = T,
  seed_number = 1234
)
```

Arguments

gobject	giotto object
cluster_method	community cluster method to use
name	name for new clustering result

nn_network_to_use
: type of NN network to use (kNN vs sNN)

network_name
: name of NN network to use

pyth_leid_resolution
: resolution for leiden

pyth_leid_weight_col
: column to use for weights

pyth_leid_part_type
: partition type to use

pyth_leid_init_memb
: initial membership

pyth_leid_iterations
: number of iterations

pyth_louv_resolution
: resolution for louvain

pyth_louv_weight_col
: python louvain param: weight column

python_louv_random
: python louvain param: random

python_path
: specify specific path to python if required

louvain_gamma
: louvain param: gamma or resolution

louvain_omega
: louvain param: omega

walk_steps
: randomwalk: number of steps

walk_clusters
: randomwalk: number of clusters

walk_weights
: randomwalk: weight column

sNNclust_k
: SNNclust: k neighbors to use

sNNclust_eps
: SNNclust: epsilon

sNNclust_minPts
: SNNclust: min points

borderPoints
: SNNclust: border points

expression_values
: expression values to use

genes_to_use
: = NULL,

dim_reduction_to_use
: dimension reduction to use

dim_reduction_name
: name of reduction 'pca',

dimensions_to_use
: dimensions to use

distance_method
: distance method

km_centers
: kmeans centers

km_iter_max
: kmeans iterations

km_nstart
: kmeans random starting points

km_algorithm
: kmeans algorithm

hc_agglomeration_method	hierarchical clustering method
hc_k	hierachical number of clusters
hc_h	hierarchical tree cutoff
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

Details

Wrapper for the different clustering methods.

Value

giotto object with new clusters appended to cell metadata

See Also

doLeidenCluster, doLouvainCluster_community, doLouvainCluster_multinet, doLouvainCluster, doRandomWalkCluster, doSNNCluster, doKmeans, doHclust

---

clusterSpatialCorFeats

clusterSpatialCorFeats

Description

Cluster based on spatially correlated features

Usage

```
clusterSpatialCorFeats(
  spatCorObject,
  name = "spat_clus",
  hclust_method = "ward.D",
  k = 10,
  return_obj = TRUE
)
```

Arguments

spatCorObject	spatial correlation object
name	name for spatial clustering results
hclust_method	method for hierarchical clustering
k	number of clusters to extract
return_obj	return spatial correlation object (spatCorObject)

Value

spatCorObject or cluster results

clusterSpatialCorGenes *clusterSpatialCorGenes*

Description

Cluster based on spatially correlated genes

Usage

```
clusterSpatialCorGenes(
  spatCorObject,
  name = "spat_clus",
  hclust_method = "ward.D",
  k = 10,
  return_obj = TRUE
)
```

Arguments

spatCorObject	spatial correlation object
name	name for spatial clustering results
hclust_method	method for hierarchical clustering
k	number of clusters to extract
return_obj	return spatial correlation object (spatCorObject)

Value

spatCorObject or cluster results

colMeans_giotto *colMeans_giotto*

Description

colMeans function that works with multiple matrix representations

Usage

```
colMeans_giotto(mymatrix)
```

Arguments

mymatrix	matrix object

Value

numeric vector

colSums_giotto *colSums_giotto*

Description

colSums function that works with multiple matrix representations

Usage

```
colSums_giotto(mymatrix)
```

Arguments

mymatrix	matrix object

Value

numeric vector

combCCcom *combCCcom*

Description

Combine spatial and expression based cell-cell communication data.tables

Usage

```
combCCcom(
  spatialCC,
  exprCC,
  min_lig_nr = 3,
  min_rec_nr = 3,
  min_padj_value = 1,
  min_log2fc = 0,
  min_av_diff = 0,
  detailed = FALSE
)
```

Arguments

spatialCC	spatial cell-cell communication scores
exprCC	expression cell-cell communication scores
min_lig_nr	minimum number of ligand cells
min_rec_nr	minimum number of receptor cells
min_padj_value	minimum adjusted p-value
min_log2fc	minimum log2 fold-change
min_av_diff	minimum average expression difference
detailed	detailed option used with spatCellCellcom (default = FALSE)

Value

combined data.table with spatial and expression communication data

---

`combineCellProximityGenes` *combineCellProximityGenes*

Description

Combine ICG scores in a pairwise manner.

Usage

```
combineCellProximityGenes(...)
```

Arguments

`...`	Arguments passed on to `combineInteractionChangedGenes`
	`cpgObject` ICG (interaction changed gene) score object
	`selected_ints` subset of selected cell-cell interactions (optional)
	`selected_genes` subset of selected genes (optional)
	`specific_genes_1` specific geneset combo (need to position match specific_genes_2)
	`specific_genes_2` specific geneset combo (need to position match specific_genes_1)
	`min_cells` minimum number of target cell type
	`min_int_cells` minimum number of interacting cell type
	`min_fdr` minimum adjusted p-value
	`min_spat_diff` minimum absolute spatial expression difference
	`min_log2_fc` minimum absolute log2 fold-change
	`do_parallel` run calculations in parallel with mclapply
	`cores` number of cores to use if do_parallel = TRUE
	`verbose` verbose

See Also

`combineInteractionChangedGenes`

combineCPG *combineCPG*

Description

Combine ICG scores in a pairwise manner.

Usage

```
combineCPG(...)
```

Arguments

...	Arguments passed on to combineICG
	cpgObject ICG (interaction changed gene) score object
	selected_ints subset of selected cell-cell interactions (optional)
	selected_genes subset of selected genes (optional)
	specific_genes_1 specific geneset combo (need to position match specific_genes_2)
	specific_genes_2 specific geneset combo (need to position match specific_genes_1)
	min_cells minimum number of target cell type
	min_int_cells minimum number of interacting cell type
	min_fdr minimum adjusted p-value
	min_spat_diff minimum absolute spatial expression difference
	min_log2_fc minimum absolute log2 fold-change
	do_parallel run calculations in parallel with mclapply
	cores number of cores to use if do_parallel = TRUE
	verbose verbose

See Also

combineICG

---

combineICG *combineICG*

Description

Combine ICG scores in a pairwise manner.

Usage

```
combineICG(
  cpgObject,
  selected_ints = NULL,
  selected_genes = NULL,
  specific_genes_1 = NULL,
  specific_genes_2 = NULL,
  min_cells = 5,
```

```
  min_int_cells = 3,
  min_fdr = 0.05,
  min_spat_diff = 0,
  min_log2_fc = 0.5,
  do_parallel = TRUE,
  cores = NA,
  verbose = T
)
```

Arguments

cpgObject	ICG (interaction changed gene) score object
selected_ints	subset of selected cell-cell interactions (optional)
selected_genes	subset of selected genes (optional)
specific_genes_1	specific geneset combo (need to position match specific_genes_2)
specific_genes_2	specific geneset combo (need to position match specific_genes_1)
min_cells	minimum number of target cell type
min_int_cells	minimum number of interacting cell type
min_fdr	minimum adjusted p-value
min_spat_diff	minimum absolute spatial expression difference
min_log2_fc	minimum absolute log2 fold-change
do_parallel	run calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
verbose	verbose

Value

cpgObject that contains the filtered differential gene scores

---

combineInteractionChangedGenes

combineInteractionChangedGenes

Description

Combine ICG scores in a pairwise manner.

Usage

```
combineInteractionChangedGenes(
  cpgObject,
  selected_ints = NULL,
  selected_genes = NULL,
  specific_genes_1 = NULL,
  specific_genes_2 = NULL,
  min_cells = 5,
```

```
  min_int_cells = 3,
  min_fdr = 0.05,
  min_spat_diff = 0,
  min_log2_fc = 0.5,
  do_parallel = TRUE,
  cores = NA,
  verbose = T
)
```

Arguments

cpgObject	ICG (interaction changed gene) score object
selected_ints	subset of selected cell-cell interactions (optional)
selected_genes	subset of selected genes (optional)
specific_genes_1	specific geneset combo (need to position match specific_genes_2)
specific_genes_2	specific geneset combo (need to position match specific_genes_1)
min_cells	minimum number of target cell type
min_int_cells	minimum number of interacting cell type
min_fdr	minimum adjusted p-value
min_spat_diff	minimum absolute spatial expression difference
min_log2_fc	minimum absolute log2 fold-change
do_parallel	run calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
verbose	verbose

Value

cpgObject that contains the filtered differential gene scores

---

combineMetadata *combineMetadata*

Description

This function combines the cell metadata with spatial locations and enrichment results from runSpatialEnrich

Usage

```
combineMetadata(gobject, feat_type = NULL, spat_enr_names = NULL)
```

Arguments

gobject	Giotto object
feat_type	feature type
spat_enr_names	names of spatial enrichment results to include

Value

Extended cell metadata in data.table format.

convertEnsemblToGeneSymbol *convertEnsemblToGeneSymbol*

Description

This function convert ensembl gene IDs from a matrix to official gene symbols

Usage

```
convertEnsemblToGeneSymbol(matrix, species = c("mouse", "human"))
```

Arguments

matrix	an expression matrix with ensembl gene IDs as rownames
species	species to use for gene symbol conversion

Details

This function requires that the biomaRt library is installed

Value

expression matrix with gene symbols as rownames

createCrossSection *createCrossSection*

Description

Create a virtual 2D cross section.

Usage

```
createCrossSection(
  gobject,
  name = "cross_section",
  spatial_network_name = "Delaunay_network",
  thickness_unit = c("cell", "natural"),
  slice_thickness = 2,
  cell_distance_estimate_method = "mean",
  extend_ratio = 0.2,
  method = c("equation", "3 points", "point and norm vector",
    "point and two plane vectors"),
  equation = NULL,
  point1 = NULL,
  point2 = NULL,
  point3 = NULL,
  normVector = NULL,
  planeVector1 = NULL,
```

```
  planeVector2 = NULL,
  mesh_grid_n = 20,
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
name	name of cress section object. (default = cross_sectino)
spatial_network_name	name of spatial network object. (default = Delaunay_network)
thickness_unit	unit of the virtual section thickness. If "cell", average size of the observed cells is used as length unit. If "natural", the unit of cell location coordinates is used.(default = cell)
slice_thickness	thickness of slice. default = 2
cell_distance_estimate_method	method to estimate average distance between neighobring cells. (default = mean)
extend_ratio	deciding the span of the cross section meshgrid, as a ratio of extension compared to the borders of the vitural tissue section. (default = 0.2)
method	method to define the cross section plane. If equation, the plane is defined by a four element numerical vector (equation) in the form of c(A,B,C,D), corresponding to a plane with equation Ax+By+Cz=D. If 3 points, the plane is define by the coordinates of 3 points, as given by point1, point2, and point3. If point and norm vector, the plane is defined by the coordinates of one point (point1) in the plane and the coordinates of one norm vector (normVector) to the plane. If point and two plane vector, the plane is defined by the coordinates of one point (point1) in the plane and the coordinates of two vectors (planeVector1, planeVector2) in the plane. (default = equation)
equation	equation required by method "equation".equations needs to be a numerical vector of length 4, in the form of c(A,B,C,D), which defines plane Ax+By+Cz=D.
point1	coordinates of the first point required by method "3 points","point and norm vector", and "point and two plane vectors".
point2	coordinates of the second point required by method "3 points"
point3	coordinates of the third point required by method "3 points"
normVector	coordinates of the norm vector required by method "point and norm vector"
planeVector1	coordinates of the first plane vector required by method "point and two plane vectors"
planeVector2	coordinates of the second plane vector required by method "point and two plane vectors"
mesh_grid_n	numer of meshgrid lines to generate along both directions for the cross section plane.
return_gobject	boolean: return giotto object (default = TRUE)

Details

Creates a virtual 2D cross section object for a given spatial network object. The users need to provide the definition of the cross section plane (see method).

Value

giotto object with updated spatial network slot

`createGiottoImage` *createGiottoImage*

Description

Creates a giotto image that can be added to a Giotto object and/or used to add an image to the spatial plotting functions

Usage

```
createGiottoImage(
  gobject = NULL,
  spatial_locs = NULL,
  mg_object,
  name = "image",
  xmax_adj = 0,
  xmin_adj = 0,
  ymax_adj = 0,
  ymin_adj = 0
)
```

Arguments

`gobject`	giotto object
`spatial_locs`	spatial locations (alternative if giobject = NULL)
`mg_object`	magick image object
`name`	name for the image
`xmax_adj`	adjustment of the maximum x-value to align the image
`xmin_adj`	adjustment of the minimum x-value to align the image
`ymax_adj`	adjustment of the maximum y-value to align the image
`ymin_adj`	adjustment of the minimum y-value to align the image

Value

a giotto image object

createGiottoInstructions *createGiottoInstructions*

Description

Function to set global instructions for giotto functions

Usage

```
createGiottoInstructions(
  python_path = NULL,
  show_plot = NULL,
  return_plot = NULL,
  save_plot = NULL,
  save_dir = NULL,
  plot_format = NULL,
  dpi = NULL,
  units = NULL,
  height = NULL,
  width = NULL,
  is_docker = FALSE
)
```

Arguments

python_path	path to python binary to use
show_plot	print plot to console, default = TRUE
return_plot	return plot as object, default = TRUE
save_plot	automatically save plot, dafault = FALSE
save_dir	path to directory where to save plots
plot_format	format of plots (defaults to png)
dpi	resolution for raster images
units	units of format (defaults to in)
height	height of plots
width	width of plots
is_docker	using docker implementation of Giotto (defaults to FALSE)

Value

named vector with giotto instructions

See Also

More online information can be found here https://rubd.github.io/Giotto_site/articles/instructions_and_plotting.html

createGiottoObject *create Giotto object*

Description

Function to create a giotto object

Usage

```
createGiottoObject(
  expression,
  expression_feat = "rna",
  spatial_locs = NULL,
  spatial_info = NULL,
  cell_metadata = NULL,
  feat_metadata = NULL,
  feat_info = NULL,
  spatial_network = NULL,
  spatial_network_name = NULL,
  spatial_grid = NULL,
  spatial_grid_name = NULL,
  spatial_enrichment = NULL,
  spatial_enrichment_name = NULL,
  dimension_reduction = NULL,
  nn_network = NULL,
  images = NULL,
  offset_file = NULL,
  instructions = NULL,
  cores = NA
)
```

Arguments

expression	expression information
expression_feat	available features (e.g. rna, protein, ...)
spatial_locs	data.table or data.frame with coordinates for cell centroids
spatial_info	information about spatial units
cell_metadata	cell annotation metadata
feat_metadata	feature annotation metadata for each unique feature
feat_info	information about features for each unique feature
spatial_network	list of spatial network(s)
spatial_network_name	list of spatial network name(s)
spatial_grid	list of spatial grid(s)
spatial_grid_name	list of spatial grid name(s)

`spatial_enrichment`
: list of spatial enrichment score(s) for each spatial region

`spatial_enrichment_name`
: list of spatial enrichment name(s)

`dimension_reduction`
: list of dimension reduction(s)

`nn_network`
: list of nearest neighbor network(s)

`images`
: list of images

`offset_file`
: file used to stitch fields together (optional)

`instructions`
: list of instructions or output result from `createGiottoInstructions`

`cores`
: how many cores or threads to use to read data if paths are provided

Details

See https://rubd.github.io/Giotto_site/articles/howto_giotto_class.html for more details

[**Requirements**] To create a giotto object you need to provide at least a matrix with genes as row names and cells as column names. This matrix can be provided as a base matrix, sparse Matrix, data.frame, data.table or as a path to any of those. To include spatial information about cells (or regions) you need to provide a matrix, data.table or data.frame (or path to them) with coordinates for all spatial dimensions. This can be 2D (x and y) or 3D (x, y, x). The row order for the cell coordinates should be the same as the column order for the provided expression data.

[**Instructions**] Additionally an instruction file, generated manually or with `createGiottoInstructions` can be provided to instructions, if not a default instruction file will be created for the Giotto object.

[**Multiple fields**] In case a dataset consists of multiple fields, like seqFISH+ for example, an offset file can be provided to stitch the different fields together. `stitchFieldCoordinates` can be used to generate such an offset file.

[**Processed data**] Processed count data, such as normalized data, can be provided using one of the different expression slots (norm_expr, norm_scaled_expr, custom_expr).

[**Metadata**] Cell and gene metadata can be provided using the cell and gene metadata slots. This data can also be added afterwards using the `addGeneMetadata` or `addCellMetadata` functions.

[**Other information**] Additional information can be provided through the appropriate slots:

- spatial networks
- spatial girds
- spatial enrichments
- dimensions reduction
- nearest neighbours networks
- images

Value

giotto object

createGiottoVisiumObject *createGiottoVisiumObject*

Description

creates Giotto object directly from a 10X visium folder

Usage

```
createGiottoVisiumObject(
  visium_dir = NULL,
  expr_data = c("raw", "filter"),
  gene_column_index = 1,
  h5_visium_path = NULL,
  h5_gene_ids = c("symbols", "ensembl"),
  h5_tissue_positions_path = NULL,
  h5_image_png_path = NULL,
  png_name = NULL,
  xmax_adj = 0,
  xmin_adj = 0,
  ymax_adj = 0,
  ymin_adj = 0,
  instructions = NULL,
  cores = NA,
  verbose = TRUE
)
```

Arguments

visium_dir	path to the 10X visium directory [required]
expr_data	raw or filtered data (see details)
gene_column_index	which column index to select (see details)
h5_visium_path	path to visium 10X .h5 file
h5_gene_ids	gene names as symbols (default) or ensemble gene ids
h5_tissue_positions_path	path to tissue locations (.csv file)
h5_image_png_path	path to tissue .png file (optional)
png_name	select name of png to use (see details)
xmax_adj	adjustment of the maximum x-value to align the image
xmin_adj	adjustment of the minimum x-value to align the image
ymax_adj	adjustment of the maximum y-value to align the image
ymin_adj	adjustment of the minimum y-value to align the image
instructions	list of instructions or output result from createGiottoInstructions
cores	how many cores or threads to use to read data if paths are provided

Details

If starting from a Visium 10X directory:

- expr_data: raw will take expression data from raw_feature_bc_matrix and filter from filtered_feature_bc_matrix
- gene_column_index: which gene identifiers (names) to use if there are multiple columns (e.g. ensemble and gene symbol)
- png_name: by default the first png will be selected, provide the png name to override this (e.g. myimage.png)

If starting from a Visium 10X .h5 file

- h5_visium_path: full path to .h5 file: /your/path/to/visium_file.h5
- h5_tissue_positions_path: full path to spatial locations file: /you/path/to/tissue_positions_list.csv
- h5_image_png_path: full path to png: /your/path/to/images/tissue_lowres_image.png

Value

giotto object

---

createNearestNetwork *createNearestNetwork*

Description

create a nearest neighbour (NN) network

Usage

```
createNearestNetwork(
  gobject,
  feat_type = NULL,
  type = c("sNN", "kNN"),
  dim_reduction_to_use = "pca",
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  feats_to_use = NULL,
  genes_to_use = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  name = "sNN.pca",
  return_gobject = TRUE,
  k = 30,
  minimum_shared = 5,
  top_shared = 3,
  verbose = T,
  ...
)
```

Arguments

gobject	giotto object
feat_type	feature type
type	sNN or kNN
dim_reduction_to_use	dimension reduction method to use
dim_reduction_name	name of dimension reduction set to use
dimensions_to_use	number of dimensions to use as input
feats_to_use	if dim_reduction_to_use = NULL, which genes to use
genes_to_use	deprecated, use feats_to_use
expression_values	expression values to use
name	arbitrary name for NN network
return_gobject	boolean: return giotto object (default = TRUE)
k	number of k neighbors to use
minimum_shared	minimum shared neighbors
top_shared	keep at ...
verbose	be verbose
...	additional parameters for kNN and sNN functions from dbscan

Details

This function creates a k-nearest neighbour (kNN) or shared nearest neighbour (sNN) network based on the provided dimension reduction space. To run it directly on the gene expression matrix set *dim_reduction_to_use = NULL*.

See also kNN and sNN for more information about how the networks are created.

Output for kNN:

- from: cell_ID for source cell
- to: cell_ID for target cell
- distance: distance between cells
- weight: weight = 1/(1 + distance)

Output for sNN:

- from: cell_ID for source cell
- to: cell_ID for target cell
- distance: distance between cells
- weight: 1/(1 + distance)
- shared: number of shared neighbours
- rank: ranking of pairwise cell neighbours

For sNN networks two additional parameters can be set:

- minimum_shared: minimum number of shared neighbours needed
- top_shared: keep this number of the top shared neighbours, irrespective of minimum_shared setting

Value

giotto object with updated NN network

Examples

```
data(mini_giotto_single_cell)

mini_giotto_single_cell <- createNearestNetwork(gobject = mini_giotto_single_cell,
                                                dimensions_to_use = 1:3, k = 3)
```

---

createSpatialDefaultGrid

createSpatialDefaultGrid

Description

Create a spatial grid using the default method

Usage

```
createSpatialDefaultGrid(
  gobject,
  sdimx_stepsize = NULL,
  sdimy_stepsize = NULL,
  sdimz_stepsize = NULL,
  minimum_padding = 1,
  name = NULL,
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
sdimx_stepsize	stepsize along the x-axis
sdimy_stepsize	stepsize along the y-axis
sdimz_stepsize	stepsize along the z-axis
minimum_padding	minimum padding on the edges
name	name for spatial grid (default = 'spatial_grid')
return_gobject	boolean: return giotto object (default = TRUE)

Details

Creates a spatial grid with defined x, y (and z) dimensions. The dimension units are based on the provided spatial location units.

Value

giotto object with updated spatial grid slot

createSpatialDelaunayNetwork
createSpatialDelaunayNetwork

Description

Create a spatial Delaunay network based on cell centroid physical distances.

Usage

```
createSpatialDelaunayNetwork(
  gobject,
  method = c("deldir", "delaunayn_geometry", "RTriangle"),
  dimensions = "all",
  name = "Delaunay_network",
  maximum_distance = "auto",
  minimum_k = 0,
  options = "Pp",
  Y = TRUE,
  j = TRUE,
  S = 0,
  verbose = T,
  return_gobject = TRUE,
  ...
)
```

Arguments

gobject	giotto object
method	package to use to create a Delaunay network
dimensions	which spatial dimensions to use. Use "sdimx" (spatial dimension x), "sdimy", "sdimz" respectively to refer to X (or the 1st), Y (or the 2nd) and Z(or the 3rd) dimension, see details. (default = all)
name	name for spatial network (default = 'delaunay_network')
maximum_distance	distance cuttof for Delaunay neighbors to consider. If "auto", "upper wisker" value of the distance vector between neighbors is used; see the boxplotgraphics documentation for more details.(default = "auto")
minimum_k	minimum number of neigbhours if maximum_distance != NULL
options	(geometry) String containing extra control options for the underlying Qhull command; see the Qhull documentation (../doc/qhull/html/qdelaun.html) for the available options. (default = 'Pp', do not report precision problems)
Y	(RTriangle) If TRUE prohibits the insertion of Steiner points on the mesh boundary.
j	(RTriangle) If TRUE jettisons vertices that are not part of the final triangulation from the output.
S	(RTriangle) Specifies the maximum number of added Steiner points.
verbose	verbose
return_gobject	boolean: return giotto object (default = TRUE)
...	Other additional parameters

Details

Creates a spatial Delaunay network as explained in delaunayn (default), deldir, or triangulate.

Value

giotto object with updated spatial network slot

---

createSpatialGrid *createSpatialGrid*

Description

Create a spatial grid using the default method

Usage

```
createSpatialGrid(
  gobject,
  name = NULL,
  method = c("default"),
  sdimx_stepsize = NULL,
  sdimy_stepsize = NULL,
  sdimz_stepsize = NULL,
  minimum_padding = 1,
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
name	name for spatial grid
method	method to create a spatial grid
sdimx_stepsize	stepsize along the x-axis
sdimy_stepsize	stepsize along the y-axis
sdimz_stepsize	stepsize along the z-axis
minimum_padding	minimum padding on the edges
return_gobject	boolean: return giotto object (default = TRUE)

Details

Creates a spatial grid with defined x, y (and z) dimensions. The dimension units are based on the provided spatial location units.

- default method: createSpatialDefaultGrid

Value

giotto object with updated spatial grid slot

createSpatialKNNnetwork *createSpatialKNNnetwork*

Description

Create a spatial knn network.

Usage

```
createSpatialKNNnetwork(
  gobject,
  method = "dbscan",
  dimensions = "all",
  name = "knn_network",
  k = 4,
  maximum_distance = NULL,
  minimum_k = 0,
  verbose = F,
  return_gobject = TRUE,
  ...
)
```

Arguments

gobject	giotto object
method	method to create kNN network
dimensions	which spatial dimensions to use (default = all)
name	name for spatial network (default = 'spatial_network')
k	number of nearest neighbors based on physical distance
maximum_distance	distance cuttof for nearest neighbors to consider for kNN network
minimum_k	minimum nearest neigbhours if maximum_distance != NULL
verbose	verbose
return_gobject	boolean: return giotto object (default = TRUE)
...	additional arguments to the selected method function

Value

giotto object with updated spatial network slot

dimensions: default = 'all' which takes all possible dimensions. Alternatively you can provide a character vector that specifiifies the spatial dimensions to use, e.g. c("sdimx', "sdimy") or a numerical vector, e.g. 2:3

maximum_distance: to create a network based on maximum distance only, you also need to set k to a very high value, e.g. k = 100

createSpatialNetwork *createSpatialNetwork*

Description

Create a spatial network based on cell centroid physical distances.

Usage

```
createSpatialNetwork(
  gobject,
  name = NULL,
  dimensions = "all",
  method = c("Delaunay", "kNN"),
  delaunay_method = c("deldir", "delaunayn_geometry", "RTriangle"),
  maximum_distance_delaunay = "auto",
  options = "Pp",
  Y = TRUE,
  j = TRUE,
  S = 0,
  minimum_k = 0,
  knn_method = "dbscan",
  k = 4,
  maximum_distance_knn = NULL,
  verbose = F,
  return_gobject = TRUE,
  ...
)
```

Arguments

gobject	giotto object
name	name for spatial network (default = 'spatial_network')
dimensions	which spatial dimensions to use (default = all)
method	which method to use to create a spatial network. (default = Delaunay)
delaunay_method	Delaunay method to use
maximum_distance_delaunay	distance cuttof for nearest neighbors to consider for Delaunay network
options	(geometry) String containing extra control options for the underlying Qhull command; see the Qhull documentation (../doc/qhull/html/qdelaun.html) for the available options. (default = 'Pp', do not report precision problems)
Y	(RTriangle) If TRUE prohibits the insertion of Steiner points on the mesh boundary.
j	(RTriangle) If TRUE jettisons vertices that are not part of the final triangulation from the output.
S	(RTriangle) Specifies the maximum number of added Steiner points.
minimum_k	minimum nearest neigbhours if maximum_distance != NULL

knn_method	method to create kNN network
k	number of nearest neighbors based on physical distance
maximum_distance_knn	distance cuttof for nearest neighbors to consider for kNN network
verbose	verbose
return_gobject	boolean: return giotto object (default = TRUE)
...	Additional parameters for the selected function

Details

Creates a spatial network connecting single-cells based on their physical distance to each other. For Delaunay method, neighbors will be decided by delaunay triangulation and a maximum distance criteria. For kNN method, number of neighbors can be determined by k, or maximum distance from each cell with or without setting a minimum k for each cell.

dimensions: default = 'all' which takes all possible dimensions. Alternatively you can provide a character vector that specififfies the spatial dimensions to use, e.g. c("sdimx', "sdimy") or a numerical vector, e.g. 2:3

Value

giotto object with updated spatial network slot

`create_crossSection_object`

create_crossSection_object

Description

create a crossSection object

Usage

```
create_crossSection_object(
  name = NULL,
  method = NULL,
  thickness_unit = NULL,
  slice_thickness = NULL,
  cell_distance_estimate_method = NULL,
  extend_ratio = NULL,
  plane_equation = NULL,
  mesh_grid_n = NULL,
  mesh_obj = NULL,
  cell_subset = NULL,
  cell_subset_spatial_locations = NULL,
  cell_subset_projection_locations = NULL,
  cell_subset_projection_PCA = NULL,
  cell_subset_projection_coords = NULL
)
```

Arguments

name	name of cress section object. (default = cross_sectino)
method	method to define the cross section plane.
thickness_unit	unit of the virtual section thickness. If "cell", average size of the observed cells is used as length unit. If "natural", the unit of cell location coordinates is used.(default = cell)
slice_thickness	thickness of slice
cell_distance_estimate_method	method to estimate average distance between neighobring cells. (default = mean)
extend_ratio	deciding the span of the cross section meshgrid, as a ratio of extension compared to the borders of the vitural tissue section. (default = 0.2)
plane_equation	a numerical vector of length 4, in the form of c(A,B,C,D), which defines plane Ax+By+Cz=D.
mesh_grid_n	numer of meshgrid lines to generate along both directions for the cross section plane.
mesh_obj	object that stores the cross section meshgrid information.
cell_subset	cells selected by the cross section
cell_subset_spatial_locations	locations of cells selected by the cross section
cell_subset_projection_locations	3D projection coordinates of selected cells onto the cross section plane
cell_subset_projection_PCA	pca of projection coordinates
cell_subset_projection_coords	2D PCA coordinates of selected cells in the cross section plane

---

crossSectionGenePlot *crossSectionGenePlot*

Description

Visualize cells and gene expression in a virtual cross section according to spatial coordinates

Usage

```
crossSectionGenePlot(
  gobject = NULL,
  crossSection_obj = NULL,
  name = NULL,
  spatial_network_name = "Delaunay_network",
  default_save_name = "crossSectionGenePlot",
  ...
)
```

Arguments

gobject	giotto object
crossSection_obj	crossSection object
name	name of virtual cross section to use
spatial_network_name	name of spatial network to use
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for spatGenePlot2D

Details

Description of parameters.

Value

ggplot

See Also

spatGenePlot3D and spatGenePlot2D

---

crossSectionGenePlot3D *crossSectionGenePlot3D*

Description

Visualize cells and gene expression in a virtual cross section according to spatial coordinates

Usage

```
crossSectionGenePlot3D(
  gobject,
  crossSection_obj = NULL,
  name = NULL,
  spatial_network_name = "Delaunay_network",
  other_cell_color = alpha("lightgrey", 0),
  default_save_name = "crossSectionGenePlot3D",
  ...
)
```

Arguments

gobject	giotto object
crossSection_obj	cross section object as alternative input. default = NULL.
name	name of virtual cross section to use

spatial_network_name
: name of spatial network to use

other_cell_color
: color of cells outside the cross section. default = transparent.

default_save_name
: default save name for saving, don't change, change save_name in save_param

...
: parameters for spatGenePlot3D

Details

Description of parameters.

Value

ggplot

`crossSectionPlot` *crossSectionPlot*

Description

Visualize cells in a virtual cross section according to spatial coordinates

Usage

```
crossSectionPlot(
  gobject,
  crossSection_obj = NULL,
  name = NULL,
  spatial_network_name = "Delaunay_network",
  default_save_name = "crossSectionPlot",
  ...
)
```

Arguments

gobject
: giotto object

crossSection_obj
: cross section object as alternative input. default = NULL.

name
: name of virtual cross section to use

spatial_network_name
: name of spatial network to use

default_save_name
: default save name for saving, don't change, change save_name in save_param

...
: parameters for spatPlot2D

Details

Description of parameters.

Value

ggplot

See Also

crossSectionPlot

`crossSectionPlot3D` *crossSectionPlot3D*

Description

Visualize cells in a virtual cross section according to spatial coordinates

Usage

```
crossSectionPlot3D(
  gobject,
  crossSection_obj = NULL,
  name = NULL,
  spatial_network_name = "Delaunay_network",
  show_other_cells = T,
  other_cell_color = alpha("lightgrey", 0),
  default_save_name = "crossSection3D",
  ...
)
```

Arguments

`gobject`	giotto object
`crossSection_obj`	cross section object as alternative input. default = NULL.
`name`	name of virtual cross section to use
`spatial_network_name`	name of spatial network to use
`show_other_cells`	display not selected cells
`other_cell_color`	color of cells outside the cross section. default = transparent.
`default_save_name`	default save name for saving, don't change, change save_name in save_param
`...`	parameters for spatPlot3D

Details

Description of parameters.

Value

ggplot

`detectSpatialCorFeatsMatrix` *detectSpatialCorFeatsMatrix*

Description

Detect genes that are spatially correlated

Usage

```
detectSpatialCorFeatsMatrix(
  expression_matrix,
  method = c("grid", "network"),
  spatial_network,
  spatial_grid,
  spatial_locs,
  subset_feats = NULL,
  network_smoothing = NULL,
  min_cells_per_grid = 4,
  cor_method = c("pearson", "kendall", "spearman")
)
```

Arguments

`expression_matrix`	provided expression matrix
`method`	method to use for spatial averaging
`spatial_network`	provided spatial network
`spatial_grid`	provided spatial grid
`spatial_locs`	provided spatial locations
`subset_feats`	subset of features to use
`network_smoothing`	smoothing factor beteen 0 and 1 (default: automatic)
`min_cells_per_grid`	minimum number of cells to consider a grid
`cor_method`	correlation method

Details

For method = network, it expects a fully connected spatial network. You can make sure to create a fully connected network by setting minimal_k > 0 in the `createSpatialNetwork` function.

- 1. grid-averaging: average gene expression values within a predefined spatial grid
- 2. network-averaging: smoothens the gene expression matrix by averaging the expression within one cell by using the neighbours within the predefined spatial network. b is a smoothening factor that defaults to 1 - 1/k, where k is the median number of k-neighbors in the selected spatial network. Setting b = 0 means no smoothing and b = 1 means no contribution from its own expression.

The spatCorObject can be further explored with showSpatialCorGenes()

Value

returns a spatial correlation object: "spatCorObject"

See Also

showSpatialCorFeats

`detectSpatialPatterns` *detectSpatialPatterns*

Description

Identify spatial patterns through PCA on average expression in a spatial grid.

Usage

```
detectSpatialPatterns(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  spatial_grid_name = "spatial_grid",
  min_cells_per_grid = 4,
  scale_unit = F,
  ncp = 100,
  show_plot = T,
  PC_zscore = 1.5
)
```

Arguments

`gobject`	giotto object
`expression_values`	expression values to use
`spatial_grid_name`	name of spatial grid to use (default = 'spatial_grid')
`min_cells_per_grid`	minimum number of cells in a grid to be considered
`scale_unit`	scale features
`ncp`	number of principal components to calculate
`show_plot`	show plots
`PC_zscore`	minimum z-score of variance explained by a PC

Details

Steps to identify spatial patterns:

- 1. average gene expression for cells within a grid, see createSpatialGrid
- 2. perform PCA on the average grid expression profiles
- 3. convert variance of principlal components (PCs) to z-scores and select PCs based on a z-score threshold

Value

spatial pattern object 'spatPatObj'

`dimCellPlot` *dimCellPlot*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimCellPlot(gobject, ...)
```

Arguments

`gobject`	giotto object
`...`	Arguments passed on to `dimCellPlot2D`
	`dim_reduction_to_use` dimension reduction to use
	`dim_reduction_name` dimension reduction name
	`dim1_to_use` dimension to use on x-axis
	`dim2_to_use` dimension to use on y-axis
	`spat_enr_names` names of spatial enrichment results to include
	`cell_annotation_values` numeric cell annotation columns
	`show_NN_network` show underlying NN network
	`nn_network_to_use` type of NN network to use (kNN vs sNN)
	`network_name` name of NN network to use, if show_NN_network = TRUE
	`cell_color_code` named vector with colors for cell annotation values
	`cell_color_gradient` vector with 3 colors for numeric data
	`gradient_midpoint` midpoint for color gradient
	`gradient_limits` vector with lower and upper limits
	`select_cell_groups` select subset of cells/clusters based on cell_color parameter
	`select_cells` select subset of cells based on cell IDs
	`show_other_cells` display not selected cells
	`other_cell_color` color of not selected cells
	`other_point_size` size of not selected cells
	`show_cluster_center` plot center of selected clusters
	`show_center_label` plot label of selected clusters
	`center_point_size` size of center points
	`center_point_border_col` border color of center points
	`center_point_border_stroke` border stroke size of center points
	`label_size` size of labels
	`label_fontface` font of labels
	`edge_alpha` column to use for alpha of the edges
	`point_shape` point with border or not (border or no_border)

point_size size of point (cell)
point_alpha transparancy of dim. reduction points
point_border_col color of border around points
point_border_stroke stroke size of border around points
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
background_color color of plot background
axis_text size of axis text
axis_title size of axis title
cow_n_col cowplot param: how many columns
cow_rel_h cowplot param: relative height
cow_rel_w cowplot param: relative width
cow_align cowplot param: how to align
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters
default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters. For 3D plots see dimCellPlot2D

Value

ggplot

See Also

Other dimension reduction cell annotation visualizations: dimCellPlot2D()

Examples

```
data(mini_giotto_single_cell)

# combine all metadata
combineMetadata(mini_giotto_single_cell, spat_enr_names = 'cluster_metagene')

# visualize total expression information
dimCellPlot(mini_giotto_single_cell, cell_annotation_values = 'total_expr')

# visualize enrichment results
dimCellPlot(mini_giotto_single_cell,
               spat_enr_names = 'cluster_metagene',
               cell_annotation_values = c('1','2'))
```

dimCellPlot2D *dimCellPlot2D*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimCellPlot2D(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  spat_enr_names = NULL,
  cell_annotation_values = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  edge_alpha = NULL,
  point_shape = c("border", "no_border"),
  point_size = 1,
  point_alpha = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
```

```
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "dimCellPlot2D"
)
```

Arguments

gobject	giotto object
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
spat_enr_names	names of spatial enrichment results to include
cell_annotation_values	numeric cell annotation columns
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
cell_color_code	named vector with colors for cell annotation values
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points

center_point_border_col
: border color of center points

center_point_border_stroke
: border stroke size of center points

label_size
: size of labels

label_fontface
: font of labels

edge_alpha
: column to use for alpha of the edges

point_shape
: point with border or not (border or no_border)

point_size
: size of point (cell)

point_alpha
: transparancy of dim. reduction points

point_border_col
: color of border around points

point_border_stroke
: stroke size of border around points

show_legend
: show legend

legend_text
: size of legend text

legend_symbol_size
: size of legend symbols

background_color
: color of plot background

axis_text
: size of axis text

axis_title
: size of axis title

cow_n_col
: cowplot param: how many columns

cow_rel_h
: cowplot param: relative height

cow_rel_w
: cowplot param: relative width

cow_align
: cowplot param: how to align

show_plot
: show plot

return_plot
: return ggplot object

save_plot
: directly save the plot [boolean]

save_param
: list of saving parameters, see showSaveParameters

default_save_name
: default save name for saving, don't change, change save_name in save_param

Details

Description of parameters. For 3D plots see dimPlot3D

Value

ggplot

See Also

Other dimension reduction cell annotation visualizations: dimCellPlot()

Examples

```
data(mini_giotto_single_cell)

# combine all metadata
combineMetadata(mini_giotto_single_cell, spat_enr_names = 'cluster_metagene')

# visualize total expression information
dimCellPlot2D(mini_giotto_single_cell, cell_annotation_values = 'total_expr')

# visualize enrichment results
dimCellPlot2D(mini_giotto_single_cell,
               spat_enr_names = 'cluster_metagene',
               cell_annotation_values = c('1','2'))
```

`dimGenePlot` *dimGenePlot*

Description

Visualize gene expression according to dimension reduction coordinates

Usage

```
dimGenePlot(...)
```

Arguments

`...`	Arguments passed on to `dimGenePlot2D` `gobject` giotto object `expression_values` gene expression values to use `genes` genes to show `dim_reduction_to_use` dimension reduction to use `dim_reduction_name` dimension reduction name `dim1_to_use` dimension to use on x-axis `dim2_to_use` dimension to use on y-axis `show_NN_network` show underlying NN network `nn_network_to_use` type of NN network to use (kNN vs sNN) `network_name` name of NN network to use, if show_NN_network = TRUE `network_color` color of NN network `edge_alpha` column to use for alpha of the edges `scale_alpha_with_expression` scale expression with ggplot alpha parameter `point_shape` point with border or not (border or no_border) `point_size` size of point (cell) `point_alpha` transparancy of points `cell_color_gradient` vector with 3 colors for numeric data `gradient_midpoint` midpoint for color gradient `gradient_limits` vector with lower and upper limits `point_border_col` color of border around points

point_border_stroke stroke size of border around points

show_legend show legend

legend_text size of legend text

background_color color of plot background

axis_text size of axis text

axis_title size of axis title

cow_n_col cowplot param: how many columns

cow_rel_h cowplot param: relative height

cow_rel_w cowplot param: relative width

cow_align cowplot param: how to align

show_plot show plots

return_plot return ggplot object

save_plot directly save the plot [boolean]

save_param list of saving parameters, see showSaveParameters

default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

dimGenePlot3D

Other dimension reduction gene expression visualizations: dimGenePlot2D(), dimGenePlot3D()

Examples

```
data(mini_giotto_single_cell)

all_genes = slot(mini_giotto_single_cell, 'gene_ID')
selected_genes = all_genes[1:2]
dimGenePlot(mini_giotto_single_cell, genes = selected_genes, point_size = 3)
```

---

dimGenePlot2D *dimGenePlot2D*

Description

Visualize gene expression according to dimension reduction coordinates

Usage

```
dimGenePlot2D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  network_color = "lightgray",
  edge_alpha = NULL,
  scale_alpha_with_expression = FALSE,
  point_shape = c("border", "no_border"),
  point_size = 1,
  point_alpha = 1,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  legend_text = 8,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "dimGenePlot2D"
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
genes	genes to show
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis

`show_NN_network`
: show underlying NN network

`nn_network_to_use`
: type of NN network to use (kNN vs sNN)

`network_name`
: name of NN network to use, if show_NN_network = TRUE

`network_color`
: color of NN network

`edge_alpha`
: column to use for alpha of the edges

`scale_alpha_with_expression`
: scale expression with ggplot alpha parameter

`point_shape`
: point with border or not (border or no_border)

`point_size`
: size of point (cell)

`point_alpha`
: transparancy of points

`cell_color_gradient`
: vector with 3 colors for numeric data

`gradient_midpoint`
: midpoint for color gradient

`gradient_limits`
: vector with lower and upper limits

`point_border_col`
: color of border around points

`point_border_stroke`
: stroke size of border around points

`show_legend`
: show legend

`legend_text`
: size of legend text

`background_color`
: color of plot background

`axis_text`
: size of axis text

`axis_title`
: size of axis title

`cow_n_col`
: cowplot param: how many columns

`cow_rel_h`
: cowplot param: relative height

`cow_rel_w`
: cowplot param: relative width

`cow_align`
: cowplot param: how to align

`show_plot`
: show plots

`return_plot`
: return ggplot object

`save_plot`
: directly save the plot [boolean]

`save_param`
: list of saving parameters, see `showSaveParameters`

`default_save_name`
: default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

dimGenePlot3D

Other dimension reduction gene expression visualizations: dimGenePlot3D(), dimGenePlot()

Examples

```
data(mini_giotto_single_cell)

all_genes = slot(mini_giotto_single_cell, 'gene_ID')
selected_genes = all_genes[1:2]
dimGenePlot2D(mini_giotto_single_cell, genes = selected_genes, point_size = 3)
```

---

dimGenePlot3D *dimGenePlot3D*

Description

Visualize cells and gene expression according to dimension reduction coordinates

Usage

```
dimGenePlot3D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = 3,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  network_color = "lightgray",
  cluster_column = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1,
  edge_alpha = NULL,
  point_size = 2,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  show_legend = T,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
```

```
  default_save_name = "dimGenePlot3D"
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
genes	genes to show
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim3_to_use	dimension to use on z-axis
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
network_color	color of NN network
cluster_column	cluster column to select groups
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
genes_high_color	color for high expression levels
genes_mid_color	color for medium expression levels
genes_low_color	color for low expression levels
show_legend	show legend
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

Other dimension reduction gene expression visualizations: `dimGenePlot2D()`, `dimGenePlot()`

`dimPlot` *dimPlot*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimPlot(...)
```

Arguments

`...`	Arguments passed on to `dimPlot2D` `gobject` giotto object `feat_type` feature type `group_by` create multiple plots based on cell annotation column `group_by_subset` subset the group_by factor column `dim_reduction_to_use` dimension reduction to use `dim_reduction_name` dimension reduction name `dim1_to_use` dimension to use on x-axis `dim2_to_use` dimension to use on y-axis `spat_enr_names` names of spatial enrichment results to include `show_NN_network` show underlying NN network `nn_network_to_use` type of NN network to use (kNN vs sNN) `network_name` name of NN network to use, if show_NN_network = TRUE `cell_color` color for cells (see details) `color_as_factor` convert color column to factor `cell_color_code` named vector with colors `cell_color_gradient` vector with 3 colors for numeric data `gradient_midpoint` midpoint for color gradient `gradient_limits` vector with lower and upper limits `select_cell_groups` select subset of cells/clusters based on cell_color parameter `select_cells` select subset of cells based on cell IDs `show_other_cells` display not selected cells `other_cell_color` color of not selected cells

other_point_size size of not selected cells

show_cluster_center plot center of selected clusters

show_center_label plot label of selected clusters

center_point_size size of center points

center_point_border_col border color of center points

center_point_border_stroke border stroke size of center points

label_size size of labels

label_fontface font of labels

edge_alpha column to use for alpha of the edges

point_shape point with border or not (border or no_border)

point_size size of point (cell)

point_alpha transparancy of point

point_border_col color of border around points

point_border_stroke stroke size of border around points

title title for plot, defaults to cell_color parameter

show_legend show legend

legend_text size of legend text

legend_symbol_size size of legend symbols

background_color color of plot background

axis_text size of axis text

axis_title size of axis title

cow_n_col cowplot param: how many columns

cow_rel_h cowplot param: relative height

cow_rel_w cowplot param: relative width

cow_align cowplot param: how to align

show_plot show plot

return_plot return ggplot object

save_plot directly save the plot [boolean]

save_param list of saving parameters, see showSaveParameters

default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters, see dimPlot2D. For 3D plots see dimPlot3D

Value

ggplot

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), plotPCA_2D(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_2D(), plotUMAP_3D(), plotUMAP()

Examples

```
data(mini_giotto_single_cell)

dimPlot(mini_giotto_single_cell)
dimPlot(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

---

dimPlot2D *dimPlot2D*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimPlot2D(
  gobject,
  feat_type = NULL,
  group_by = NULL,
  group_by_subset = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  spat_enr_names = NULL,
  show_NN_network = FALSE,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  cell_color = NULL,
  color_as_factor = TRUE,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_cluster_center = FALSE,
  show_center_label = TRUE,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  edge_alpha = NULL,
  point_shape = c("border", "no_border"),
  point_size = 1,
  point_alpha = 1,
```

```
  point_border_col = "black",
  point_border_stroke = 0.1,
  title = NULL,
  show_legend = TRUE,
  legend_text = 8,
  legend_symbol_size = 1,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "dimPlot2D"
)
```

Arguments

gobject	giotto object
feat_type	feature type
group_by	create multiple plots based on cell annotation column
group_by_subset	subset the group_by factor column
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
spat_enr_names	names of spatial enrichment results to include
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits

`select_cell_groups`
: select subset of cells/clusters based on cell_color parameter

`select_cells`
: select subset of cells based on cell IDs

`show_other_cells`
: display not selected cells

`other_cell_color`
: color of not selected cells

`other_point_size`
: size of not selected cells

`show_cluster_center`
: plot center of selected clusters

`show_center_label`
: plot label of selected clusters

`center_point_size`
: size of center points

`center_point_border_col`
: border color of center points

`center_point_border_stroke`
: border stroke size of center points

`label_size`
: size of labels

`label_fontface`
: font of labels

`edge_alpha`
: column to use for alpha of the edges

`point_shape`
: point with border or not (border or no_border)

`point_size`
: size of point (cell)

`point_alpha`
: transparancy of point

`point_border_col`
: color of border around points

`point_border_stroke`
: stroke size of border around points

`title`
: title for plot, defaults to cell_color parameter

`show_legend`
: show legend

`legend_text`
: size of legend text

`legend_symbol_size`
: size of legend symbols

`background_color`
: color of plot background

`axis_text`
: size of axis text

`axis_title`
: size of axis title

`cow_n_col`
: cowplot param: how many columns

`cow_rel_h`
: cowplot param: relative height

`cow_rel_w`
: cowplot param: relative width

`cow_align`
: cowplot param: how to align

`show_plot`
: show plot

`return_plot`
: return ggplot object

`save_plot`
: directly save the plot [boolean]

`save_param`
: list of saving parameters, see `showSaveParameters`

`default_save_name`
: default save name for saving, don't change, change save_name in save_param

Details

Description of parameters. For 3D plots see dimPlot3D

Value

ggplot

See Also

Other reduced dimension visualizations: dimPlot3D(), dimPlot(), plotPCA_2D(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_2D(), plotUMAP_3D(), plotUMAP()

Examples

```
data(mini_giotto_single_cell)

dimPlot2D(mini_giotto_single_cell)
dimPlot2D(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

---

dimPlot3D *dimPlot3D*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimPlot3D(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = 3,
  spat_enr_names = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 2,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  color_as_factor = T,
  cell_color = NULL,
  cell_color_code = NULL,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 4,
```

```
  edge_alpha = NULL,
  point_size = 3,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "dim3D"
)
```

Arguments

gobject	giotto object
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim3_to_use	dimension to use on z-axis
spat_enr_names	names of spatial enrichment results to include
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
color_as_factor	convert color column to factor
cell_color	color for cells (see details)
cell_color_code	named vector with colors
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)

show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

plotly

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot(), plotPCA_2D(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_2D(), plotUMAP_3D(), plotUMAP()

---

doHclust *doHclust*

Description

cluster cells using hierarchical clustering algorithm

Usage

```
doHclust(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes_to_use = NULL,
  dim_reduction_to_use = c("cells", "pca", "umap", "tsne"),
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  distance_method = c("pearson", "spearman", "original", "euclidean", "maximum",
    "manhattan", "canberra", "binary", "minkowski"),
  agglomeration_method = c("ward.D2", "ward.D", "single", "complete", "average",
    "mcquitty", "median", "centroid"),
  k = 10,
  h = NULL,
  name = "hclust",
  return_gobject = TRUE,
  set_seed = T,
  seed_number = 1234
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
genes_to_use	subset of genes to use
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimensions reduction name
dimensions_to_use	dimensions to use
distance_method	distance method
agglomeration_method	agglomeration method for hclust
k	number of final clusters
h	cut hierarchical tree at height = h
name	name for hierarchical clustering
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

Details

Description on how to use Kmeans clustering method.

Value

giotto object with new clusters appended to cell metadata

See Also

hclust

Examples

```
data(mini_giotto_single_cell)

mini_giotto_single_cell = doHclust(mini_giotto_single_cell, k = 4, name = 'hier_clus')
plotUMAP_2D(mini_giotto_single_cell, cell_color = 'hier_clus', point_size = 3)
```

doHMRF *doHMRF*

Description

Run HMRF

Usage

```
doHMRF(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  spatial_network_name = "Delaunay_network",
  spatial_genes = NULL,
  spatial_dimensions = c("sdimx", "sdimy", "sdimz"),
  dim_reduction_to_use = NULL,
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  seed = 100,
  name = "test",
  k = 10,
  betas = c(0, 2, 50),
  tolerance = 1e-10,
  zscore = c("none", "rowcol", "colrow"),
  numinit = 100,
  python_path = NULL,
  output_folder = NULL,
  overwrite_output = TRUE
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
spatial_network_name	name of spatial network to use for HMRF
spatial_genes	spatial genes to use for HMRF
spatial_dimensions	select spatial dimensions to use, default is all possible dimensions
dim_reduction_to_use	use another dimension reduction set as input
dim_reduction_name	name of dimension reduction set to use
dimensions_to_use	number of dimensions to use as input
seed	seed to fix random number generator (for creating initialization of HMRF) (-1 if no fixing)
name	name of HMRF run

k	number of HMRF domains
betas	betas to test for. three numbers: start_beta, beta_increment, num_betas e.g. c(0, 2.0, 50)
tolerance	tolerance
zscore	zscore
numinit	number of initializations
python_path	python path to use
output_folder	output folder to save results
overwrite_output	overwrite output folder

Details

Description of HMRF parameters ...

Value

Creates a directory with results that can be viewed with viewHMRFresults

---

`doKmeans` *doKmeans*

Description

cluster cells using kmeans algorithm

Usage

```
doKmeans(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes_to_use = NULL,
  dim_reduction_to_use = c("cells", "pca", "umap", "tsne"),
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  distance_method = c("original", "pearson", "spearman", "euclidean", "maximum",
    "manhattan", "canberra", "binary", "minkowski"),
  centers = 10,
  iter_max = 100,
  nstart = 1000,
  algorithm = "Hartigan-Wong",
  name = "kmeans",
  return_gobject = TRUE,
  set_seed = T,
  seed_number = 1234
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
genes_to_use	subset of genes to use
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimensions reduction name
dimensions_to_use	dimensions to use
distance_method	distance method
centers	number of final clusters
iter_max	kmeans maximum iterations
nstart	kmeans nstart
algorithm	kmeans algorithm
name	name for kmeans clustering
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

Details

Description on how to use Kmeans clustering method.

Value

giotto object with new clusters appended to cell metadata

See Also

kmeans

Examples

```
data(mini_giotto_single_cell)

mini_giotto_single_cell = doKmeans(mini_giotto_single_cell, centers = 4, name = 'kmeans_clus')
plotUMAP_2D(mini_giotto_single_cell, cell_color = 'kmeans_clus', point_size = 3)
```

doLeidenCluster *doLeidenCluster*

Description

cluster cells using a NN-network and the Leiden community detection algorithm

Usage

```
doLeidenCluster(
  gobject,
  feat_type = NULL,
  name = "leiden_clus",
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  python_path = NULL,
  resolution = 1,
  weight_col = "weight",
 partition_type = c("RBConfigurationVertexPartition", "ModularityVertexPartition"),
  init_membership = NULL,
  n_iterations = 1000,
  return_gobject = TRUE,
  set_seed = T,
  seed_number = 1234
)
```

Arguments

gobject	giotto object
feat_type	feature type
name	name for cluster
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
python_path	specify specific path to python if required
resolution	resolution
weight_col	weight column to use for edges
partition_type	The type of partition to use for optimisation.
init_membership	initial membership of cells for the partition
n_iterations	number of interations to run the Leiden algorithm. If the number of iterations is negative, the Leiden algorithm is run until an iteration in which there was no improvement.
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

Details

This function is a wrapper for the Leiden algorithm implemented in python, which can detect communities in graphs of millions of nodes (cells), as long as they can fit in memory. See the https://github.com/vtraag/leidenalgleidenalg github page or the https://leidenalg.readthedocs.io/en/stable/index.htmlreadthedocs page for more information.

Partition types available and information:

- RBConfigurationVertexPartition: Implements Reichardt and Bornholdt's Potts model with a configuration null model. This quality function is well-defined only for positive edge weights. This quality function uses a linear resolution parameter.
- ModularityVertexPartition: Implements modularity. This quality function is well-defined only for positive edge weights. It does *not* use the resolution parameter

Set *weight_col* = *NULL* to give equal weight (=1) to each edge.

Value

giotto object with new clusters appended to cell metadata

`doLeidenSubCluster` *doLeidenSubCluster*

Description

Further subcluster cells using a NN-network and the Leiden algorithm

Usage

```
doLeidenSubCluster(
  gobject,
  name = "sub_pleiden_clus",
  cluster_column = NULL,
  selected_clusters = NULL,
 hvg_param = list(reverse_log_scale = T, difference_in_cov = 1, expression_values =
    "normalized"),
  hvg_min_perc_cells = 5,
  hvg_mean_expr_det = 1,
  use_all_genes_as_hvg = FALSE,
  min_nr_of_hvg = 5,
  pca_param = list(expression_values = "normalized", scale_unit = T),
  nn_param = list(dimensions_to_use = 1:20),
  k_neighbors = 10,
  resolution = 0.5,
  n_iterations = 500,
  python_path = NULL,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  return_gobject = TRUE,
  verbose = T
)
```

Arguments

gobject	giotto object
name	name for new clustering result
cluster_column	cluster column to subcluster
selected_clusters	only do subclustering on these clusters
hvg_param	parameters for calculateHVG
hvg_min_perc_cells	threshold for detection in min percentage of cells
hvg_mean_expr_det	threshold for mean expression level in cells with detection
use_all_genes_as_hvg	forces all genes to be HVG and to be used as input for PCA
min_nr_of_hvg	minimum number of HVG, or all genes will be used as input for PCA
pca_param	parameters for runPCA
nn_param	parameters for parameters for createNearestNetwork
k_neighbors	number of k for createNearestNetwork
resolution	resolution of Leiden clustering
n_iterations	number of interations to run the Leiden algorithm.
python_path	specify specific path to python if required
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
return_gobject	boolean: return giotto object (default = TRUE)
verbose	verbose

Details

This function performs subclustering using the Leiden algorithm on selected clusters. The systematic steps are:

- 1. subset Giotto object
- 2. identify highly variable genes
- 3. run PCA
- 4. create nearest neighbouring network
- 5. do Leiden clustering

Value

giotto object with new subclusters appended to cell metadata

See Also

doLeidenCluster

doLouvainCluster *doLouvainCluster*

Description

cluster cells using a NN-network and the Louvain algorithm.

Usage

```
doLouvainCluster(
  gobject,
  version = c("community", "multinet"),
  name = "louvain_clus",
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  python_path = NULL,
  resolution = 1,
  weight_col = NULL,
  gamma = 1,
  omega = 1,
  louv_random = F,
  return_gobject = TRUE,
  set_seed = F,
  seed_number = 1234,
  ...
)
```

Arguments

gobject	giotto object
version	implemented version of Louvain clustering to use
name	name for cluster
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
python_path	[community] specify specific path to python if required
resolution	[community] resolution
weight_col	weight column name
gamma	[multinet] Resolution parameter for modularity in the generalized louvain method.
omega	[multinet] Inter-layer weight parameter in the generalized louvain method
louv_random	[community] Will randomize the node evaluation order and the community evaluation order to get different partitions at each call
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed
...	additional parameters

Details

Louvain clustering using the community or multinet implementation of the louvain clustering algorithm.

Value

giotto object with new clusters appended to cell metadata

See Also

doLouvainCluster_community and doLouvainCluster_multinet

---

doLouvainSubCluster *doLouvainSubCluster*

Description

subcluster cells using a NN-network and the Louvain algorithm

Usage

```
doLouvainSubCluster(
  gobject,
  name = "sub_louvain_clus",
  version = c("community", "multinet"),
  cluster_column = NULL,
  selected_clusters = NULL,
 hvg_param = list(reverse_log_scale = T, difference_in_cov = 1, expression_values =
    "normalized"),
  hvg_min_perc_cells = 5,
  hvg_mean_expr_det = 1,
  use_all_genes_as_hvg = FALSE,
  min_nr_of_hvg = 5,
  pca_param = list(expression_values = "normalized", scale_unit = T),
  nn_param = list(dimensions_to_use = 1:20),
  k_neighbors = 10,
  resolution = 0.5,
  gamma = 1,
  omega = 1,
  python_path = NULL,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  return_gobject = TRUE,
  verbose = T
)
```

Arguments

gobject	giotto object
name	name for new clustering result
version	version of Louvain algorithm to use

cluster_column	cluster column to subcluster
selected_clusters	only do subclustering on these clusters
hvg_param	parameters for calculateHVG
hvg_min_perc_cells	threshold for detection in min percentage of cells
hvg_mean_expr_det	threshold for mean expression level in cells with detection
use_all_genes_as_hvg	forces all genes to be HVG and to be used as input for PCA
min_nr_of_hvg	minimum number of HVG, or all genes will be used as input for PCA
pca_param	parameters for runPCA
nn_param	parameters for parameters for createNearestNetwork
k_neighbors	number of k for createNearestNetwork
resolution	resolution for community algorithm
gamma	gamma
omega	omega
python_path	specify specific path to python if required
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
return_gobject	boolean: return giotto object (default = TRUE)
verbose	verbose

Details

This function performs subclustering using the Louvain algorithm on selected clusters. The systematic steps are:

- 1. subset Giotto object
- 2. identify highly variable genes
- 3. run PCA
- 4. create nearest neighbouring network
- 5. do Louvain clustering

Value

giotto object with new subclusters appended to cell metadata

See Also

doLouvainCluster_multinet and doLouvainCluster_community

doRandomWalkCluster *doRandomWalkCluster*

Description

Cluster cells using a random walk approach.

Usage

```
doRandomWalkCluster(
  gobject,
  name = "random_walk_clus",
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  walk_steps = 4,
  walk_clusters = 10,
  walk_weights = NA,
  return_gobject = TRUE,
  set_seed = F,
  seed_number = 1234
)
```

Arguments

gobject	giotto object
name	name for cluster
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
walk_steps	number of walking steps
walk_clusters	number of final clusters
walk_weights	cluster column defining the walk weights
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

Details

See cluster_walktrap function from the igraph package in R for more information.

Value

giotto object with new clusters appended to cell metadata

doSNNCluster *doSNNCluster*

Description

Cluster cells using a SNN cluster approach.

Usage

```
doSNNCluster(
  gobject,
  name = "sNN_clus",
  nn_network_to_use = "kNN",
  network_name = "kNN.pca",
  k = 20,
  eps = 4,
  minPts = 16,
  borderPoints = TRUE,
  return_gobject = TRUE,
  set_seed = F,
  seed_number = 1234
)
```

Arguments

gobject	giotto object
name	name for cluster
nn_network_to_use	type of NN network to use (only works on kNN)
network_name	name of kNN network to use
k	Neighborhood size for nearest neighbor sparsification to create the shared NN graph.
eps	Two objects are only reachable from each other if they share at least eps nearest neighbors.
minPts	minimum number of points that share at least eps nearest neighbors for a point to be considered a core points.
borderPoints	should borderPoints be assigned to clusters like in DBSCAN?
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

Details

See sNNclust from dbscan package

Value

giotto object with new clusters appended to cell metadata

`estimateImageBg` *estimateImageBg*

Description

helps to estimate which color is the background color of your plot

Usage

```
estimateImageBg(mg_object, top_color_range = 1:50)
```

Arguments

`mg_object`	magick image or Giotto image object
`top_color_range`	top possible background colors to return

Value

vector of pixel color frequencies and an associated barplot

`exportGiottoViewer` *exportGiottoViewer*

Description

compute highly variable genes

Usage

```
exportGiottoViewer(
  gobject,
  output_directory = NULL,
  spat_enr_names = NULL,
  factor_annotations = NULL,
  numeric_annotations = NULL,
  dim_reductions,
  dim_reduction_names,
  expression_values = c("scaled", "normalized", "custom"),
  dim_red_rounding = NULL,
  dim_red_rescale = c(-20, 20),
  expression_rounding = 2,
  overwrite_dir = T,
  verbose = T
)
```

Arguments

gobject	giotto object
output_directory	directory where to save the files
spat_enr_names	spatial enrichment results to include for annotations
factor_annotations	giotto cell annotations to view as factor
numeric_annotations	giotto cell annotations to view as numeric
dim_reductions	high level dimension reductions to view
dim_reduction_names	specific dimension reduction names
expression_values	expression values to use in Viewer
dim_red_rounding	numerical indicating how to round the coordinates
dim_red_rescale	numericals to rescale the coordinates
expression_rounding	numerical indicating how to round the expression data
overwrite_dir	overwrite files in the directory if it already existed
verbose	be verbose

Details

Giotto Viewer expects the results from Giotto Analyzer in a specific format, which is provided by this function. To include enrichment results from createSpatialEnrich include the provided spatial enrichment name (default PAGE or rank) and add the gene signature names (.e.g cell types) to the numeric annotations parameter.

Value

writes the necessary output to use in Giotto Viewer

Examples

```
## Not run:

data(mini_giotto_single_cell)
exportGiottoViewer(mini_giotto_single_cell)


## End(Not run)
```

exprCellCellcom *exprCellCellcom*

Description

Cell-Cell communication scores based on expression only

Usage

```
exprCellCellcom(
  gobject,
  cluster_column = "cell_types",
  random_iter = 1000,
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  detailed = FALSE,
  adjust_method = c("fdr", "bonferroni", "BH", "holm", "hochberg", "hommel", "BY",
    "none"),
  adjust_target = c("genes", "cells"),
  set_seed = TRUE,
  seed_number = 1234,
  verbose = T
)
```

Arguments

gobject	giotto object to use
cluster_column	cluster column with cell type information
random_iter	number of iterations
gene_set_1	first specific gene set from gene pairs
gene_set_2	second specific gene set from gene pairs
log2FC_addendum	addendum to add when calculating log2FC
detailed	provide more detailed information (random variance and z-score)
adjust_method	which method to adjust p-values
adjust_target	adjust multiple hypotheses at the cell or gene level
set_seed	set seed for random simulations (default = TRUE)
seed_number	seed number
verbose	verbose

Details

Statistical framework to identify if pairs of genes (such as ligand-receptor combinations) are expressed at higher levels than expected based on a reshuffled null distribution of gene expression values, without considering the spatial position of cells. More details will follow soon.

Value

Cell-Cell communication scores for gene pairs based on expression only

fDataDT *fDataDT*

Description

show gene metadata

Usage

```
fDataDT(gobject, feat_type = NULL)
```

Arguments

gobject	giotto object
feat_type	feature type

Value

data.table with gene metadata

Examples

```
data(mini_giotto_single_cell) # loads existing Giotto object
fDataDT(mini_giotto_single_cell)
```

filterCombinations *filterCombinations*

Description

Shows how many genes and cells are lost with combinations of thresholds.

Usage

```
filterCombinations(
  gobject,
  expression_values = c("raw", "normalized", "scaled", "custom"),
  expression_thresholds = c(1, 2),
  gene_det_in_min_cells = c(5, 50),
  min_det_genes_per_cell = c(200, 400),
  scale_x_axis = "identity",
  x_axis_offset = 0,
  scale_y_axis = "identity",
  y_axis_offset = 0,
  show_plot = TRUE,
  return_plot = FALSE,
  save_plot = NA,
  save_param = list(),
  default_save_name = "filterCombinations"
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
expression_thresholds	all thresholds to consider a gene expressed
gene_det_in_min_cells	minimum number of cells that should express a gene to consider that gene further
min_det_genes_per_cell	minimum number of expressed genes per cell to consider that cell further
scale_x_axis	ggplot transformation for x-axis (e.g. log2)
x_axis_offset	x-axis offset to be used together with the scaling transformation
scale_y_axis	ggplot transformation for y-axis (e.g. log2)
y_axis_offset	y-axis offset to be used together with the scaling transformation
show_plot	show plot
return_plot	return only ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Creates a scatterplot that visualizes the number of genes and cells that are lost with a specific combination of a gene and cell threshold given an arbitrary cutoff to call a gene expressed. This function can be used to make an informed decision at the filtering step with filterGiotto.

Value

list of data.table and ggplot object

Examples

```
data(mini_giotto_single_cell)

# assess the effect of multiple filter criteria
filterCombinations(mini_giotto_single_cell,
gene_det_in_min_cells = c(2, 4, 8),
min_det_genes_per_cell = c(5, 10, 20))
```

filterCPG *filterCPG*

Description

Filter Interaction Changed Gene scores.

Usage

```
filterCPG(...)
```

Arguments

...	Arguments passed on to filterICF
	cpgObject ICF (interaction changed feature) score object
	min_cells minimum number of source cell type
	min_cells_expr minimum expression level for source cell type
	min_int_cells minimum number of interacting neighbor cell type
	min_int_cells_expr minimum expression level for interacting neighbor cell type
	min_fdr minimum adjusted p-value
	min_spat_diff minimum absolute spatial expression difference
	min_log2_fc minimum log2 fold-change
	min_zscore minimum z-score change
	zscores_column calculate z-scores over cell types or features
	direction differential expression directions to keep

See Also

filterICF

filterDistributions *filterDistributions*

Description

show gene or cell distribution after filtering on expression threshold

Usage

```
filterDistributions(
  gobject,
  expression_values = c("raw", "normalized", "scaled", "custom"),
  expression_threshold = 1,
  detection = c("genes", "cells"),
  plot_type = c("histogram", "violin"),
  nr_bins = 30,
  fill_color = "lightblue",
```

```
  scale_axis = "identity",
  axis_offset = 0,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "filterDistributions"
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
expression_threshold	threshold to consider a gene expressed
detection	consider genes or cells
plot_type	type of plot
nr_bins	number of bins for histogram plot
fill_color	fill color for plots
scale_axis	ggplot transformation for axis (e.g. log2)
axis_offset	offset to be used together with the scaling transformation
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot object

Examples

```
data(mini_giotto_single_cell)

# distribution plot of genes
filterDistributions(mini_giotto_single_cell, detection = 'genes')

# distribution plot of cells
filterDistributions(mini_giotto_single_cell, detection = 'cells')
```

`filterGiotto` *filterGiotto*

Description

filter Giotto object based on expression threshold

Usage

```
filterGiotto(
  gobject,
  feat_type = NULL,
  expression_values = c("raw", "normalized", "scaled", "custom"),
  expression_threshold = 1,
  feat_det_in_min_cells = 100,
  gene_det_in_min_cells = NULL,
  min_det_feats_per_cell = 100,
  min_det_genes_per_cell = NULL,
  verbose = F
)
```

Arguments

`gobject`	giotto object
`feat_type`	feature type
`expression_values`	expression values to use
`expression_threshold`	threshold to consider a gene expressed
`feat_det_in_min_cells`	minimum # of cells that need to express a feature
`gene_det_in_min_cells`	deprecated, use feat_det_in_min_cells
`min_det_feats_per_cell`	minimum # of features that need to be detected in a cell
`min_det_genes_per_cell`	deprecated, use min_det_genes_per_cell
`verbose`	verbose

Details

The function `filterCombinations` can be used to explore the effect of different parameter values.

Value

giotto object

findCPG *findCPG*

Description

Identifies cell-to-cell Interaction Changed Genes (ICG), i.e. genes that are differentially expressed due to proximity to other cell types.

Usage

```
findCPG(...)
```

Arguments

...	Arguments passed on to findICF
	gobject giotto object
	feat_type feature type
	expression_values expression values to use
	selected_feats subset of selected features (optional)
	cluster_column name of column to use for cell types
	spatial_network_name name of spatial network to use
	minimum_unique_cells minimum number of target cells required
	minimum_unique_int_cells minimum number of interacting cells required
	diff_test which differential expression test
	mean_method method to use to calculate the mean
	offset offset value to use when calculating log2 ratio
	adjust_method which method to adjust p-values
	nr_permutations number of permutations if diff_test = permutation
	exclude_selected_cells_from_test exclude interacting cells other cells
	do_parallel run calculations in parallel with mclapply
	cores number of cores to use if do_parallel = TRUE
	set_seed set a seed for reproducibility
	seed_number seed number

See Also

findICF

`findGiniMarkers` *findGiniMarkers*

Description

Identify marker genes for selected clusters based on gini detection and expression scores.

Usage

```
findGiniMarkers(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  subset_clusters = NULL,
  group_1 = NULL,
  group_2 = NULL,
  min_expr_gini_score = 0.2,
  min_det_gini_score = 0.2,
  detection_threshold = 0,
  rank_score = 1,
  min_genes = 5
)
```

Arguments

`gobject`	giotto object
`expression_values`	gene expression values to use
`cluster_column`	clusters to use
`subset_clusters`	selection of clusters to compare
`group_1`	group 1 cluster IDs from cluster_column for pairwise comparison
`group_2`	group 2 cluster IDs from cluster_column for pairwise comparison
`min_expr_gini_score`	filter on minimum gini coefficient for expression
`min_det_gini_score`	filter on minimum gini coefficient for detection
`detection_threshold`	detection threshold for gene expression
`rank_score`	rank scores for both detection and expression to include
`min_genes`	minimum number of top genes to return

Details

Detection of marker genes using the https://en.wikipedia.org/wiki/Gini_coefficientgini coefficient is based on the following steps/principles per gene:

- 1. calculate average expression per cluster
- 2. calculate detection fraction per cluster

- 3. calculate gini-coefficient for av. expression values over all clusters
- 4. calculate gini-coefficient for detection fractions over all clusters
- 5. convert gini-scores to rank scores
- 6. for each gene create combined score = detection rank x expression rank x expr gini-coefficient x detection gini-coefficient
- 7. for each gene sort on expression and detection rank and combined score

As a results "top gini" genes are genes that are very selectivily expressed in a specific cluster, however not always expressed in all cells of that cluster. In other words highly specific, but not necessarily sensitive at the single-cell level.

To perform differential expression between cluster groups you need to specificy cluster IDs to the parameters *group_1* and *group_2*.

Value

data.table with marker genes

Examples

```
data(mini_giotto_single_cell)

gini_markers = findGiniMarkers(gobject = mini_giotto_single_cell,
                               cluster_column = 'leiden_clus',
                               group_1 = 1,
                               group_2 = 2)
```

`findGiniMarkers_one_vs_all`

findGiniMarkers_one_vs_all

Description

Identify marker genes for all clusters in a one vs all manner based on gini detection and expression scores.

Usage

```
findGiniMarkers_one_vs_all(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  subset_clusters = NULL,
  min_expr_gini_score = 0.5,
  min_det_gini_score = 0.5,
  detection_threshold = 0,
  rank_score = 1,
  min_genes = 4,
  verbose = TRUE
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
cluster_column	clusters to use
subset_clusters	selection of clusters to compare
min_expr_gini_score	filter on minimum gini coefficient on expression
min_det_gini_score	filter on minimum gini coefficient on detection
detection_threshold	detection threshold for gene expression
rank_score	rank scores for both detection and expression to include
min_genes	minimum number of top genes to return
verbose	be verbose

Value

data.table with marker genes

See Also

findGiniMarkers

Examples

```
data(mini_giotto_single_cell)

gini_markers = findGiniMarkers_one_vs_all(gobject = mini_giotto_single_cell,
                                          cluster_column = 'leiden_clus')
```

---

findICG *findICG*

Description

Identifies cell-to-cell Interaction Changed Genes (ICG), i.e. genes that are differentially expressed due to proximity to other cell types.

Usage

```
findICG(
  gobject,
  expression_values = "normalized",
  selected_genes = NULL,
  cluster_column,
  spatial_network_name = "Delaunay_network",
```

```
  minimum_unique_cells = 1,
  minimum_unique_int_cells = 1,
  diff_test = c("permutation", "limma", "t.test", "wilcox"),
  mean_method = c("arithmic", "geometric"),
  offset = 0.1,
  adjust_method = c("bonferroni", "BH", "holm", "hochberg", "hommel", "BY", "fdr",
    "none"),
  nr_permutations = 100,
  exclude_selected_cells_from_test = T,
  do_parallel = TRUE,
  cores = NA,
  set_seed = TRUE,
  seed_number = 1234
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
selected_genes	subset of selected genes (optional)
cluster_column	name of column to use for cell types
spatial_network_name	name of spatial network to use
minimum_unique_cells	minimum number of target cells required
minimum_unique_int_cells	minimum number of interacting cells required
diff_test	which differential expression test
mean_method	method to use to calculate the mean
offset	offset value to use when calculating log2 ratio
adjust_method	which method to adjust p-values
nr_permutations	number of permutations if diff_test = permutation
exclude_selected_cells_from_test	exclude interacting cells other cells
do_parallel	run calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
set_seed	set a seed for reproducibility
seed_number	seed number

Details

Function to calculate if genes are differentially expressed in cell types when they interact (approximated by physical proximity) with other cell types. The results data.table in the cpgObject contains - at least - the following columns:

- genes: All or selected list of tested genes
- sel: average gene expression in the interacting cells from the target cell type

- other: average gene expression in the NOT-interacting cells from the target cell type
- log2fc: log2 fold-change between sel and other
- diff: spatial expression difference between sel and other
- p.value: associated p-value
- p.adj: adjusted p-value
- cell_type: target cell type
- int_cell_type: interacting cell type
- nr_select: number of cells for selected target cell type
- int_nr_select: number of cells for interacting cell type
- nr_other: number of other cells of selected target cell type
- int_nr_other: number of other cells for interacting cell type
- unif_int: cell-cell interaction

Value

cpgObject that contains the differential gene scores

See Also

findICF

`findMarkers` *findMarkers*

Description

Identify marker genes for selected clusters.

Usage

```
findMarkers(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column = NULL,
  method = c("scran", "gini", "mast"),
  subset_clusters = NULL,
  group_1 = NULL,
  group_2 = NULL,
  min_expr_gini_score = 0.5,
  min_det_gini_score = 0.5,
  detection_threshold = 0,
  rank_score = 1,
  min_genes = 4,
  group_1_name = NULL,
  group_2_name = NULL,
  adjust_columns = NULL,
  ...
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
cluster_column	clusters to use
method	method to use to detect differentially expressed genes
subset_clusters	selection of clusters to compare
group_1	group 1 cluster IDs from cluster_column for pairwise comparison
group_2	group 2 cluster IDs from cluster_column for pairwise comparison
min_expr_gini_score	gini: filter on minimum gini coefficient for expression
min_det_gini_score	gini: filter minimum gini coefficient for detection
detection_threshold	gini: detection threshold for gene expression
rank_score	gini: rank scores to include
min_genes	minimum number of top genes to return (for gini)
group_1_name	mast: custom name for group_1 clusters
group_2_name	mast: custom name for group_2 clusters
adjust_columns	mast: column in pDataDT to adjust for (e.g. detection rate)
...	additional parameters for the findMarkers function in scran or zlm function in MAST

Details

Wrapper for all individual functions to detect marker genes for clusters.

Value

data.table with marker genes

See Also

findScranMarkers, findGiniMarkers and findMastMarkers

---

findMarkers_one_vs_all

findMarkers_one_vs_all

Description

Identify marker genes for all clusters in a one vs all manner.

Usage

```
findMarkers_one_vs_all(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  subset_clusters = NULL,
  method = c("scran", "gini", "mast"),
  pval = 0.01,
  logFC = 0.5,
  min_genes = 10,
  min_expr_gini_score = 0.5,
  min_det_gini_score = 0.5,
  detection_threshold = 0,
  rank_score = 1,
  adjust_columns = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
cluster_column	clusters to use
subset_clusters	selection of clusters to compare
method	method to use to detect differentially expressed genes
pval	scran & mast: filter on minimal p-value
logFC	scan & mast: filter on logFC
min_genes	minimum genes to keep per cluster, overrides pval and logFC
min_expr_gini_score	gini: filter on minimum gini coefficient for expression
min_det_gini_score	gini: filter minimum gini coefficient for detection
detection_threshold	gini: detection threshold for gene expression
rank_score	gini: rank scores to include
adjust_columns	mast: column in pDataDT to adjust for (e.g. detection rate)
verbose	be verbose
...	additional parameters for the findMarkers function in scran or zlm function in MAST

Details

Wrapper for all one vs all functions to detect marker genes for clusters.

Value

data.table with marker genes

See Also

findScranMarkers_one_vs_all, findGiniMarkers_one_vs_all and findMastMarkers_one_vs_all

---

findMastMarkers *findMastMarkers*

Description

Identify marker genes for selected clusters based on the MAST package.

Usage

```
findMastMarkers(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  group_1 = NULL,
  group_1_name = NULL,
  group_2 = NULL,
  group_2_name = NULL,
  adjust_columns = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
cluster_column	clusters to use
group_1	group 1 cluster IDs from cluster_column for pairwise comparison
group_1_name	custom name for group_1 clusters
group_2	group 2 cluster IDs from cluster_column for pairwise comparison
group_2_name	custom name for group_2 clusters
adjust_columns	column in pDataDT to adjust for (e.g. detection rate)
verbose	be verbose
...	additional parameters for the zlm function in MAST

Details

This is a minimal convenience wrapper around the zlm from the MAST package to detect differentially expressed genes. Caution: with large datasets MAST might take a long time to run and finish

Value

data.table with marker genes

Examples

```
## Not run:
data(mini_giotto_single_cell)

mast_markers = findMastMarkers(gobject = mini_giotto_single_cell,
                               cluster_column = 'leiden_clus',
                               group_1 = 1,
                               group_2 = 2)

## End(Not run)
```

`findMastMarkers_one_vs_all` *findMastMarkers_one_vs_all*

Description

Identify marker genes for all clusters in a one vs all manner based on the MAST package.

Usage

```
findMastMarkers_one_vs_all(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  subset_clusters = NULL,
  adjust_columns = NULL,
  pval = 0.001,
  logFC = 1,
  min_genes = 10,
  verbose = TRUE,
  ...
)
```

Arguments

`gobject`	giotto object
`expression_values`	gene expression values to use
`cluster_column`	clusters to use
`subset_clusters`	selection of clusters to compare
`adjust_columns`	column in pDataDT to adjust for (e.g. detection rate)
`pval`	filter on minimal p-value
`logFC`	filter on logFC
`min_genes`	minimum genes to keep per cluster, overrides pval and logFC
`verbose`	be verbose
`...`	additional parameters for the zlm function in MAST

Value

data.table with marker genes

See Also

findMastMarkers

Examples

```
data(mini_giotto_single_cell)

mast_markers = findMastMarkers_one_vs_all(gobject = mini_giotto_single_cell,
                                          cluster_column = 'leiden_clus')
```

---

findNetworkNeighbors *findNetworkNeighbors*

Description

Find the spatial neighbors for a selected group of cells within the selected spatial network.

Usage

```
findNetworkNeighbors(
  gobject,
  spatial_network_name,
  source_cell_ids = NULL,
  name = "nb_cells"
)
```

Arguments

gobject	Giotto object
spatial_network_name	name of spatial network
source_cell_ids	cell ids for which you want to know the spatial neighbors
name	name of the results

Value

data.table

Examples

```
data(mini_giotto_single_cell)

# get all cells
all_cells = slot(mini_giotto_single_cell, 'cell_ID')

# find all the spatial neighbours for the first 5 cells
# within the Delaunay network
findNetworkNeighbors(mini_giotto_single_cell,
                     spatial_network_name = 'Delaunay_network',
                     source_cell_ids = all_cells[1:5])
```

`findScranMarkers` *findScranMarkers*

Description

Identify marker genes for all or selected clusters based on scran's implementation of findMarkers.

Usage

```
findScranMarkers(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  subset_clusters = NULL,
  group_1 = NULL,
  group_2 = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

`gobject`	giotto object
`expression_values`	gene expression values to use
`cluster_column`	clusters to use
`subset_clusters`	selection of clusters to compare
`group_1`	group 1 cluster IDs from cluster_column for pairwise comparison
`group_2`	group 2 cluster IDs from cluster_column for pairwise comparison
`verbose`	be verbose (default = FALSE)
`...`	additional parameters for the findMarkers function in scran

Details

This is a minimal convenience wrapper around the `findMarkers` function from the scran package.

To perform differential expression between cluster groups you need to specificy cluster IDs to the parameters *group_1* and *group_2*.

Value

data.table with marker genes

Examples

```
data(mini_giotto_single_cell)

scran_markers = findScranMarkers(gobject = mini_giotto_single_cell,
                                 cluster_column = 'leiden_clus',
                                 group_1 = 1,
                                 group_2 = 2)
```

---

findScranMarkers_one_vs_all

findScranMarkers_one_vs_all

Description

Identify marker genes for all clusters in a one vs all manner based on scran's implementation of findMarkers.

Usage

```
findScranMarkers_one_vs_all(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  subset_clusters = NULL,
  pval = 0.01,
  logFC = 0.5,
  min_genes = 10,
  verbose = TRUE,
  ...
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
cluster_column	clusters to use
subset_clusters	subset of clusters to use
pval	filter on minimal p-value
logFC	filter on logFC
min_genes	minimum genes to keep per cluster, overrides pval and logFC
verbose	be verbose
...	additional parameters for the findMarkers function in scran

Value

data.table with marker genes

See Also

findScranMarkers

Examples

```
data(mini_giotto_single_cell)

scran_markers = findScranMarkers_one_vs_all(gobject = mini_giotto_single_cell,
                                            cluster_column = 'leiden_clus')
```

`get10Xmatrix` *get10Xmatrix*

Description

This function creates an expression matrix from a 10X structured folder

Usage

```
get10Xmatrix(path_to_data, gene_column_index = 1)
```

Arguments

`path_to_data`	path to the 10X folder
`gene_column_index`	which column from the features or genes .tsv file to use for row ids

Details

A typical 10X folder is named raw_feature_bc_matrix or raw_feature_bc_matrix and it has 3 files:

- barcodes.tsv(.gz)
- features.tsv(.gz) or genes.tsv(.gz)
- matrix.mtx(.gz)

By default the first column of the features or genes .tsv file will be used, however if multiple annotations are provided (e.g. ensembl gene ids and gene symbols) the user can select another column.

Value

sparse expression matrix from 10X

get10Xmatrix_h5 *get10Xmatrix_h5*

Description

This function creates an expression matrix from a 10X h5 file path

Usage

```
get10Xmatrix_h5(path_to_data, gene_ids = c("symbols", "ensembl"))
```

Arguments

path_to_data	path to the 10X .h5 file
gene_ids	use gene symbols (default) or ensembl ids for the gene expression matrix

Details

If the .h5 10x file has multiple modalities (e.g. RNA and protein), multiple matrices will be returned

Value

(list of) sparse expression matrix from 10X

getClusterSimilarity *getClusterSimilarity*

Description

Creates data.table with pairwise correlation scores between each cluster.

Usage

```
getClusterSimilarity(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  cor = c("pearson", "spearman")
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
cluster_column	name of column to use for clusters
cor	correlation score to calculate distance

Details

Creates data.table with pairwise correlation scores between each cluster and the group size (# of cells) for each cluster. This information can be used together with mergeClusters to combine very similar or small clusters into bigger clusters.

Value

data.table

Examples

```
data("mini_giotto_single_cell")

cluster_similarities = getClusterSimilarity(mini_giotto_single_cell,
                                            cluster_column = 'leiden_clus')
```

---

getDendrogramSplits *getDendrogramSplits*

Description

Split dendrogram at each node and keep the leave (label) information..

Usage

```
getDendrogramSplits(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  cor = c("pearson", "spearman"),
  distance = "ward.D",
  h = NULL,
  h_color = "red",
  show_dend = TRUE,
  verbose = TRUE
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
cluster_column	name of column to use for clusters
cor	correlation score to calculate distance
distance	distance method to use for hierarchical clustering
h	height of horizontal lines to plot
h_color	color of horizontal lines
show_dend	show dendrogram
verbose	be verbose

Details

Creates a data.table with three columns and each row represents a node in the dendrogram. For each node the height of the node is given together with the two subdendrograms. This information can be used to determine in a hierarchical manner differentially expressed marker genes at each node.

Value

data.table object

Examples

```
data("mini_giotto_single_cell")

splits = getDendrogramSplits(mini_giotto_single_cell, cluster_column = 'leiden_clus')
```

---

getDistinctColors *getDistinctColors*

Description

Returns a number of distint colors based on the RGB scale

Usage

```
getDistinctColors(n)
```

Arguments

n	number of colors wanted

Value

number of distinct colors

---

getGiottoImage *getGiottoImage*

Description

get get a giotto image from a giotto object

Usage

```
getGiottoImage(gobject, image_name)
```

Arguments

gobject	giotto object
image_name	name of giotto image showGiottoImageNames

Value

a giotto image

`getSpatialDataset` *getSpatialDataset*

Description

This package will automatically download the spatial locations and expression matrix for the chosen dataset. These files are already in the right format to create a Giotto object. If wget is installed on your machine, you can add 'method = wget' to the parameters to download files faster.

Usage

```
getSpatialDataset(
 dataset = c("ST_OB1", "ST_OB2", "codex_spleen", "cycif_PDAC", "starmap_3D_cortex",
    "osmfish_SS_cortex", "merfish_preoptic", "seqfish_SS_cortex", "seqfish_OB",
    "slideseq_cerebellum"),
  directory = getwd(),
  ...
)
```

Arguments

`dataset`	dataset to download
`directory`	directory to save the data to
`...`	additional parameters to `download.file`

`giotto-class` *S4 giotto Class*

Description

Framework of giotto object to store and work with spatial expression data

Details

[**expression**] There are several ways to provide expression information:

[**expression_feat**] The different featurs or modalities such as rna, protein, metabolites, ... that are provided in the expression slot.

Slots

`expression` expression information

`expression_feat` available features (e.g. rna, protein, ...)

`spatial_locs` spatial location coordinates for cells

`spatial_info` information about spatial units

`cell_metadata` metadata for cells

`feat_metadata` metadata for available features

`feat_info` information about features

`cell_ID` unique cell IDs

`feat_ID` unique feature IDs for all features or modalities

`spatial_network` spatial network in data.table/data.frame format

`spatial_grid` spatial grid in data.table/data.frame format

`spatial_enrichment` slot to save spatial enrichment-like results

`dimension_reduction` slot to save dimension reduction coordinates

`nn_network` nearest neighbor network in igraph format

`images` slot to store giotto images

`parameters` slot to save parameters that have been used

`instructions` slot for global function instructions

`offset_file` offset file used to stitch together image fields

`OS_platform` Operating System to run Giotto analysis on

`hyperGeometricEnrich` *hyperGeometricEnrich*

Description

Function to calculate gene signature enrichment scores per spatial position using a hypergeometric test.

Usage

```
hyperGeometricEnrich(...)
```

Arguments

`...`	Arguments passed on to `runHyperGeometricEnrich` `gobject` Giotto object `sign_matrix` Matrix of signature genes for each cell type / process `expression_values` expression values to use `reverse_log_scale` reverse expression values from log scale `logbase` log base to use if reverse_log_scale = TRUE `top_percentage` percentage of cells that will be considered to have gene expression with matrix binarization `output_enrichment` how to return enrichment output `p_value` calculate p-values (boolean, default = FALSE) `name` to give to spatial enrichment results, default = rank `return_gobject` return giotto object

See Also

runHyperGeometricEnrich

---

insertCrossSectionGenePlot3D *insertCrossSectionGenePlot3D*

Description

Visualize cells and gene expression in a virtual cross section according to spatial coordinates

Usage

```
insertCrossSectionGenePlot3D(
  gobject,
  crossSection_obj = NULL,
  name = NULL,
  spatial_network_name = "Delaunay_network",
  mesh_grid_color = "#1f77b4",
  mesh_grid_width = 3,
  mesh_grid_style = "dot",
  sdimx = "sdimx",
  sdimy = "sdimy",
  sdimz = "sdimz",
  show_other_cells = F,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatGenePlot3D_with_cross_section",
  ...
)
```

Arguments

gobject	giotto object
crossSection_obj	cross section object as alternative input. default = NULL.
name	name of virtual cross section to use
spatial_network_name	name of spatial network to use
mesh_grid_color	color for the meshgrid lines
mesh_grid_width	width for the meshgrid lines
mesh_grid_style	style for the meshgrid lines

sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimy')
show_other_cells	display not selected cells
axis_scale	axis_scale
custom_ratio	custom_ratio
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for spatGenePlot3D

Details

Description of parameters.

Value

ggplot

`insertCrossSectionSpatPlot3D` *insertCrossSectionSpatPlot3D*

Description

Visualize the meshgrid lines of cross section together with cells

Usage

```
insertCrossSectionSpatPlot3D(
  gobject,
  crossSection_obj = NULL,
  name = NULL,
  spatial_network_name = "Delaunay_network",
  mesh_grid_color = "#1f77b4",
  mesh_grid_width = 3,
  mesh_grid_style = "dot",
  sdimx = "sdimx",
  sdimy = "sdimy",
  sdimz = "sdimz",
  show_other_cells = F,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  default_save_name = "spat3D_with_cross_section",
  ...
)
```

Arguments

gobject	giotto object
crossSection_obj	cross section object as alternative input. default = NULL.
name	name of virtual cross section to use
spatial_network_name	name of spatial network to use
mesh_grid_color	color for the meshgrid lines
mesh_grid_width	width for the meshgrid lines
mesh_grid_style	style for the meshgrid lines
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimy')
show_other_cells	display not selected cells
axis_scale	axis_scale
custom_ratio	custom_ratio
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for spatPlot3D

Details

Description of parameters.

Value

ggplot

---

installGiottoEnvironment *installGiottoEnvironment*

Description

Installs a giotto environment

Usage

```
installGiottoEnvironment(
  packages_to_install = c("pandas", "networkx", "python-igraph", "leidenalg",
    "python-louvain", "python.app", "scikit-learn"),
  force_miniconda = FALSE,
  force_environment = FALSE,
  verbose = TRUE
)
```

Arguments

packages_to_install	all python modules (packages) that should be installed for Giotto to work
force_miniconda	force reinstallation of miniconda
force_environment	force reinstallation of the giotto environment
verbose	be verbose

Details

This function will install a local giotto environment using the miniconda system as implemented by reticulate. Once this giotto environment is installed it will be automatically detected when you run the Giotto toolbox. If you want to use your own python path then you can set the python_path in the createGiottoInstructions and provide the instructions to the createGiottoObject function.

Value

installs a giotto environment using the reticulate miniconda system

Examples

```
## Not run:

  # this command will install r-miniconda
  # and a giotto environment with all necessary python modules
  installGiottoEnvironment()

## End(Not run)
```

---

jackstrawPlot *jackstrawPlot*

Description

identify significant prinicipal components (PCs)

Usage

```
jackstrawPlot(
  gobject,
  feat_type = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "feats"),
  feats_to_use = NULL,
  genes_to_use = NULL,
  center = FALSE,
  scale_unit = FALSE,
  ncp = 20,
  ylim = c(0, 1),
```

```
  iter = 10,
  threshold = 0.01,
  verbose = TRUE,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "jackstrawPlot"
)
```

Arguments

gobject	giotto object
feat_type	feature type
expression_values	expression values to use
reduction	cells or genes
feats_to_use	subset of features to use for PCA
genes_to_use	deprecated, use feats_to_use
center	center data before PCA
scale_unit	scale features before PCA
ncp	number of principal components to calculate
ylim	y-axis limits on jackstraw plot
iter	number of interations for jackstraw
threshold	p-value threshold to call a PC significant
verbose	show progress of jackstraw method
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function()
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

The Jackstraw method uses the permutationPA function. By systematically permuting genes it identifies robust, and thus significant, PCs.

Value

ggplot object for jackstraw method

Examples

```
data(mini_giotto_single_cell)

# jackstraw package is required to run
jackstrawPlot(mini_giotto_single_cell, ncp = 10)
```

`loadHMRF` *loadHMRF*

Description

load previous HMRF

Usage

```
loadHMRF(
  name_used = "test",
  output_folder_used,
  k_used = 10,
  betas_used,
  python_path_used
)
```

Arguments

`name_used`	name of HMRF that was run
`output_folder_used`	output folder that was used
`k_used`	number of HMRF domains that was tested
`betas_used`	betas that were tested
`python_path_used`	python path that was used

Details

Description of HMRF parameters ...

Value

reloads a previous ran HMRF from doHRMF

makeSignMatrixPAGE *makeSignMatrixPAGE*

Description

Function to convert a list of signature genes (e.g. for cell types or processes) into a binary matrix format that can be used with the PAGE enrichment option. Each cell type or process should have a vector of cell-type or process specific genes. These vectors need to be combined into a list (sign_list). The names of the cell types or processes that are provided in the list need to be given (sign_names).

Usage

```
makeSignMatrixPAGE(sign_names, sign_list)
```

Arguments

sign_names	vector with names for each provided gene signature
sign_list	list of genes (signature)

Value

matrix

See Also

PAGEEnrich

makeSignMatrixRank *makeSignMatrixRank*

Description

Function to convert a single-cell count matrix and a corresponding single-cell cluster vector into a rank matrix that can be used with the Rank enrichment option.

Usage

```
makeSignMatrixRank(
  sc_matrix,
  sc_cluster_ids,
  ties_method = c("random", "max"),
  gobject = NULL
)
```

Arguments

sc_matrix	matrix of single-cell RNAseq expression data
sc_cluster_ids	vector of cluster ids
ties_method	how to handle rank ties
gobject	if giotto object is given then only genes present in both datasets will be considered

Value

matrix

See Also

rankEnrich

---

mean_giotto *mean_giotto*

Description

mean function that works with multiple matrix representations

Usage

```
mean_giotto(x, ...)
```

Arguments

x	vector
...	additional parameters

Value

numeric

---

mergeClusters *mergeClusters*

Description

Merge selected clusters based on pairwise correlation scores and size of cluster.

Usage

```
mergeClusters(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  cor = c("pearson", "spearman"),
  new_cluster_name = "merged_cluster",
  min_cor_score = 0.8,
  max_group_size = 20,
  force_min_group_size = 10,
  max_sim_clusters = 10,
  return_gobject = TRUE,
  verbose = TRUE
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
cluster_column	name of column to use for clusters
cor	correlation score to calculate distance
new_cluster_name	new name for merged clusters
min_cor_score	min correlation score to merge pairwise clusters
max_group_size	max cluster size that can be merged
force_min_group_size	size of clusters that will be merged with their most similar neighbor(s)
max_sim_clusters	maximum number of clusters to potentially merge to reach force_min_group_size
return_gobject	return giotto object
verbose	be verbose

Details

Merge selected clusters based on pairwise correlation scores and size of cluster. To avoid large clusters to merge the max_group_size can be lowered. Small clusters can be forcibly merged with their most similar pairwise cluster by adjusting the force_min_group_size parameter. Clusters smaller than this value will be merged independent on the provided min_cor_score value. The force_min_group_size might not always be reached if clusters have already been merged before
A giotto object is returned by default, if FALSE then the merging vector will be returned.

Value

Giotto object

Examples

```
data("mini_giotto_single_cell")

pDataDT(mini_giotto_single_cell)
mini_giotto_single_cell = mergeClusters(mini_giotto_single_cell,
                                        cluster_column = 'leiden_clus',
                                        min_cor_score = 0.7,
                                        force_min_group_size = 4)
pDataDT(mini_giotto_single_cell)
plotUMAP_2D(mini_giotto_single_cell, cell_color = 'merged_cluster', point_size = 3)
```

---

mini_giotto_3D *mini Giotto object for spatial single-cell 3D data*

Description

Mini Giotto object created from the STARmap data.

Usage

```
data(mini_giotto_3D)
```

Format

An object of class "giotto"; see createGiottoObject.

References

Wang et al. (2018) Science (PubMed)

Examples

```
data(mini_giotto_3D)

## Not run: spatPlot3D(mini_giotto_3D, cell_color = 'cell_types', point_size = 5)
```

---

mini_giotto_multi_cell *mini Giotto object for spatial multi-cell resolution data*

Description

Mini Giotto object created from the Brain Visium 10X data.

Usage

```
data(mini_giotto_multi_cell)
```

Format

An object of class "giotto"; see createGiottoObject.

References

10 Genomics Visium technology (10xgenomics)

Examples

```
data(mini_giotto_multi_cell)

## Not run: spatPlot(mini_giotto_multi_cell, cell_color = 'cell_types', point_size = 5)
```

---

mini_giotto_single_cell

mini Giotto object for spatial single-cell resolution data

Description

Mini Giotto object created from the seqFISH+ data.

Usage

```
data(mini_giotto_single_cell)
```

Format

An object of class "giotto"; see createGiottoObject.

References

Eng et al. (2019) Nature (PubMed)

Examples

```
data(mini_giotto_single_cell)

## Not run: spatPlot2D(mini_giotto_single_cell,cell_color = 'cell_types', point_size = 5)
```

normalizeGiotto *normalizeGiotto*

Description

fast normalize and/or scale expresion values of Giotto object

Usage

```
normalizeGiotto(
  gobject,
  feat_type = NULL,
  norm_methods = c("standard", "osmFISH"),
  library_size_norm = TRUE,
  scalefactor = 6000,
  log_norm = TRUE,
  log_offset = 1,
  logbase = 2,
  scale_feats = TRUE,
  scale_genes = NULL,
  scale_cells = TRUE,
  scale_order = c("first_feats", "first_cells"),
  verbose = FALSE
)
```

Arguments

gobject	giotto object
feat_type	feature type
norm_methods	normalization method to use
library_size_norm	normalize cells by library size
scalefactor	scale factor to use after library size normalization
log_norm	transform values to log-scale
log_offset	offset value to add to expression matrix, default = 1
logbase	log base to use to log normalize expression values
scale_feats	z-score genes over all cells
scale_genes	deprecated, use scale_feats
scale_cells	z-score cells over all genes
scale_order	order to scale feats and cells
verbose	be verbose

Details

Currently there are two 'methods' to normalize your raw counts data.

A. The standard method follows the standard protocol which can be adjusted using the provided parameters and follows the following order:

- 1. Data normalization for total library size and scaling by a custom scale-factor.
- 2. Log transformation of data.
- 3. Z-scoring of data by genes and/or cells.

B. The normalization method as provided by the osmFISH paper is also implemented:

- 1. First normalize genes, for each gene divide the counts by the total gene count and multiply by the total number of genes.
- 2. Next normalize cells, for each cell divide the normalized gene counts by the total counts per cell and multiply by the total number of cells.

This data will be saved in the Giotto slot for custom expression.

Value

giotto object

Examples

```
data(mini_giotto_single_cell)

norm_gobject = normalizeGiotto(mini_giotto_single_cell)
```

`PAGEEnrich` *PAGEEnrich*

Description

Function to calculate gene signature enrichment scores per spatial position using PAGE.

Usage

```
PAGEEnrich(...)
```

Arguments

`...`	Arguments passed on to `runPAGEEnrich` `gobject` Giotto object `sign_matrix` Matrix of signature genes for each cell type / process `expression_values` expression values to use `min_overlap_genes` minimum number of overlapping genes in sign_matrix required to calculate enrichment `reverse_log_scale` reverse expression values from log scale `logbase` log base to use if reverse_log_scale = TRUE `output_enrichment` how to return enrichment output `p_value` calculate p-values (boolean, default = FALSE) `include_depletion` calculate both enrichment and depletion

n_times number of permutations to calculate for p_value
max_block number of lines to process together (default = 20e6)
name to give to spatial enrichment results, default = PAGE
verbose be verbose
return_gobject return giotto object

See Also

runPAGEEnrich

---

pDataDT *pDataDT*

Description

show cell metadata

Usage

```
pDataDT(gobject, feat_type = NULL)
```

Arguments

gobject	giotto object
feat_type	feature type

Value

data.table with cell metadata

Examples

```
data(mini_giotto_single_cell) # loads existing Giotto object
pDataDT(mini_giotto_single_cell)
```

---

plotCCcomDotplot *plotCCcomDotplot*

Description

Plots dotplot for ligand-receptor communication scores in cell-cell interactions

Usage

```
plotCCcomDotplot(
  gobject,
  comScores,
  selected_LR = NULL,
  selected_cell_LR = NULL,
  show_LR_names = TRUE,
  show_cell_LR_names = TRUE,
  cluster_on = c("PI", "LR_expr", "log2fc"),
  cor_method = c("pearson", "kendall", "spearman"),
 aggl_method = c("ward.D", "ward.D2", "single", "complete", "average", "mcquitty",
    "median", "centroid"),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCCcomDotplot"
)
```

Arguments

gobject	giotto object
comScores	communinication scores from exprCellCellcom or spatCellCellcom
selected_LR	selected ligand-receptor combinations
selected_cell_LR	selected cell-cell combinations for ligand-receptor combinations
show_LR_names	show ligand-receptor names
show_cell_LR_names	show cell-cell names
cluster_on	values to use for clustering of cell-cell and ligand-receptor pairs
cor_method	correlation method used for clustering
aggl_method	agglomeration method used by hclust
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

plotCCcomHeatmap *plotCCcomHeatmap*

Description

Plots heatmap for ligand-receptor communication scores in cell-cell interactions

Usage

```
plotCCcomHeatmap(
  gobject,
  comScores,
  selected_LR = NULL,
  selected_cell_LR = NULL,
  show_LR_names = TRUE,
  show_cell_LR_names = TRUE,
  show = c("PI", "LR_expr", "log2fc"),
  cor_method = c("pearson", "kendall", "spearman"),
 aggl_method = c("ward.D", "ward.D2", "single", "complete", "average", "mcquitty",
    "median", "centroid"),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCCcomHeatmap"
)
```

Arguments

gobject	giotto object
comScores	communinication scores from exprCellCellcom or spatCellCellcom
selected_LR	selected ligand-receptor combinations
selected_cell_LR	selected cell-cell combinations for ligand-receptor combinations
show_LR_names	show ligand-receptor names
show_cell_LR_names	show cell-cell names
show	values to show on heatmap
cor_method	correlation method used for clustering
aggl_method	agglomeration method used by hclust
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

`plotCellProximityGenes` *plotCellProximityGenes*

Description

Create visualization for cell proximity gene scores

Usage

```
plotCellProximityGenes(
  gobject,
  cpgObject,
  method = c("volcano", "cell_barplot", "cell-cell", "cell_sankey", "heatmap",
    "dotplot"),
  min_cells = 4,
  min_cells_expr = 1,
  min_int_cells = 4,
  min_int_cells_expr = 1,
  min_fdr = 0.1,
  min_spat_diff = 0.2,
  min_log2_fc = 0.2,
  min_zscore = 2,
  zscores_column = c("cell_type", "genes"),
  direction = c("both", "up", "down"),
  cell_color_code = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCellProximityGenes"
)
```

Arguments

`gobject`	giotto object
`cpgObject`	ICG (interaction changed gene) score object
`method`	plotting method to use
`min_cells`	minimum number of source cell type
`min_cells_expr`	minimum expression level for source cell type
`min_int_cells`	minimum number of interacting neighbor cell type
`min_int_cells_expr`	minimum expression level for interacting neighbor cell type
`min_fdr`	minimum adjusted p-value
`min_spat_diff`	minimum absolute spatial expression difference

min_log2_fc	minimum log2 fold-change
min_zscore	minimum z-score change
zscores_column	calculate z-scores over cell types or genes
direction	differential expression directions to keep
cell_color_code	vector of colors with cell types as names
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

plot

---

plotCombineCCcom *plotCombineCCcom*

Description

Create visualization for combined (pairwise) cell proximity gene scores

Usage

```
plotCombineCCcom(
  gobject,
  combCCcom,
  selected_LR = NULL,
  selected_cell_LR = NULL,
  detail_plot = T,
  simple_plot = F,
  simple_plot_facet = c("interaction", "genes"),
  facet_scales = "fixed",
  facet_ncol = length(selected_LR),
  facet_nrow = length(selected_cell_LR),
  colors = c("#9932CC", "#FF8C00"),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCombineCCcom"
)
```

Arguments

gobject	giotto object
combCCcom	combined communcation scores, output from combCCcom()
selected_LR	selected ligand-receptor pair
selected_cell_LR	selected cell-cell interaction pair for ligand-receptor pair
detail_plot	show detailed info in both interacting cell types
simple_plot	show a simplified plot
simple_plot_facet	facet on interactions or genes with simple plot
facet_scales	ggplot facet scales paramter
facet_ncol	ggplot facet ncol parameter
facet_nrow	ggplot facet nrow parameter
colors	vector with two colors to use
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

---

plotCombineCellCellCommunication
plotCombineCellCellCommunication

Description

Create visualization for combined (pairwise) cell proximity gene scores

Usage

```
plotCombineCellCellCommunication(
  gobject,
  combCCcom,
  selected_LR = NULL,
  selected_cell_LR = NULL,
  detail_plot = T,
  simple_plot = F,
  simple_plot_facet = c("interaction", "genes"),
  facet_scales = "fixed",
  facet_ncol = length(selected_LR),
  facet_nrow = length(selected_cell_LR),
```

```
  colors = c("#9932CC", "#FF8C00"),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCombineCellCellCommunication"
)
```

Arguments

gobject	giotto object
combCCcom	combined communcation scores, output from combCCcom()
selected_LR	selected ligand-receptor pair
selected_cell_LR	selected cell-cell interaction pair for ligand-receptor pair
detail_plot	show detailed info in both interacting cell types
simple_plot	show a simplified plot
simple_plot_facet	facet on interactions or genes with simple plot
facet_scales	ggplot facet scales paramter
facet_ncol	ggplot facet ncol parameter
facet_nrow	ggplot facet nrow parameter
colors	vector with two colors to use
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

---

plotCombineCellProximityGenes *plotCombineCellProximityGenes*

Description

Create visualization for combined (pairwise) ICG scores

Usage

```
plotCombineCellProximityGenes(...)
```

Arguments

...	Arguments passed on to plotCombineInteractionChangedGenes
	gobject giotto object
	combCpgObject ICGscores, output from combineInteractionChangedGenes()
	selected_interactions interactions to show
	selected_gene_to_gene pairwise gene combinations to show
	detail_plot show detailed info in both interacting cell types
	simple_plot show a simplified plot
	simple_plot_facet facet on interactions or genes with simple plot
	facet_scales ggplot facet scales paramter
	facet_ncol ggplot facet ncol parameter
	facet_nrow ggplot facet nrow parameter
	colors vector with two colors to use
	show_plot show plots
	return_plot return plotting object
	save_plot directly save the plot [boolean]
	save_param list of saving parameters from all_plots_save_function
	default_save_name default save name for saving, don't change, change save_name in save_param

See Also

plotCombineInteractionChangedGenes

---

plotCombineCPG *plotCombineCPG*

Description

Create visualization for combined (pairwise) ICG scores

Usage

```
plotCombineCPG(...)
```

Arguments

...	Arguments passed on to plotCombineICG
	gobject giotto object
	combCpgObject ICGscores, output from combineInteractionChangedGenes()
	selected_interactions interactions to show
	selected_gene_to_gene pairwise gene combinations to show
	detail_plot show detailed info in both interacting cell types
	simple_plot show a simplified plot
	simple_plot_facet facet on interactions or genes with simple plot
	facet_scales ggplot facet scales paramter
	facet_ncol ggplot facet ncol parameter

facet_nrow ggplot facet nrow parameter
colors vector with two colors to use
show_plot show plots
return_plot return plotting object
save_plot directly save the plot [boolean]
save_param list of saving parameters from all_plots_save_function
default_save_name default save name for saving, don't change, change save_name in save_param

See Also

plotCombineICG

---

plotCombineICG *plotCombineICG*

Description

Create visualization for combined (pairwise) ICG scores

Usage

```
plotCombineICG(
  gobject,
  combCpgObject,
  selected_interactions = NULL,
  selected_gene_to_gene = NULL,
  detail_plot = T,
  simple_plot = F,
  simple_plot_facet = c("interaction", "genes"),
  facet_scales = "fixed",
  facet_ncol = length(selected_gene_to_gene),
  facet_nrow = length(selected_interactions),
  colors = c("#9932CC", "#FF8C00"),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCombineICG"
)
```

Arguments

gobject	giotto object
combCpgObject	ICGscores, output from combineInteractionChangedGenes()
selected_interactions	interactions to show
selected_gene_to_gene	pairwise gene combinations to show
detail_plot	show detailed info in both interacting cell types

simple_plot	show a simplified plot
simple_plot_facet	facet on interactions or genes with simple plot
facet_scales	ggplot facet scales paramter
facet_ncol	ggplot facet ncol parameter
facet_nrow	ggplot facet nrow parameter
colors	vector with two colors to use
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

---

plotCombineInteractionChangedGenes *plotCombineInteractionChangedGenes*

Description

Create visualization for combined (pairwise) ICG scores

Usage

```
plotCombineInteractionChangedGenes(
  gobject,
  combCpgObject,
  selected_interactions = NULL,
  selected_gene_to_gene = NULL,
  detail_plot = T,
  simple_plot = F,
  simple_plot_facet = c("interaction", "genes"),
  facet_scales = "fixed",
  facet_ncol = length(selected_gene_to_gene),
  facet_nrow = length(selected_interactions),
  colors = c("#9932CC", "#FF8C00"),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCombineICG"
)
```

Arguments

gobject	giotto object
combCpgObject	ICGscores, output from combineInteractionChangedGenes()
selected_interactions	interactions to show
selected_gene_to_gene	pairwise gene combinations to show
detail_plot	show detailed info in both interacting cell types
simple_plot	show a simplified plot
simple_plot_facet	facet on interactions or genes with simple plot
facet_scales	ggplot facet scales paramter
facet_ncol	ggplot facet ncol parameter
facet_nrow	ggplot facet nrow parameter
colors	vector with two colors to use
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

---

plotCPG *plotCPG*

Description

Create visualization for cell proximity gene scores

Usage

```
plotCPG(
  gobject,
  cpgObject,
  method = c("volcano", "cell_barplot", "cell-cell", "cell_sankey", "heatmap",
    "dotplot"),
  min_cells = 5,
  min_cells_expr = 1,
  min_int_cells = 3,
  min_int_cells_expr = 1,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
```

```
  min_log2_fc = 0.2,
  min_zscore = 2,
  zscores_column = c("cell_type", "genes"),
  direction = c("both", "up", "down"),
  cell_color_code = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCPG"
)
```

Arguments

gobject	giotto object
cpgObject	ICG (interaction changed gene) score object
method	plotting method to use
min_cells	minimum number of source cell type
min_cells_expr	minimum expression level for source cell type
min_int_cells	minimum number of interacting neighbor cell type
min_int_cells_expr	minimum expression level for interacting neighbor cell type
min_fdr	minimum adjusted p-value
min_spat_diff	minimum absolute spatial expression difference
min_log2_fc	minimum log2 fold-change
min_zscore	minimum z-score change
zscores_column	calculate z-scores over cell types or genes
direction	differential expression directions to keep
cell_color_code	vector of colors with cell types as names
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

plot

plotGiottoImage *plotGiottoImage*

Description

get plot a giotto image from a giotto object

Usage

```
plotGiottoImage(gobject, image_name)
```

Arguments

gobject	giotto object
image_name	name of giotto image showGiottoImageNames

Value

plot

plotHeatmap *plotHeatmap*

Description

Creates heatmap for genes and clusters.

Usage

```
plotHeatmap(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  cluster_column = NULL,
  cluster_order = c("size", "correlation", "custom"),
  cluster_custom_order = NULL,
  cluster_color_code = NULL,
  cluster_cor_method = "pearson",
  cluster_hclust_method = "ward.D",
  gene_order = c("correlation", "custom"),
  gene_custom_order = NULL,
  gene_cor_method = "pearson",
  gene_hclust_method = "complete",
  show_values = c("rescaled", "z-scaled", "original"),
  size_vertical_lines = 1.1,
  gradient_colors = c("blue", "yellow", "red"),
  gene_label_selection = NULL,
  axis_text_y_size = NULL,
  legend_nrows = 1,
```

```
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotHeatmap"
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
genes	genes to use
cluster_column	name of column to use for clusters
cluster_order	method to determine cluster order
cluster_custom_order	custom order for clusters
cluster_color_code	color code for clusters
cluster_cor_method	method for cluster correlation
cluster_hclust_method	method for hierarchical clustering of clusters
gene_order	method to determine gene order
gene_custom_order	custom order for genes
gene_cor_method	method for gene correlation
gene_hclust_method	method for hierarchical clustering of genes
show_values	which values to show on heatmap
size_vertical_lines	sizes for vertical lines
gradient_colors	colors for heatmap gradient
gene_label_selection	subset of genes to show on y-axis
axis_text_y_size	size for y-axis text
legend_nrows	number of rows for the cluster legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name

Details

If you want to display many genes there are 2 ways to proceed:

- 1. set axis_text_y_size to a really small value and show all genes
- 2. provide a subset of genes to display to gene_label_selection

Value

ggplot

Examples

```
## Not run:

data(mini_giotto_single_cell)

# get all genes
all_genes = slot(mini_giotto_single_cell, 'gene_ID')

# plot heatmap
plotHeatmap(mini_giotto_single_cell,
            genes = all_genes[1:10])

# look at cell metadata
cell_metadata = pDataDT(mini_giotto_single_cell)

# plot heatmap per cell type, a column name from cell_metadata
plotHeatmap(mini_giotto_single_cell,
            genes = all_genes[1:10],
            cluster_column = 'cell_types')


## End(Not run)
```

---

plotICG *plotICG*

Description

Create barplot to visualize interaction changed genes

Usage

```
plotICG(
  gobject,
  cpgObject,
  source_type,
  source_markers,
  ICG_genes,
  cell_color_code = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
```

```
  save_param = list(),
  default_save_name = "plotICG"
)
```

Arguments

gobject	giotto object
cpgObject	ICG (interaction changed gene) score object
source_type	cell type of the source cell
source_markers	markers for the source cell type
ICG_genes	named character vector of ICG genes
cell_color_code	cell color code for the interacting cell types
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

plot

`plotInteractionChangedGenes` *plotInteractionChangedGenes*

Description

Create barplot to visualize interaction changed genes

Usage

```
plotInteractionChangedGenes(
  gobject,
  cpgObject,
  source_type,
  source_markers,
  ICG_genes,
  cell_color_code = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotInteractionChangedGenes"
)
```

Arguments

gobject	giotto object
cpgObject	ICG (interaction changed gene) score object
source_type	cell type of the source cell
source_markers	markers for the source cell type
ICG_genes	named character vector of ICG genes
cell_color_code	cell color code for the interacting cell types
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

plot

---

plotMetaDataCellsHeatmap *plotMetaDataCellsHeatmap*

Description

Creates heatmap for numeric cell metadata within aggregated clusters.

Usage

```
plotMetaDataCellsHeatmap(
  gobject,
  metadata_cols = NULL,
  spat_enr_names = NULL,
  value_cols = NULL,
  first_meta_col = NULL,
  second_meta_col = NULL,
  show_values = c("zscores", "original", "zscores_rescaled"),
  custom_cluster_order = NULL,
  clus_cor_method = "pearson",
  clus_cluster_method = "complete",
  custom_values_order = NULL,
  values_cor_method = "pearson",
  values_cluster_method = "complete",
  midpoint = 0,
  x_text_size = 8,
  x_text_angle = 45,
  y_text_size = 8,
  strip_text_size = 8,
```

```
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotMetaDataCellsHeatmap"
)
```

Arguments

gobject	giotto object
metadata_cols	annotation columns found in pDataDT(gobject)
spat_enr_names	spatial enrichment results to include
value_cols	value columns to use
first_meta_col	if more than 1 metadata column, select the x-axis factor
second_meta_col	if more than 1 metadata column, select the facetting factor
show_values	which values to show on heatmap
custom_cluster_order	custom cluster order (default = NULL)
clus_cor_method	correlation method for clusters
clus_cluster_method	hierarchical cluster method for the clusters
custom_values_order	custom values order (default = NULL)
values_cor_method	correlation method for values
values_cluster_method	hierarchical cluster method for the values
midpoint	midpoint of show_values
x_text_size	size of x-axis text
x_text_angle	angle of x-axis text
y_text_size	size of y-axis text
strip_text_size	size of strip text
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Creates heatmap for the average values of selected value columns in the different annotation groups.

Value

ggplot or data.table

See Also

plotMetaDataHeatmap for gene expression instead of numeric cell annotation data.

---

plotMetaDataHeatmap *plotMetaDataHeatmap*

Description

Creates heatmap for genes within aggregated clusters.

Usage

```
plotMetaDataHeatmap(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  metadata_cols = NULL,
  selected_genes = NULL,
  first_meta_col = NULL,
  second_meta_col = NULL,
  show_values = c("zscores", "original", "zscores_rescaled"),
  custom_cluster_order = NULL,
  clus_cor_method = "pearson",
  clus_cluster_method = "complete",
  custom_gene_order = NULL,
  gene_cor_method = "pearson",
  gene_cluster_method = "complete",
  gradient_color = c("blue", "white", "red"),
  gradient_midpoint = 0,
  gradient_limits = NULL,
  x_text_size = 10,
  x_text_angle = 45,
  y_text_size = 10,
  strip_text_size = 8,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotMetaDataHeatmap"
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
metadata_cols	annotation columns found in pDataDT(gobject)
selected_genes	subset of genes to use
first_meta_col	if more than 1 metadata column, select the x-axis factor
second_meta_col	if more than 1 metadata column, select the facetting factor

show_values which values to show on heatmap

custom_cluster_order
custom cluster order (default = NULL)

clus_cor_method
correlation method for clusters

clus_cluster_method
hierarchical cluster method for the clusters

custom_gene_order
custom gene order (default = NULL)

gene_cor_method
correlation method for genes

gene_cluster_method
hierarchical cluster method for the genes

gradient_color vector with 3 colors for numeric data

gradient_midpoint
midpoint for color gradient

gradient_limits
vector with lower and upper limits

x_text_size size of x-axis text

x_text_angle angle of x-axis text

y_text_size size of y-axis text

strip_text_size
size of strip text

show_plot show plot

return_plot return ggplot object

save_plot directly save the plot [boolean]

save_param list of saving parameters, see showSaveParameters

default_save_name
default save name

Details

Creates heatmap for the average expression of selected genes in the different annotation/cluster groups. Calculation of cluster or gene order is done on the provided expression values, but visualization is by default on the z-scores. Other options are the original values or z-scores rescaled per gene (-1 to 1).

Value

ggplot or data.table

See Also

plotMetaDataCellsHeatmap for numeric cell annotation instead of gene expression.

Examples

```
## Not run:

data(mini_giotto_single_cell)

# get all genes
all_genes = slot(mini_giotto_single_cell, 'gene_ID')

# look at cell metadata
cell_metadata = pDataDT(mini_giotto_single_cell)

# plot heatmap per cell type, a column name from cell_metadata
plotMetaDataHeatmap(mini_giotto_single_cell,
                    selected_genes = all_genes[1:10],
                    metadata_cols = 'cell_types')


## End(Not run)
```

`plotPCA` *plotPCA*

Description

Short wrapper for PCA visualization

Usage

```
plotPCA(gobject, dim_reduction_name = "pca", default_save_name = "PCA", ...)
```

Arguments

`gobject`	giotto object
`dim_reduction_name`	name of PCA
`default_save_name`	default save name of PCA plot
`...`	Arguments passed on to `dimPlot2D` `feat_type` feature type `group_by` create multiple plots based on cell annotation column `group_by_subset` subset the group_by factor column `dim1_to_use` dimension to use on x-axis `dim2_to_use` dimension to use on y-axis `spat_enr_names` names of spatial enrichment results to include `show_NN_network` show underlying NN network `nn_network_to_use` type of NN network to use (kNN vs sNN) `network_name` name of NN network to use, if show_NN_network = TRUE `cell_color` color for cells (see details) `color_as_factor` convert color column to factor

`cell_color_code` named vector with colors
`cell_color_gradient` vector with 3 colors for numeric data
`gradient_midpoint` midpoint for color gradient
`gradient_limits` vector with lower and upper limits
`select_cell_groups` select subset of cells/clusters based on cell_color parameter
`select_cells` select subset of cells based on cell IDs
`show_other_cells` display not selected cells
`other_cell_color` color of not selected cells
`other_point_size` size of not selected cells
`show_cluster_center` plot center of selected clusters
`show_center_label` plot label of selected clusters
`center_point_size` size of center points
`center_point_border_col` border color of center points
`center_point_border_stroke` border stroke size of center points
`label_size` size of labels
`label_fontface` font of labels
`edge_alpha` column to use for alpha of the edges
`point_shape` point with border or not (border or no_border)
`point_size` size of point (cell)
`point_alpha` transparancy of point
`point_border_col` color of border around points
`point_border_stroke` stroke size of border around points
`title` title for plot, defaults to cell_color parameter
`show_legend` show legend
`legend_text` size of legend text
`legend_symbol_size` size of legend symbols
`background_color` color of plot background
`axis_text` size of axis text
`axis_title` size of axis title
`cow_n_col` cowplot param: how many columns
`cow_rel_h` cowplot param: relative height
`cow_rel_w` cowplot param: relative width
`cow_align` cowplot param: how to align
`show_plot` show plot
`return_plot` return ggplot object
`save_plot` directly save the plot [boolean]
`save_param` list of saving parameters, see `showSaveParameters`

Details

Description of parameters, see `dimPlot2D`. For 3D plots see `plotPCA_3D`

Value

ggplot

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), dimPlot(), plotPCA_2D(), plotPCA_3D(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_2D(), plotUMAP_3D(), plotUMAP()

Examples

```
data(mini_giotto_single_cell)

plotPCA(mini_giotto_single_cell)
plotPCA(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

---

plotPCA_2D *plotPCA_2D*

Description

Short wrapper for PCA visualization

Usage

```
plotPCA_2D(
  gobject,
  dim_reduction_name = "pca",
  default_save_name = "PCA_2D",
  ...
)
```

Arguments

gobject	giotto object
dim_reduction_name	name of PCA
default_save_name	default save name of PCA plot
...	Arguments passed on to dimPlot2D
	feat_type feature type
	group_by create multiple plots based on cell annotation column
	group_by_subset subset the group_by factor column
	dim1_to_use dimension to use on x-axis
	dim2_to_use dimension to use on y-axis
	spat_enr_names names of spatial enrichment results to include
	show_NN_network show underlying NN network
	nn_network_to_use type of NN network to use (kNN vs sNN)
	network_name name of NN network to use, if show_NN_network = TRUE
	cell_color color for cells (see details)
	color_as_factor convert color column to factor
	cell_color_code named vector with colors

`cell_color_gradient` vector with 3 colors for numeric data

`gradient_midpoint` midpoint for color gradient

`gradient_limits` vector with lower and upper limits

`select_cell_groups` select subset of cells/clusters based on cell_color parameter

`select_cells` select subset of cells based on cell IDs

`show_other_cells` display not selected cells

`other_cell_color` color of not selected cells

`other_point_size` size of not selected cells

`show_cluster_center` plot center of selected clusters

`show_center_label` plot label of selected clusters

`center_point_size` size of center points

`center_point_border_col` border color of center points

`center_point_border_stroke` border stroke size of center points

`label_size` size of labels

`label_fontface` font of labels

`edge_alpha` column to use for alpha of the edges

`point_shape` point with border or not (border or no_border)

`point_size` size of point (cell)

`point_alpha` transparancy of point

`point_border_col` color of border around points

`point_border_stroke` stroke size of border around points

`title` title for plot, defaults to cell_color parameter

`show_legend` show legend

`legend_text` size of legend text

`legend_symbol_size` size of legend symbols

`background_color` color of plot background

`axis_text` size of axis text

`axis_title` size of axis title

`cow_n_col` cowplot param: how many columns

`cow_rel_h` cowplot param: relative height

`cow_rel_w` cowplot param: relative width

`cow_align` cowplot param: how to align

`show_plot` show plot

`return_plot` return ggplot object

`save_plot` directly save the plot [boolean]

`save_param` list of saving parameters, see `showSaveParameters`

Details

Description of parameters, see `dimPlot2D`. For 3D plots see `plotPCA_3D`

Value

ggplot

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), dimPlot(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_2D(), plotUMAP_3D(), plotUMAP()

Examples

```
data(mini_giotto_single_cell)

plotPCA_2D(mini_giotto_single_cell)
plotPCA_2D(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

---

plotPCA_3D *plotPCA_3D*

Description

Visualize cells according to 3D PCA dimension reduction

Usage

```
plotPCA_3D(
  gobject,
  dim_reduction_name = "pca",
  default_save_name = "PCA_3D",
  ...
)
```

Arguments

gobject	giotto object
dim_reduction_name	name of PCA
default_save_name	default save name of PCA plot
...	Arguments passed on to dimPlot3D
	dim1_to_use dimension to use on x-axis
	dim2_to_use dimension to use on y-axis
	dim3_to_use dimension to use on z-axis
	spat_enr_names names of spatial enrichment results to include
	show_NN_network show underlying NN network
	nn_network_to_use type of NN network to use (kNN vs sNN)
	network_name name of NN network to use, if show_NN_network = TRUE
	cell_color color for cells (see details)
	color_as_factor convert color column to factor
	cell_color_code named vector with colors
	select_cell_groups select subset of cells/clusters based on cell_color parameter
	select_cells select subset of cells based on cell IDs

show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size size of not selected cells
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
label_size size of labels
edge_alpha column to use for alpha of the edges
point_size size of point (cell)
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters

Details

Description of parameters.

Value

plotly

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), dimPlot(), plotPCA_2D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_2D(), plotUMAP_3D(), plotUMAP()

---

plotRankSpatvsExpr *plotRankSpatvsExpr*

Description

Plots dotplot to compare ligand-receptor rankings from spatial and expression information

Usage

```
plotRankSpatvsExpr(
  gobject,
  combCC,
  expr_rnk_column = "LR_expr_rnk",
  spat_rnk_column = "LR_spat_rnk",
  midpoint = 10,
  size_range = c(0.01, 1.5),
  xlims = NULL,
  ylims = NULL,
  selected_ranks = c(1, 10, 20),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotRankSpatvsExpr"
)
```

Arguments

gobject	giotto object
combCC	combined communinication scores from combCCcom
expr_rnk_column	column with expression rank information to use
spat_rnk_column	column with spatial rank information to use
midpoint	midpoint of colors
size_range	size ranges of dotplot
xlims	x-limits, numerical vector of 2
ylims	y-limits, numerical vector of 2
selected_ranks	numerical vector, will be used to print out the percentage of top spatial ranks are recovered
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

---

plotRecovery *plotRecovery*

Description

Plots recovery plot to compare ligand-receptor rankings from spatial and expression information

Usage

```
plotRecovery(
  gobject,
  combCC,
  expr_rnk_column = "exprPI_rnk",
  spat_rnk_column = "spatPI_rnk",
  ground_truth = c("spatial", "expression"),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotRecovery"
)
```

Arguments

gobject	giotto object
combCC	combined communinication scores from combCCcom
expr_rnk_column	column with expression rank information to use
spat_rnk_column	column with spatial rank information to use
ground_truth	what to consider as ground truth (default: spatial)
show_plot	show plots
return_plot	return plotting object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

---

plotRecovery_sub *plotRecovery_sub*

Description

Plots recovery plot to compare ligand-receptor rankings from spatial and expression information

Usage

```
plotRecovery_sub(combCC, first_col = "LR_expr_rnk", second_col = "LR_spat_rnk")
```

Arguments

combCC	combined communinication scores from combCCcom
first_col	first column to use
second_col	second column to use

plotStatDelaunayNetwork *plotStatDelaunayNetwork*

Description

Plots network statistics for a Delaunay network..

Usage

```
plotStatDelaunayNetwork(
  gobject,
  method = c("deldir", "delaunayn_geometry", "RTriangle"),
  dimensions = "all",
  maximum_distance = "auto",
  minimum_k = 0,
  options = "Pp",
  Y = TRUE,
  j = TRUE,
  S = 0,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotStatDelaunayNetwork",
  ...
)
```

Arguments

gobject	giotto object
method	package to use to create a Delaunay network
dimensions	which spatial dimensions to use (maximum 2 dimensions)
maximum_distance	distance cuttof for Delaunay neighbors to consider
minimum_k	minimum neigbhours if maximum_distance != NULL
options	(geometry) String containing extra control options for the underlying Qhull command; see the Qhull documentation (../doc/qhull/html/qdelaun.html) for the available options. (default = 'Pp', do not report precision problems)
Y	(RTriangle) If TRUE prohibits the insertion of Steiner points on the mesh boundary.
j	(RTriangle) If TRUE jettisons vertices that are not part of the final triangulation from the output.
S	(RTriangle) Specifies the maximum number of added Steiner points.
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]

save_param list of saving parameters, see showSaveParameters

default_save_name
default save name for saving, don't change, change save_name in save_param

... Other parameters

Value

giotto object with updated spatial network slot

---

plotTSNE *plotTSNE*

Description

Short wrapper for tSNE visualization

Usage

```
plotTSNE(gobject, dim_reduction_name = "tsne", default_save_name = "tSNE", ...)
```

Arguments

gobject giotto object

dim_reduction_name
name of TSNE

default_save_name
default save name of TSNE plot

... Arguments passed on to dimPlot2D

feat_type feature type

group_by create multiple plots based on cell annotation column

group_by_subset subset the group_by factor column

dim1_to_use dimension to use on x-axis

dim2_to_use dimension to use on y-axis

spat_enr_names names of spatial enrichment results to include

show_NN_network show underlying NN network

nn_network_to_use type of NN network to use (kNN vs sNN)

network_name name of NN network to use, if show_NN_network = TRUE

cell_color color for cells (see details)

color_as_factor convert color column to factor

cell_color_code named vector with colors

cell_color_gradient vector with 3 colors for numeric data

gradient_midpoint midpoint for color gradient

gradient_limits vector with lower and upper limits

select_cell_groups select subset of cells/clusters based on cell_color parameter

select_cells select subset of cells based on cell IDs

show_other_cells display not selected cells

other_cell_color color of not selected cells
other_point_size size of not selected cells
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
center_point_border_col border color of center points
center_point_border_stroke border stroke size of center points
label_size size of labels
label_fontface font of labels
edge_alpha column to use for alpha of the edges
point_shape point with border or not (border or no_border)
point_size size of point (cell)
point_alpha transparancy of point
point_border_col color of border around points
point_border_stroke stroke size of border around points
title title for plot, defaults to cell_color parameter
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
background_color color of plot background
axis_text size of axis text
axis_title size of axis title
cow_n_col cowplot param: how many columns
cow_rel_h cowplot param: relative height
cow_rel_w cowplot param: relative width
cow_align cowplot param: how to align
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters

Details

Description of parameters, see dimPlot2D. For 3D plots see plotTSNE_3D

Value

ggplot

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), dimPlot(), plotPCA_2D(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotUMAP_2D(), plotUMAP_3D(), plotUMAP()

Examples

```
data(mini_giotto_single_cell)

plotTSNE(mini_giotto_single_cell)
plotTSNE(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

`plotTSNE_2D` *plotTSNE_2D*

Description

Short wrapper for tSNE visualization

Usage

```
plotTSNE_2D(
  gobject,
  dim_reduction_name = "tsne",
  default_save_name = "tSNE_2D",
  ...
)
```

Arguments

`gobject`	giotto object
`dim_reduction_name`	name of TSNE
`default_save_name`	default save name of TSNE plot
`...`	Arguments passed on to `dimPlot2D` `feat_type` feature type `group_by` create multiple plots based on cell annotation column `group_by_subset` subset the group_by factor column `dim1_to_use` dimension to use on x-axis `dim2_to_use` dimension to use on y-axis `spat_enr_names` names of spatial enrichment results to include `show_NN_network` show underlying NN network `nn_network_to_use` type of NN network to use (kNN vs sNN) `network_name` name of NN network to use, if show_NN_network = TRUE `cell_color` color for cells (see details) `color_as_factor` convert color column to factor `cell_color_code` named vector with colors `cell_color_gradient` vector with 3 colors for numeric data `gradient_midpoint` midpoint for color gradient `gradient_limits` vector with lower and upper limits `select_cell_groups` select subset of cells/clusters based on cell_color parameter

`select_cells` select subset of cells based on cell IDs
`show_other_cells` display not selected cells
`other_cell_color` color of not selected cells
`other_point_size` size of not selected cells
`show_cluster_center` plot center of selected clusters
`show_center_label` plot label of selected clusters
`center_point_size` size of center points
`center_point_border_col` border color of center points
`center_point_border_stroke` border stroke size of center points
`label_size` size of labels
`label_fontface` font of labels
`edge_alpha` column to use for alpha of the edges
`point_shape` point with border or not (border or no_border)
`point_size` size of point (cell)
`point_alpha` transparancy of point
`point_border_col` color of border around points
`point_border_stroke` stroke size of border around points
`title` title for plot, defaults to cell_color parameter
`show_legend` show legend
`legend_text` size of legend text
`legend_symbol_size` size of legend symbols
`background_color` color of plot background
`axis_text` size of axis text
`axis_title` size of axis title
`cow_n_col` cowplot param: how many columns
`cow_rel_h` cowplot param: relative height
`cow_rel_w` cowplot param: relative width
`cow_align` cowplot param: how to align
`show_plot` show plot
`return_plot` return ggplot object
`save_plot` directly save the plot [boolean]
`save_param` list of saving parameters, see `showSaveParameters`

Details

Description of parameters, see `dimPlot2D`. For 3D plots see `plotTSNE_3D`

Value

ggplot

See Also

Other reduced dimension visualizations: `dimPlot2D()`, `dimPlot3D()`, `dimPlot()`, `plotPCA_2D()`, `plotPCA_3D()`, `plotPCA()`, `plotTSNE_3D()`, `plotTSNE()`, `plotUMAP_2D()`, `plotUMAP_3D()`, `plotUMAP()`

Examples

```
data(mini_giotto_single_cell)

plotTSNE_2D(mini_giotto_single_cell)
plotTSNE_2D(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

`plotTSNE_3D` *plotTSNE_3D*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
plotTSNE_3D(
  gobject,
  dim_reduction_name = "tsne",
  default_save_name = "TSNE_3D",
  ...
)
```

Arguments

`gobject`	giotto object
`dim_reduction_name`	name of TSNE
`default_save_name`	default save name of TSNE plot
`...`	Arguments passed on to `dimPlot3D`
	`dim1_to_use` dimension to use on x-axis
	`dim2_to_use` dimension to use on y-axis
	`dim3_to_use` dimension to use on z-axis
	`spat_enr_names` names of spatial enrichment results to include
	`show_NN_network` show underlying NN network
	`nn_network_to_use` type of NN network to use (kNN vs sNN)
	`network_name` name of NN network to use, if show_NN_network = TRUE
	`cell_color` color for cells (see details)
	`color_as_factor` convert color column to factor
	`cell_color_code` named vector with colors
	`select_cell_groups` select subset of cells/clusters based on cell_color parameter
	`select_cells` select subset of cells based on cell IDs
	`show_other_cells` display not selected cells
	`other_cell_color` color of not selected cells
	`other_point_size` size of not selected cells
	`show_cluster_center` plot center of selected clusters

show_center_label plot label of selected clusters
center_point_size size of center points
label_size size of labels
edge_alpha column to use for alpha of the edges
point_size size of point (cell)
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters

Details

Description of parameters.

Value

plotly

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), dimPlot(), plotPCA_2D(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE(), plotUMAP_2D(), plotUMAP_3D(), plotUMAP()

---

plotUMAP *plotUMAP*

Description

Short wrapper for UMAP visualization

Usage

```
plotUMAP(gobject, dim_reduction_name = "umap", default_save_name = "UMAP", ...)
```

Arguments

gobject giotto object
dim_reduction_name
name of UMAP
default_save_name
default save name of UMAP plot
... Arguments passed on to dimPlot2D
feat_type feature type
group_by create multiple plots based on cell annotation column
group_by_subset subset the group_by factor column
dim1_to_use dimension to use on x-axis
dim2_to_use dimension to use on y-axis
spat_enr_names names of spatial enrichment results to include
show_NN_network show underlying NN network

nn_network_to_use type of NN network to use (kNN vs sNN)
network_name name of NN network to use, if show_NN_network = TRUE
cell_color color for cells (see details)
color_as_factor convert color column to factor
cell_color_code named vector with colors
cell_color_gradient vector with 3 colors for numeric data
gradient_midpoint midpoint for color gradient
gradient_limits vector with lower and upper limits
select_cell_groups select subset of cells/clusters based on cell_color parameter
select_cells select subset of cells based on cell IDs
show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size size of not selected cells
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
center_point_border_col border color of center points
center_point_border_stroke border stroke size of center points
label_size size of labels
label_fontface font of labels
edge_alpha column to use for alpha of the edges
point_shape point with border or not (border or no_border)
point_size size of point (cell)
point_alpha transparancy of point
point_border_col color of border around points
point_border_stroke stroke size of border around points
title title for plot, defaults to cell_color parameter
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
background_color color of plot background
axis_text size of axis text
axis_title size of axis title
cow_n_col cowplot param: how many columns
cow_rel_h cowplot param: relative height
cow_rel_w cowplot param: relative width
cow_align cowplot param: how to align
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters

Details

Description of parameters, see dimPlot2D. For 3D plots see plotUMAP_3D

Value

ggplot

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), dimPlot(), plotPCA_2D(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_2D(), plotUMAP_3D()

Examples

```
data(mini_giotto_single_cell)

plotUMAP(mini_giotto_single_cell)
plotUMAP(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

---

plotUMAP_2D *plotUMAP_2D*

Description

Short wrapper for UMAP visualization

Usage

```
plotUMAP_2D(
  gobject,
  dim_reduction_name = "umap",
  default_save_name = "UMAP_2D",
  ...
)
```

Arguments

gobject	giotto object
dim_reduction_name	name of UMAP
default_save_name	default save name of UMAP plot
...	Arguments passed on to dimPlot2D
	feat_type feature type
	group_by create multiple plots based on cell annotation column
	group_by_subset subset the group_by factor column
	dim1_to_use dimension to use on x-axis
	dim2_to_use dimension to use on y-axis
	spat_enr_names names of spatial enrichment results to include
	show_NN_network show underlying NN network
	nn_network_to_use type of NN network to use (kNN vs sNN)
	network_name name of NN network to use, if show_NN_network = TRUE

`cell_color` color for cells (see details)
`color_as_factor` convert color column to factor
`cell_color_code` named vector with colors
`cell_color_gradient` vector with 3 colors for numeric data
`gradient_midpoint` midpoint for color gradient
`gradient_limits` vector with lower and upper limits
`select_cell_groups` select subset of cells/clusters based on cell_color parameter
`select_cells` select subset of cells based on cell IDs
`show_other_cells` display not selected cells
`other_cell_color` color of not selected cells
`other_point_size` size of not selected cells
`show_cluster_center` plot center of selected clusters
`show_center_label` plot label of selected clusters
`center_point_size` size of center points
`center_point_border_col` border color of center points
`center_point_border_stroke` border stroke size of center points
`label_size` size of labels
`label_fontface` font of labels
`edge_alpha` column to use for alpha of the edges
`point_shape` point with border or not (border or no_border)
`point_size` size of point (cell)
`point_alpha` transparancy of point
`point_border_col` color of border around points
`point_border_stroke` stroke size of border around points
`title` title for plot, defaults to cell_color parameter
`show_legend` show legend
`legend_text` size of legend text
`legend_symbol_size` size of legend symbols
`background_color` color of plot background
`axis_text` size of axis text
`axis_title` size of axis title
`cow_n_col` cowplot param: how many columns
`cow_rel_h` cowplot param: relative height
`cow_rel_w` cowplot param: relative width
`cow_align` cowplot param: how to align
`show_plot` show plot
`return_plot` return ggplot object
`save_plot` directly save the plot [boolean]
`save_param` list of saving parameters, see `showSaveParameters`

Details

Description of parameters, see `dimPlot2D`. For 3D plots see `plotUMAP_3D`

Value

ggplot

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), dimPlot(), plotPCA_2D(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_3D(), plotUMAP()

Examples

```
data(mini_giotto_single_cell)

plotUMAP_2D(mini_giotto_single_cell)
plotUMAP_2D(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

---

plotUMAP_3D *plotUMAP_3D*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
plotUMAP_3D(
  gobject,
  dim_reduction_name = "umap",
  default_save_name = "UMAP_3D",
  ...
)
```

Arguments

gobject	giotto object
dim_reduction_name	name of UMAP
default_save_name	default save name of UMAP plot
...	Arguments passed on to dimPlot3D
	dim1_to_use dimension to use on x-axis
	dim2_to_use dimension to use on y-axis
	dim3_to_use dimension to use on z-axis
	spat_enr_names names of spatial enrichment results to include
	show_NN_network show underlying NN network
	nn_network_to_use type of NN network to use (kNN vs sNN)
	network_name name of NN network to use, if show_NN_network = TRUE
	cell_color color for cells (see details)
	color_as_factor convert color column to factor
	cell_color_code named vector with colors
	select_cell_groups select subset of cells/clusters based on cell_color parameter
	select_cells select subset of cells based on cell IDs

show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size size of not selected cells
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
label_size size of labels
edge_alpha column to use for alpha of the edges
point_size size of point (cell)
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters

Details

Description of parameters.

Value

plotly

See Also

Other reduced dimension visualizations: dimPlot2D(), dimPlot3D(), dimPlot(), plotPCA_2D(), plotPCA_3D(), plotPCA(), plotTSNE_2D(), plotTSNE_3D(), plotTSNE(), plotUMAP_2D(), plotUMAP()

---

processGiotto *processGiotto*

Description

Wrapper for the different Giotto object processing functions

Usage

```
processGiotto(
  gobject,
  filter_params = list(),
  norm_params = list(),
  stat_params = list(),
  adjust_params = list(),
  verbose = TRUE
)
```

Arguments

gobject	giotto object
filter_params	additional parameters to filterGiotto
norm_params	additional parameters to normalizeGiotto
stat_params	additional parameters to addStatistics
adjust_params	additional parameters to adjustGiottoMatrix
verbose	be verbose (default is TRUE)

Details

See filterGiotto, normalizeGiotto, addStatistics and adjustGiottoMatrix for more information about the different parameters in each step. If you do not provide them it will use the default values.

Value

giotto object

Examples

```
data(mini_giotto_single_cell)

processed_object = processGiotto(mini_giotto_single_cell,
                                 filter_params = list(gene_det_in_min_cells = 10,
                                 min_det_genes_per_cell = 10))
```

---

rankEnrich *rankEnrich*

Description

Function to calculate gene signature enrichment scores per spatial position using a rank based approach.

Usage

```
rankEnrich(...)
```

Arguments

...	Arguments passed on to runRankEnrich
	gobject Giotto object
	sign_matrix Matrix of signature genes for each cell type / process
	expression_values expression values to use
	reverse_log_scale reverse expression values from log scale
	logbase log base to use if reverse_log_scale = TRUE
	output_enrichment how to return enrichment output
	ties_method how to handle rank ties

p_value	calculate p-values (boolean, default = FALSE)
n_times	number of permutations to calculate for p_value
rbp_p	fractional binarization threshold (default = 0.99)
num_agg	number of top genes to aggregate (default = 100)
name	to give to spatial enrichment results, default = rank
return_gobject	return giotto object

See Also

runRankEnrich

---

rankSpatialCorGroups *rankSpatialCorGroups*

Description

Rank spatial correlated clusters according to correlation structure

Usage

```
rankSpatialCorGroups(
  gobject,
  spatCorObject,
  use_clus_name = NULL,
  show_plot = NA,
  return_plot = FALSE,
  save_plot = NA,
  save_param = list(),
  default_save_name = "rankSpatialCorGroups"
)
```

Arguments

gobject	giotto object
spatCorObject	spatial correlation object
use_clus_name	name of clusters to visualize (from clusterSpatialCorGenes())
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

data.table with positive (within group) and negative (outside group) scores

`readExprMatrix` *readExprMatrix*

Description

Function to read an expression matrix into a sparse matrix.

Usage

```
readExprMatrix(path, cores = NA, transpose = FALSE)
```

Arguments

`path`	path to the expression matrix
`cores`	number of cores to use
`transpose`	transpose matrix

Details

The expression matrix needs to have both unique column names and row names

Value

sparse matrix

`readGiottoInstructions` *readGiottoInstrunctions*

Description

Retrieves the instruction associated with the provided parameter

Usage

```
readGiottoInstructions(giotto_instructions, param = NULL)
```

Arguments

`giotto_instructions`	giotto object or result from createGiottoInstructions()
`param`	parameter to retrieve

Value

specific parameter

removeCellAnnotation *removeCellAnnotation*

Description

removes cell annotation of giotto object

Usage

```
removeCellAnnotation(gobject, columns = NULL, return_gobject = TRUE)
```

Arguments

gobject	giotto object
columns	names of columns to remove
return_gobject	boolean: return giotto object (default = TRUE)

Details

if return_gobject = FALSE, it will return the cell metadata

Value

giotto object

Examples

```
data(mini_giotto_single_cell) # load full mini giotto object

# show cell metadata
pDataDT(mini_giotto_single_cell)

# remove cell_types column
mini_giotto_single_cell = removeCellAnnotation(mini_giotto_single_cell,
                                               columns = 'cell_types')
```

removeGeneAnnotation *removeGeneAnnotation*

Description

removes gene annotation of giotto object

Usage

```
removeGeneAnnotation(gobject, columns = NULL, return_gobject = TRUE)
```

Arguments

gobject	giotto object
columns	names of columns to remove
return_gobject	boolean: return giotto object (default = TRUE)

Details

if return_gobject = FALSE, it will return the gene metadata

Value

giotto object

Examples

```
data(mini_giotto_single_cell) # load full mini giotto object

# show gene metadata
fDataDT(mini_giotto_single_cell)

# remove nr_cells column
mini_giotto_single_cell = removeGeneAnnotation(mini_giotto_single_cell,
                                               columns = 'nr_cells')
```

---

removeGiottoEnvironment

removeGiottoEnvironment

Description

removeGiottoEnvironment

Usage

```
removeGiottoEnvironment(verbose = TRUE)
```

Arguments

verbose	be verbose

Details

Removes a previously installed giotto environment. See installGiottoEnvironment.

`replaceGiottoInstructions` *replaceGiottoInstructions*

Description

Function to replace all instructions from giotto object

Usage

```
replaceGiottoInstructions(gobject, instructions = NULL)
```

Arguments

`gobject`	giotto object
`instructions`	new instructions (e.g. result from createGiottoInstructions)

Value

giotto object with replaces instructions

`rowMeans_giotto` *rowMeans_giotto*

Description

rowMeans function that works with multiple matrix representations

Usage

```
rowMeans_giotto(mymatrix)
```

Arguments

`mymatrix`	matrix object

Value

numeric vector

`rowSums_giotto` *rowSums_giotto*

Description

rowSums function that works with multiple matrix representations

Usage

```
rowSums_giotto(mymatrix)
```

Arguments

`mymatrix`	matrix object

Value

numeric vector

`runDWLSDeconv` *runDWLSDeconv*

Description

Function to perform DWLS deconvolution based on single cell expression data

Usage

```
runDWLSDeconv(
  gobject,
  expression_values = c("normalized"),
  logbase = 2,
  cluster_column = "leiden_clus",
  sign_matrix,
  n_cell = 50,
  cutoff = 2,
  name = NULL,
  return_gobject = TRUE
)
```

Arguments

`gobject`	giotto object
`expression_values`	expression values to use
`logbase`	base used for log normalization
`cluster_column`	name of cluster column
`sign_matrix`	sig matrix for deconvolution

n_cell	number of cells per spot
cutoff	cut off (default = 2)
name	name to give to spatial deconvolution results, default = DWLS
return_gobject	return giotto object

Value

giotto object or deconvolution results

---

runHyperGeometricEnrich

runHyperGeometricEnrich

Description

Function to calculate gene signature enrichment scores per spatial position using a hypergeometric test.

Usage

```
runHyperGeometricEnrich(
  gobject,
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
  top_percentage = 5,
  output_enrichment = c("original", "zscore"),
  p_value = FALSE,
  name = NULL,
  return_gobject = TRUE
)
```

Arguments

gobject	Giotto object
sign_matrix	Matrix of signature genes for each cell type / process
expression_values	expression values to use
reverse_log_scale	reverse expression values from log scale
logbase	log base to use if reverse_log_scale = TRUE
top_percentage	percentage of cells that will be considered to have gene expression with matrix binarization
output_enrichment	how to return enrichment output
p_value	calculate p-values (boolean, default = FALSE)
name	to give to spatial enrichment results, default = rank
return_gobject	return giotto object

Details

The enrichment score is calculated based on the p-value from the hypergeometric test, -log10(p-value).

Value

data.table with enrichment results

`runPAGEEnrich` *runPAGEEnrich*

Description

Function to calculate gene signature enrichment scores per spatial position using PAGE.

Usage

```
runPAGEEnrich(
  gobject,
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  min_overlap_genes = 5,
  reverse_log_scale = TRUE,
  logbase = 2,
  output_enrichment = c("original", "zscore"),
  p_value = FALSE,
  include_depletion = FALSE,
  n_times = 1000,
  max_block = 2e+07,
  name = NULL,
  verbose = TRUE,
  return_gobject = TRUE
)
```

Arguments

`gobject`	Giotto object
`sign_matrix`	Matrix of signature genes for each cell type / process
`expression_values`	expression values to use
`min_overlap_genes`	minimum number of overlapping genes in sign_matrix required to calculate enrichment
`reverse_log_scale`	reverse expression values from log scale
`logbase`	log base to use if reverse_log_scale = TRUE
`output_enrichment`	how to return enrichment output
`p_value`	calculate p-values (boolean, default = FALSE)

include_depletion	calculate both enrichment and depletion
n_times	number of permutations to calculate for p_value
max_block	number of lines to process together (default = 20e6)
name	to give to spatial enrichment results, default = PAGE
verbose	be verbose
return_gobject	return giotto object

Details

sign_matrix: a binary matrix with genes as row names and cell-types as column names. Alternatively a list of signature genes can be provided to makeSignMatrixPAGE, which will create the matrix for you.

The enrichment Z score is calculated by using method (PAGE) from Kim SY et al., BMC bioinformatics, 2005 as $Z = ((Sm \breve{} mu) * m \hat{} (1/2))/delta$. For each gene in each spot, mu is the fold change values versus the mean expression and delta is the standard deviation. Sm is the mean fold change value of a specific marker gene set and m is the size of a given marker gene set.

Value

data.table with enrichment results

See Also

makeSignMatrixPAGE

---

runPAGEEnrich_OLD *runPAGEEnrich_OLD*

Description

Function to calculate gene signature enrichment scores per spatial position using PAGE.

Usage

```
runPAGEEnrich_OLD(
  gobject,
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
  output_enrichment = c("original", "zscore"),
  p_value = FALSE,
  n_times = 1000,
  name = NULL,
  return_gobject = TRUE
)
```

Arguments

gobject	Giotto object
sign_matrix	Matrix of signature genes for each cell type / process
expression_values	expression values to use
reverse_log_scale	reverse expression values from log scale
logbase	log base to use if reverse_log_scale = TRUE
output_enrichment	how to return enrichment output
p_value	calculate p-values (boolean, default = FALSE)
n_times	number of permutations to calculate for p_value
name	to give to spatial enrichment results, default = PAGE
return_gobject	return giotto object

Details

sign_matrix: a binary matrix with genes as row names and cell-types as column names. Alternatively a list of signature genes can be provided to makeSignMatrixPAGE, which will create the matrix for you.

The enrichment Z score is calculated by using method (PAGE) from Kim SY et al., BMC bioinformatics, 2005 as $Z = ((Sm \breve{} mu) * m \hat{} (1/2))/delta$. For each gene in each spot, mu is the fold change values versus the mean expression and delta is the standard deviation. Sm is the mean fold change value of a specific marker gene set and m is the size of a given marker gene set.

Value

data.table with enrichment results

See Also

makeSignMatrixPAGE

---

runPatternSimulation *runPatternSimulation*

Description

Creates a known spatial pattern for selected genes one-by-one and runs the different spatial gene detection tests

Usage

```
runPatternSimulation(
  gobject,
  pattern_name = "pattern",
  pattern_colors = c(`in` = "green", out = "red"),
  pattern_cell_ids = NULL,
  gene_names = NULL,
  spatial_probs = c(0.5, 1),
  reps = 2,
  spatial_network_name = "kNN_network",
  spat_methods = c("binSpect_single", "binSpect_multi", "spatialDE", "spark",
    "silhouetteRank"),
  spat_methods_params = list(NA, NA, NA, NA, NA),
 spat_methods_names = c("binSpect_single", "binSpect_multi", "spatialDE", "spark",
    "silhouetteRank"),
  scalefactor = 6000,
  save_plot = T,
  save_raw = T,
  save_norm = T,
  save_dir = "~",
  max_col = 4,
  height = 7,
  width = 7,
  run_simulations = TRUE,
  ...
)
```

Arguments

gobject	giotto object
pattern_name	name of spatial pattern
pattern_colors	2 color vector for the spatial pattern
pattern_cell_ids	cell ids that make up the spatial pattern
gene_names	selected genes
spatial_probs	probabilities to test for a high expressing gene value to be part of the spatial pattern
reps	number of random simulation repetitions
spatial_network_name	which spatial network to use for binSpectSingle
spat_methods	vector of spatial methods to test
spat_methods_params	list of parameters list for each element in the vector of spatial methods to test
spat_methods_names	name for each element in the vector of spatial elements to test
scalefactor	library size scaling factor when re-normalizing dataset
save_plot	save intermediate random simulation plots or not
save_raw	save the raw expression matrix of the simulation

save_norm	save the normalized expression matrix of the simulation
save_dir	directory to save results to
max_col	maximum number of columns for final plots
height	height of final plots
width	width of final plots
run_simulations	run simulations (default = TRUE)
...	additional parameters for renormalization

Value

data.table with results

---

runPCA *runPCA*

Description

runs a Principal Component Analysis

Usage

```
runPCA(
  gobject,
  feat_type = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "feats"),
  name = "pca",
  feats_to_use = "hvf",
  genes_to_use = NULL,
  return_gobject = TRUE,
  center = TRUE,
  scale_unit = TRUE,
  ncp = 100,
  method = c("irlba", "factominer"),
  rev = FALSE,
  set_seed = TRUE,
  seed_number = 1234,
  verbose = TRUE,
  ...
)
```

Arguments

gobject	giotto object
feat_type	feature type
expression_values	expression values to use
reduction	cells or genes

name	arbitrary name for PCA run
feats_to_use	subset of features to use for PCA
genes_to_use	deprecated use feats_to_use
return_gobject	boolean: return giotto object (default = TRUE)
center	center data first (default = TRUE)
scale_unit	scale features before PCA (default = TRUE)
ncp	number of principal components to calculate
method	which implementation to use
rev	do a reverse PCA
set_seed	use of seed
seed_number	seed number to use
verbose	verbosity of the function
...	additional parameters for PCA (see details)

Details

See prcomp_irlba and PCA for more information about other parameters.

- feats_to_use = NULL: will use all features from the selected matrix
- feats_to_use = <hvg name>: can be used to select a column name of highly variable features, created by (see calculateHVF)
- feats_to_use = c('geneA', 'geneB', ...): will use all manually provided features

Value

giotto object with updated PCA dimension recuction

Examples

```
data(mini_giotto_single_cell)

# run PCA
mini_giotto_single_cell <- runPCA(gobject = mini_giotto_single_cell,
                                  center = TRUE, scale_unit = TRUE)

# plot PCA results
plotPCA(mini_giotto_single_cell)
```

runRankEnrich *runRankEnrich*

Description

Function to calculate gene signature enrichment scores per spatial position using a rank based approach.

Usage

```
runRankEnrich(
  gobject,
  sign_matrix,
  expression_values = c("normalized", "raw", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
  output_enrichment = c("original", "zscore"),
  ties_method = c("random", "max"),
  p_value = FALSE,
  n_times = 1000,
  rbp_p = 0.99,
  num_agg = 100,
  name = NULL,
  return_gobject = TRUE
)
```

Arguments

gobject	Giotto object
sign_matrix	Matrix of signature genes for each cell type / process
expression_values	expression values to use
reverse_log_scale	reverse expression values from log scale
logbase	log base to use if reverse_log_scale = TRUE
output_enrichment	how to return enrichment output
ties_method	how to handle rank ties
p_value	calculate p-values (boolean, default = FALSE)
n_times	number of permutations to calculate for p_value
rbp_p	fractional binarization threshold (default = 0.99)
num_agg	number of top genes to aggregate (default = 100)
name	to give to spatial enrichment results, default = rank
return_gobject	return giotto object

Details

sign_matrix: a rank-fold matrix with genes as row names and cell-types as column names. Alternatively a scRNA-seq matrix and vector with clusters can be provided to makeSignMatrixRank, which will create the matrix for you.

First a new rank is calculated as R = (R1*R2)^(1/2), where R1 is the rank of fold-change for each gene in each spot and R2 is the rank of each marker in each cell type. The Rank-Biased Precision is then calculated as: RBP = (1 - 0.99) * (0.99)^(R - 1) and the final enrichment score is then calculated as the sum of top 100 RBPs.

Value

data.table with enrichment results

See Also

makeSignMatrixRank

`runSpatialDeconv` *runSpatialDeconv*

Description

Function to perform deconvolution based on single cell expression data

Usage

```
runSpatialDeconv(
  gobject,
  deconv_method = c("DWLS"),
  expression_values = c("normalized"),
  logbase = 2,
  cluster_column = "leiden_clus",
  sign_matrix,
  n_cell = 50,
  cutoff = 2,
  name = NULL,
  return_gobject = TRUE
)
```

Arguments

`gobject`	giotto object
`deconv_method`	method to use for deconvolution
`expression_values`	expression values to use
`logbase`	base used for log normalization
`cluster_column`	name of cluster column
`sign_matrix`	signature matrix for deconvolution

n_cell	number of cells per spot
cutoff	cut off (default = 2)
name	name to give to spatial deconvolution results
return_gobject	return giotto object

Value

giotto object or deconvolution results

---

runSpatialEnrich *runSpatialEnrich*

Description

Function to calculate gene signature enrichment scores per spatial position using an enrichment test.

Usage

```
runSpatialEnrich(
  gobject,
  enrich_method = c("PAGE", "rank", "hypergeometric"),
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  min_overlap_genes = 5,
  reverse_log_scale = TRUE,
  logbase = 2,
  p_value = FALSE,
  n_times = 1000,
  rbp_p = 0.99,
  num_agg = 100,
  max_block = 2e+07,
  top_percentage = 5,
  output_enrichment = c("original", "zscore"),
  name = NULL,
  verbose = TRUE,
  return_gobject = TRUE
)
```

Arguments

gobject	Giotto object
enrich_method	method for gene signature enrichment calculation
sign_matrix	Matrix of signature genes for each cell type / process
expression_values	expression values to use
min_overlap_genes	minimum number of overlapping genes in sign_matrix required to calculate enrichment (PAGE)
reverse_log_scale	reverse expression values from log scale

logbase	log base to use if reverse_log_scale = TRUE
p_value	calculate p-value (default = FALSE)
n_times	(page/rank) number of permutation iterations to calculate p-value
rbp_p	(rank) fractional binarization threshold (default = 0.99)
num_agg	(rank) number of top genes to aggregate (default = 100)
max_block	number of lines to process together (default = 20e6)
top_percentage	(hyper) percentage of cells that will be considered to have gene expression with matrix binarization
output_enrichment	how to return enrichment output
name	to give to spatial enrichment results, default = PAGE
verbose	be verbose
return_gobject	return giotto object

Details

For details see the individual functions:

- PAGE: runPAGEEnrich
- Rank: runRankEnrich
- Hypergeometric: runHyperGeometricEnrich

Value

Giotto object or enrichment results if return_gobject = FALSE

---

runtSNE *runtSNE*

Description

run tSNE

Usage

```
runtSNE(
  gobject,
  feat_type = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "feats"),
  dim_reduction_to_use = "pca",
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  name = "tsne",
  feats_to_use = NULL,
  genes_to_use = NULL,
  return_gobject = TRUE,
  dims = 2,
```

```
  perplexity = 30,
  theta = 0.5,
  do_PCA_first = F,
  set_seed = T,
  seed_number = 1234,
  verbose = TRUE,
  ...
)
```

Arguments

gobject	giotto object
feat_type	feature type
expression_values	expression values to use
reduction	cells or genes
dim_reduction_to_use	use another dimension reduction set as input
dim_reduction_name	name of dimension reduction set to use
dimensions_to_use	number of dimensions to use as input
name	arbitrary name for tSNE run
feats_to_use	if dim_reduction_to_use = NULL, which genes to use
genes_to_use	deprecated, use feats_to_use
return_gobject	boolean: return giotto object (default = TRUE)
dims	tSNE param: number of dimensions to return
perplexity	tSNE param: perplexity
theta	tSNE param: theta
do_PCA_first	tSNE param: do PCA before tSNE (default = FALSE)
set_seed	use of seed
seed_number	seed number to use
verbose	verbosity of the function
...	additional tSNE parameters

Details

See Rtsne for more information about these and other parameters.

- Input for tSNE dimension reduction can be another dimension reduction (default = 'pca')
- To use gene expression as input set dim_reduction_to_use = NULL
- If dim_reduction_to_use = NULL, genes_to_use can be used to select a column name of highly variable genes (see calculateHVG) or simply provide a vector of genes
- multiple tSNE results can be stored by changing the *name* of the analysis

Value

giotto object with updated tSNE dimension recuction

Examples

```
data(mini_giotto_single_cell)

mini_giotto_single_cell <- runtSNE(mini_giotto_single_cell,
                                   dimensions_to_use = 1:3,
                                   n_threads = 1,
                                   n_neighbors = 3,
                                   perplexity = 1)

plotTSNE(gobject = mini_giotto_single_cell)
```

---

runUMAP *runUMAP*

Description

run UMAP

Usage

```
runUMAP(
  gobject,
  feat_type = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "feats"),
  dim_reduction_to_use = "pca",
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  name = "umap",
  feats_to_use = NULL,
  genes_to_use = NULL,
  return_gobject = TRUE,
  n_neighbors = 40,
  n_components = 2,
  n_epochs = 400,
  min_dist = 0.01,
  n_threads = NA,
  spread = 5,
  set_seed = TRUE,
  seed_number = 1234,
  verbose = T,
  ...
)
```

Arguments

gobject	giotto object
feat_type	feature type
expression_values	expression values to use

reduction	cells or genes
dim_reduction_to_use	use another dimension reduction set as input
dim_reduction_name	name of dimension reduction set to use
dimensions_to_use	number of dimensions to use as input
name	arbitrary name for UMAP run
feats_to_use	if dim_reduction_to_use = NULL, which genes to use
genes_to_use	deprecated, use feats_to_use
return_gobject	boolean: return giotto object (default = TRUE)
n_neighbors	UMAP param: number of neighbors
n_components	UMAP param: number of components
n_epochs	UMAP param: number of epochs
min_dist	UMAP param: minimum distance
n_threads	UMAP param: threads/cores to use
spread	UMAP param: spread
set_seed	use of seed
seed_number	seed number to use
verbose	verbosity of function
...	additional UMAP parameters

Details

See umap for more information about these and other parameters.

- Input for UMAP dimension reduction can be another dimension reduction (default = 'pca')
- To use gene expression as input set dim_reduction_to_use = NULL
- If dim_reduction_to_use = NULL, genes_to_use can be used to select a column name of highly variable genes (see calculateHVG) or simply provide a vector of genes
- multiple UMAP results can be stored by changing the *name* of the analysis

Value

giotto object with updated UMAP dimension recuction

Examples

```
data(mini_giotto_single_cell)

mini_giotto_single_cell <- runUMAP(mini_giotto_single_cell,
                                   dimensions_to_use = 1:3,
                                   n_threads = 1,
                                   n_neighbors = 3)

plotUMAP(gobject = mini_giotto_single_cell)
```

screePlot *screePlot*

Description

identify significant principal components (PCs) using an screeplot (a.k.a. elbowplot)

Usage

```
screePlot(
  gobject,
  feat_type = NULL,
  name = "pca",
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "feats"),
  method = c("irlba", "factominer"),
  rev = FALSE,
  feats_to_use = NULL,
  genes_to_use = NULL,
  center = F,
  scale_unit = F,
  ncp = 100,
  ylim = c(0, 20),
  verbose = T,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "screePlot",
  ...
)
```

Arguments

gobject	giotto object
feat_type	feature type
name	name of PCA object if available
expression_values	expression values to use
reduction	cells or features
method	which implementation to use
rev	do a reverse PCA
feats_to_use	subset of features to use for PCA
genes_to_use	deprecated, use feats_to_use
center	center data before PCA
scale_unit	scale features before PCA
ncp	number of principal components to calculate
ylim	y-axis limits on scree plot

verbose	verobsity
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function()
default_save_name	default save name for saving, don't change, change save_name in save_param
...	additional arguments to pca function, see runPCA

Details

Screeplot works by plotting the explained variance of each individual PC in a barplot allowing you to identify which PC provides a significant contribution (a.k.a 'elbow method').
Screeplot will use an available pca object, based on the parameter 'name', or it will create it if it's not available (see runPCA)

Value

ggplot object for scree method

Examples

```
data(mini_giotto_single_cell)

screePlot(mini_giotto_single_cell, ncp = 10)
```

---

selectPatternGenes *selectPatternGenes*

Description

Select genes correlated with spatial patterns

Usage

```
selectPatternGenes(
  spatPatObj,
  dimensions = 1:5,
  top_pos_genes = 10,
  top_neg_genes = 10,
  min_pos_cor = 0.5,
  min_neg_cor = -0.5,
  return_top_selection = FALSE
)
```

Arguments

spatPatObj	Output from detectSpatialPatterns
dimensions	dimensions to identify correlated genes for.
top_pos_genes	Top positively correlated genes.
top_neg_genes	Top negatively correlated genes.
min_pos_cor	Minimum positive correlation score to include a gene.
min_neg_cor	Minimum negative correlation score to include a gene.
return_top_selection	only return selection based on correlation criteria (boolean)

Details

Description.

Value

Data.table with genes associated with selected dimension (PC).

---

show,giotto-method *show method for giotto class*

Description

show method for giotto class

Usage

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

Arguments

object	giotto object

---

showClusterDendrogram *showClusterDendrogram*

Description

Creates dendrogram for selected clusters.

Usage

```
showClusterDendrogram(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  cor = c("pearson", "spearman"),
  distance = "ward.D",
  h = NULL,
  h_color = "red",
  rotate = FALSE,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "showClusterDendrogram",
  ...
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
cluster_column	name of column to use for clusters
cor	correlation score to calculate distance
distance	distance method to use for hierarchical clustering
h	height of horizontal lines to plot
h_color	color of horizontal lines
rotate	rotate dendrogram 90 degrees
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param
...	additional parameters for ggdendrogram()

Details

Expression correlation dendrogram for selected clusters.

Value

ggplot

Examples

```
data(mini_giotto_single_cell)

# cell metadata
cell_metadata = pDataDT(mini_giotto_single_cell)

# create heatmap
showClusterDendrogram(mini_giotto_single_cell,
                      cluster_column = 'cell_types')
```

---

showClusterHeatmap *showClusterHeatmap*

Description

Creates heatmap based on identified clusters

Usage

```
showClusterHeatmap(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = "all",
  cluster_column,
  cor = c("pearson", "spearman"),
  distance = "ward.D",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "showClusterHeatmap",
  ...
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
genes	vector of genes to use, default to 'all'
cluster_column	name of column to use for clusters
cor	correlation score to calculate distance
distance	distance method to use for hierarchical clustering
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param
...	additional parameters for the Heatmap function from ComplexHeatmap

Details

Correlation heatmap of selected clusters.

Value

ggplot

Examples

```
data(mini_giotto_single_cell)

# cell metadata
cell_metadata = pDataDT(mini_giotto_single_cell)

# create heatmap
showClusterHeatmap(mini_giotto_single_cell,
                   cluster_column = 'cell_types')
```

---

showGiottoImageNames *showGiottoImageNames*

Description

Prints the available giotto images that are attached to the Giotto object

Usage

```
showGiottoImageNames(gobject, verbose = TRUE)
```

Arguments

gobject	a giotto object
verbose	verbosity of function

Value

a vector of giotto image names attached to the giotto object

showGiottoInstructions *showGiottoInstructions*

Description

Function to display all instructions from giotto object

Usage

```
showGiottoInstructions(gobject)
```

Arguments

gobject	giotto object

Value

named vector with giotto instructions

showGrids *showGrids*

Description

Prints the available spatial grids that are attached to the Giotto object

Usage

```
showGrids(gobject, verbose = TRUE)
```

Arguments

gobject	a giotto object
verbose	verbosity of function#'

Value

vector

showNetworks *showNetworks*

Description

Prints the available spatial networks that are attached to the Giotto object

Usage

```
showNetworks(gobject, verbose = TRUE)
```

Arguments

gobject	a giotto object
verbose	verbosity of function#'

Value

vector

showPattern *showPattern*

Description

show patterns for 2D spatial data

Usage

```
showPattern(gobject, spatPatObj, ...)
```

Arguments

gobject	giotto object
spatPatObj	Output from detectSpatialPatterns
...	Arguments passed on to showPattern2D dimension dimension to plot trim Trim ends of the PC values. background_color background color for plot grid_border_color color for grid show_legend show legend of ggplot point_size size of points show_plot show plot return_plot return ggplot object save_plot directly save the plot [boolean] save_param list of saving parameters, see showSaveParameters default_save_name default save name for saving, don't change, change save_name in save_param

Value

ggplot

See Also

showPattern2D

---

showPattern2D *showPattern2D*

Description

show patterns for 2D spatial data

Usage

```
showPattern2D(
  gobject,
  spatPatObj,
  dimension = 1,
  trim = c(0.02, 0.98),
  background_color = "white",
  grid_border_color = "grey",
  show_legend = T,
  point_size = 1,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "showPattern2D"
)
```

Arguments

gobject	giotto object
spatPatObj	Output from detectSpatialPatterns
dimension	dimension to plot
trim	Trim ends of the PC values.
background_color	background color for plot
grid_border_color	color for grid
show_legend	show legend of ggplot
point_size	size of points
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

---

showPattern3D *showPattern3D*

Description

show patterns for 3D spatial data

Usage

```
showPattern3D(
  gobject,
  spatPatObj,
  dimension = 1,
  trim = c(0.02, 0.98),
  background_color = "white",
  grid_border_color = "grey",
  show_legend = T,
  point_size = 1,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "showPattern3D"
)
```

Arguments

gobject	giotto object
spatPatObj	Output from detectSpatialPatterns
dimension	dimension to plot
trim	Trim ends of the PC values.
background_color	background color for plot
grid_border_color	color for grid
show_legend	show legend of plot
point_size	adjust the point size
axis_scale	scale the axis
custom_ratio	cutomize the scale of the axis
x_ticks	the tick number of x_axis

y_ticks	the tick number of y_axis
z_ticks	the tick number of z_axis
show_plot	show plot
return_plot	return plot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

plotly

---

showPatternGenes *showPatternGenes*

Description

show genes correlated with spatial patterns

Usage

```
showPatternGenes(
  gobject,
  spatPatObj,
  dimension = 1,
  top_pos_genes = 5,
  top_neg_genes = 5,
  point_size = 1,
  return_DT = FALSE,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "showPatternGenes"
)
```

Arguments

gobject	giotto object
spatPatObj	Output from detectSpatialPatterns
dimension	dimension to plot genes for.
top_pos_genes	Top positively correlated genes.
top_neg_genes	Top negatively correlated genes.
point_size	size of points
return_DT	if TRUE, it will return the data.table used to generate the plots
show_plot	show plot

return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

---

showProcessingSteps *showProcessingSteps*

Description

shows the sequential processing steps that were performed on a Giotto object in a summarized format

Usage

```
showProcessingSteps(gobject)
```

Arguments

gobject	giotto object

Value

list of processing steps and names

Examples

```
data(mini_giotto_single_cell)

showProcessingSteps(mini_giotto_single_cell)
```

---

showSaveParameters *showSaveParameters*

Description

Description of Giotto saving options, links to all_plots_save_function

Usage

```
showSaveParameters()
```

Value

Instruction on how to use the automatic plot saving options within Giotto

Examples

```
showSaveParameters()
```

---

signPCA *signPCA*

Description

identify significant prinicipal components (PCs)

Usage

```
signPCA(
  gobject,
  feat_type = NULL,
  name = "pca",
  method = c("screeplot", "jackstraw"),
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "feats"),
  pca_method = c("irlba", "factominer"),
  rev = FALSE,
  feats_to_use = NULL,
  genes_to_use = NULL,
  center = T,
  scale_unit = T,
  ncp = 50,
  scree_ylim = c(0, 10),
  jack_iter = 10,
  jack_threshold = 0.01,
  jack_ylim = c(0, 1),
  verbose = TRUE,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "signPCA"
)
```

Arguments

gobject	giotto object
feat_type	feature type
name	name of PCA object if available
method	method to use to identify significant PCs
expression_values	expression values to use
reduction	cells or genes
pca_method	which implementation to use
rev	do a reverse PCA

feats_to_use	subset of features to use for PCA
genes_to_use	deprecated, use feats_to_use
center	center data before PCA
scale_unit	scale features before PCA
ncp	number of principal components to calculate
scree_ylim	y-axis limits on scree plot
jack_iter	number of interations for jackstraw
jack_threshold	p-value threshold to call a PC significant
jack_ylim	y-axis limits on jackstraw plot
verbose	verbosity
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function()
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Two different methods can be used to assess the number of relevant or significant prinicipal components (PC's).
1. Screeplot works by plotting the explained variance of each individual PC in a barplot allowing you to identify which PC provides a significant contribution (a.k.a. 'elbow method').
2. The Jackstraw method uses the permutationPA function. By systematically permuting genes it identifies robust, and thus significant, PCs.

Value

ggplot object for scree method and maxtrix of p-values for jackstraw

---

silhouetteRank *silhouetteRank*

Description

Previously: calculate_spatial_genes_python. This method computes a silhouette score per gene based on the spatial distribution of two partitions of cells (expressed L1, and non-expressed L0). Here, rather than L2 Euclidean norm, it uses a rank-transformed, exponentially weighted function to represent the local physical distance between two cells. New multi aggregator implementation can be found at silhouetteRankTest

Usage

```
silhouetteRank(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  metric = "euclidean",
  subset_genes = NULL,
  rbp_p = 0.95,
  examine_top = 0.3,
  python_path = NULL
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
metric	distance metric to use
subset_genes	only run on this subset of genes
rbp_p	fractional binarization threshold
examine_top	top fraction to evaluate with silhouette
python_path	specify specific path to python if required

Value

data.table with spatial scores

---

silhouetteRankTest *silhouetteRankTest*

Description

Multi parameter aggregator version of silhouetteRank

Usage

```
silhouetteRankTest(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  subset_genes = NULL,
  overwrite_input_bin = TRUE,
  rbp_ps = c(0.95, 0.99),
  examine_tops = c(0.005, 0.01, 0.05, 0.1, 0.3),
  matrix_type = "dissim",
  num_core = 4,
  parallel_path = "/usr/bin",
  output = NULL,
  query_sizes = 10L,
  verbose = FALSE
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
subset_genes	only run on this subset of genes
overwrite_input_bin	overwrite input bin
rbp_ps	fractional binarization thresholds
examine_tops	top fractions to evaluate with silhouette
matrix_type	type of matrix
num_core	number of cores to use
parallel_path	path to GNU parallel function
output	output directory
query_sizes	size of query
verbose	be verbose

Value

data.table with spatial scores

---

simulateOneGenePatternGiottoObject *simulateOneGenePatternGiottoObject*

Description

Create a simulated spatial pattern for one selected gnee

Usage

```
simulateOneGenePatternGiottoObject(
  gobject,
  pattern_name = "pattern",
  pattern_cell_ids = NULL,
  gene_name = NULL,
  spatial_prob = 0.95,
  gradient_direction = NULL,
  show_pattern = TRUE,
  pattern_colors = c(`in` = "green", out = "red"),
  ...
)
```

Arguments

gobject	giotto object
pattern_name	name of spatial pattern
pattern_cell_ids	cell ids that make up the spatial pattern
gene_name	selected gene
spatial_prob	probability for a high expressing gene value to be part of the spatial pattern
gradient_direction	direction of gradient
show_pattern	show the discrete spatial pattern
pattern_colors	2 color vector for the spatial pattern
...	additional parameters for (re-)normalizing

Value

Reprocessed Giotto object for which one gene has a forced spatial pattern

---

spark *spark*

Description

Compute spatially expressed genes with SPARK method

Usage

```
spark(
  gobject,
  percentage = 0.1,
  min_count = 10,
  expression_values = "raw",
  num_core = 5,
  covariates = NULL,
  return_object = c("data.table", "spark"),
  ...
)
```

Arguments

gobject	giotto object
percentage	The percentage of cells that are expressed for analysis
min_count	minimum number of counts for a gene to be included
expression_values	type of values to use (raw by default)
num_core	number of cores to use
covariates	The covariates in experiments, i.e. confounding factors/batch effect. Column name of giotto cell metadata.
return_object	type of result to return (data.table or spark object)
...	Additional parameters to the spark.vc function

Details

This function is a wrapper for the method implemented in the SPARK package:

- 1. CreateSPARKObject create a SPARK object from a Giotto object
- 2. spark.vc Fits the count-based spatial model to estimate the parameters, see spark.vc for additional parameters
- 3. spark.test Testing multiple kernel matrices

Value

data.table with SPARK spatial genes results or the SPARK object

---

`spatCellCellcom` *spatCellCellcom*

Description

Spatial Cell-Cell communication scores based on spatial expression of interacting cells

Usage

```
spatCellCellcom(
  gobject,
  spatial_network_name = "Delaunay_network",
  cluster_column = "cell_types",
  random_iter = 1000,
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  min_observations = 2,
  detailed = FALSE,
  adjust_method = c("fdr", "bonferroni", "BH", "holm", "hochberg", "hommel", "BY",
    "none"),
  adjust_target = c("genes", "cells"),
  do_parallel = TRUE,
  cores = NA,
  set_seed = TRUE,
  seed_number = 1234,
  verbose = c("a little", "a lot", "none")
)
```

Arguments

`gobject`	giotto object to use
`spatial_network_name`	spatial network to use for identifying interacting cells
`cluster_column`	cluster column with cell type information
`random_iter`	number of iterations
`gene_set_1`	first specific gene set from gene pairs

gene_set_2	second specific gene set from gene pairs
log2FC_addendum	addendum to add when calculating log2FC
min_observations	minimum number of interactions needed to be considered
detailed	provide more detailed information (random variance and z-score)
adjust_method	which method to adjust p-values
adjust_target	adjust multiple hypotheses at the cell or gene level
do_parallel	run calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
set_seed	set a seed for reproducibility
seed_number	seed number
verbose	verbose

Details

Statistical framework to identify if pairs of genes (such as ligand-receptor combinations) are expressed at higher levels than expected based on a reshuffled null distribution of gene expression values in cells that are spatially in proximity to eachother..

- LR_comb:Pair of ligand and receptor
- lig_cell_type: cell type to assess expression level of ligand
- lig_expr: average expression of ligand in lig_cell_type
- ligand: ligand name
- rec_cell_type: cell type to assess expression level of receptor
- rec_expr: average expression of receptor in rec_cell_type
- receptor: receptor name
- LR_expr: combined average ligand and receptor expression
- lig_nr: total number of cells from lig_cell_type that spatially interact with cells from rec_cell_type
- rec_nr: total number of cells from rec_cell_type that spatially interact with cells from lig_cell_type
- rand_expr: average combined ligand and receptor expression from random spatial permutations
- av_diff: average difference between LR_expr and rand_expr over all random spatial permutations
- sd_diff: (optional) standard deviation of the difference between LR_expr and rand_expr over all random spatial permutations
- z_score: (optinal) z-score
- log2fc: log2 fold-change (LR_expr/rand_expr)
- pvalue: p-value
- LR_cell_comb: cell type pair combination
- p.adj: adjusted p-value
- PI: significanc score: log2fc * -log10(p.adj)

Value

Cell-Cell communication scores for gene pairs based on spatial interaction

spatCellPlot *spatCellPlot*

Description

Visualize cells according to spatial coordinates

Usage

```
spatCellPlot(...)
```

Arguments

...	Arguments passed on to spatCellPlot2D
	gobject giotto object
	feat_type feature type
	show_image show a tissue background image
	gimage a giotto image
	image_name name of a giotto image
	sdimx x-axis dimension name (default = 'sdimx')
	sdimy y-axis dimension name (default = 'sdimy')
	spat_enr_names names of spatial enrichment results to include
	cell_annotation_values numeric cell annotation columns
	cell_color_gradient vector with 3 colors for numeric data
	gradient_midpoint midpoint for color gradient
	gradient_limits vector with lower and upper limits
	select_cell_groups select subset of cells/clusters based on cell_color parameter
	select_cells select subset of cells based on cell IDs
	point_shape shape of points (border, no_border or voronoi)
	point_size size of point (cell)
	point_alpha transparancy of spatial points
	point_border_col color of border around points
	point_border_stroke stroke size of border around points
	show_cluster_center plot center of selected clusters
	show_center_label plot label of selected clusters
	center_point_size size of center points
	center_point_border_col border color of center points
	center_point_border_stroke border stroke size of center points
	label_size size of labels
	label_fontface font of labels
	show_network show underlying spatial network
	spatial_network_name name of spatial network to use
	network_color color of spatial network
	network_alpha alpha of spatial network
	show_grid show spatial grid

spatial_grid_name name of spatial grid to use
grid_color color of spatial grid
show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size point size of not selected cells
other_cells_alpha alpha of not selected cells
coord_fix_ratio fix ratio between x and y-axis
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
background_color color of plot background
vor_border_color border colorr for voronoi plot
vor_max_radius maximum radius for voronoi 'cells'
vor_alpha transparancy of voronoi 'cells'
axis_text size of axis text
axis_title size of axis title
cow_n_col cowplot param: how many columns
cow_rel_h cowplot param: relative height
cow_rel_w cowplot param: relative width
cow_align cowplot param: how to align
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters
default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

Other spatial cell annotation visualizations: spatCellPlot2D()

Examples

```
data(mini_giotto_single_cell)

# combine all metadata
combineMetadata(mini_giotto_single_cell, spat_enr_names = 'cluster_metagene')

# visualize total expression information
spatCellPlot(mini_giotto_single_cell, cell_annotation_values = 'total_expr')

# visualize enrichment results
```

```
spatCellPlot(mini_giotto_single_cell,
               spat_enr_names = 'cluster_metagene',
               cell_annotation_values = c('1','2'))
```

`spatDimCellPlot` *spatDimCellPlot*

Description

Visualize numerical features of cells according to spatial AND dimension reduction coordinates in 2D

Usage

```
spatDimCellPlot(...)
```

Arguments

`...`	Arguments passed on to `spatDimCellPlot2D` `gobject` giotto object `show_image` show a tissue background image `gimage` a giotto image `image_name` name of a giotto image `plot_alignment` direction to align plot `spat_enr_names` names of spatial enrichment results to include `cell_annotation_values` numeric cell annotation columns `dim_reduction_to_use` dimension reduction to use `dim_reduction_name` dimension reduction name `dim1_to_use` dimension to use on x-axis `dim2_to_use` dimension to use on y-axis `sdimx` = spatial dimension to use on x-axis `sdimy` = spatial dimension to use on y-axis `cell_color_gradient` vector with 3 colors for numeric data `gradient_midpoint` midpoint for color gradient `gradient_limits` vector with lower and upper limits `select_cell_groups` select subset of cells/clusters based on cell_color parameter `select_cells` select subset of cells based on cell IDs `dim_point_shape` dim reduction points with border or not (border or no_border) `dim_point_size` size of points in dim. reduction space `dim_point_alpha` transparancy of dim. reduction points `dim_point_border_col` border color of points in dim. reduction space `dim_point_border_stroke` border stroke of points in dim. reduction space `spat_point_shape` shape of points (border, no_border or voronoi) `spat_point_size` size of spatial points `spat_point_alpha` transparancy of spatial points

spat_point_border_col border color of spatial points
spat_point_border_stroke border stroke of spatial points
dim_show_cluster_center show the center of each cluster
dim_show_center_label provide a label for each cluster
dim_center_point_size size of the center point
dim_center_point_border_col border color of center point
dim_center_point_border_stroke stroke size of center point
dim_label_size size of the center label
dim_label_fontface font of the center label
spat_show_cluster_center show the center of each cluster
spat_show_center_label provide a label for each cluster
spat_center_point_size size of the spatial center points
spat_center_point_border_col border color of the spatial center points
spat_center_point_border_stroke stroke size of the spatial center points
spat_label_size size of the center label
spat_label_fontface font of the center label
show_NN_network show underlying NN network
nn_network_to_use type of NN network to use (kNN vs sNN)
nn_network_name name of NN network to use, if show_NN_network = TRUE
dim_edge_alpha column to use for alpha of the edges
spat_show_network show spatial network
spatial_network_name name of spatial network to use
spat_network_color color of spatial network
spat_network_alpha alpha of spatial network
spat_show_grid show spatial grid
spatial_grid_name name of spatial grid to use
spat_grid_color color of spatial grid
show_other_cells display not selected cells
other_cell_color color of not selected cells
dim_other_point_size size of not selected dim cells
spat_other_point_size size of not selected spat cells
spat_other_cells_alpha alpha of not selected spat cells
coord_fix_ratio ratio for coordinates
cow_n_col cowplot param: how many columns
cow_rel_h cowplot param: relative height
cow_rel_w cowplot param: relative width
cow_align cowplot param: how to align
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
dim_background_color background color of points in dim. reduction space
spat_background_color background color of spatial points
vor_border_color border colorr for voronoi plot
vor_max_radius maximum radius for voronoi 'cells'
vor_alpha transparancy of voronoi 'cells'

axis_text size of axis text

axis_title size of axis title

show_plot show plot

return_plot return ggplot object

save_plot directly save the plot [boolean]

save_param list of saving parameters, see showSaveParameters

default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

Other spatial and dimension reduction cell annotation visualizations: spatDimCellPlot2D()

Examples

```
data(mini_giotto_single_cell)

# combine all metadata
combineMetadata(mini_giotto_single_cell, spat_enr_names = 'cluster_metagene')

# visualize total expression information
spatDimCellPlot(mini_giotto_single_cell, cell_annotation_values = 'total_expr')

# visualize enrichment results
spatDimCellPlot(mini_giotto_single_cell,
                spat_enr_names = 'cluster_metagene',
                cell_annotation_values = c('1','2'))
```

---

spatDimCellPlot2D *spatDimCellPlot2D*

Description

Visualize numerical features of cells according to spatial AND dimension reduction coordinates in 2D

Usage

```
spatDimCellPlot2D(
  gobject,
  show_image = F,
  gimage = NULL,
  image_name = "image",
```

```
  plot_alignment = c("vertical", "horizontal"),
  spat_enr_names = NULL,
  cell_annotation_values = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  sdimx = "sdimx",
  sdimy = "sdimy",
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  dim_point_shape = c("border", "no_border"),
  dim_point_size = 1,
  dim_point_alpha = 1,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  spat_point_shape = c("border", "no_border", "voronoi"),
  spat_point_size = 1,
  spat_point_alpha = 1,
  spat_point_border_col = "black",
  spat_point_border_stroke = 0.1,
  dim_show_cluster_center = F,
  dim_show_center_label = T,
  dim_center_point_size = 4,
  dim_center_point_border_col = "black",
  dim_center_point_border_stroke = 0.1,
  dim_label_size = 4,
  dim_label_fontface = "bold",
  spat_show_cluster_center = F,
  spat_show_center_label = F,
  spat_center_point_size = 4,
  spat_center_point_border_col = "black",
  spat_center_point_border_stroke = 0.1,
  spat_label_size = 4,
  spat_label_fontface = "bold",
  show_NN_network = F,
  nn_network_to_use = "sNN",
  nn_network_name = "sNN.pca",
  dim_edge_alpha = 0.5,
  spat_show_network = F,
  spatial_network_name = "Delaunay_network",
  spat_network_color = "red",
  spat_network_alpha = 0.5,
  spat_show_grid = F,
  spatial_grid_name = "spatial_grid",
  spat_grid_color = "green",
  show_other_cells = TRUE,
  other_cell_color = "grey",
  dim_other_point_size = 0.5,
```

```
  spat_other_point_size = 0.5,
  spat_other_cells_alpha = 0.5,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  dim_background_color = "white",
  spat_background_color = "white",
  vor_border_color = "white",
  vor_max_radius = 200,
  vor_alpha = 1,
  axis_text = 8,
  axis_title = 8,
  coord_fix_ratio = NULL,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatDimCellPlot2D"
)
```

Arguments

gobject	giotto object
show_image	show a tissue background image
gimage	a giotto image
image_name	name of a giotto image
plot_alignment	direction to align plot
spat_enr_names	names of spatial enrichment results to include
cell_annotation_values	numeric cell annotation columns
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
sdimx	= spatial dimension to use on x-axis
sdimy	= spatial dimension to use on y-axis
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits
select_cell_groups	select subset of cells/clusters based on cell_color parameter

`select_cells` select subset of cells based on cell IDs

`dim_point_shape`
dim reduction points with border or not (border or no_border)

`dim_point_size` size of points in dim. reduction space

`dim_point_alpha`
transparancy of dim. reduction points

`dim_point_border_col`
border color of points in dim. reduction space

`dim_point_border_stroke`
border stroke of points in dim. reduction space

`spat_point_shape`
shape of points (border, no_border or voronoi)

`spat_point_size`
size of spatial points

`spat_point_alpha`
transparancy of spatial points

`spat_point_border_col`
border color of spatial points

`spat_point_border_stroke`
border stroke of spatial points

`dim_show_cluster_center`
show the center of each cluster

`dim_show_center_label`
provide a label for each cluster

`dim_center_point_size`
size of the center point

`dim_center_point_border_col`
border color of center point

`dim_center_point_border_stroke`
stroke size of center point

`dim_label_size` size of the center label

`dim_label_fontface`
font of the center label

`spat_show_cluster_center`
show the center of each cluster

`spat_show_center_label`
provide a label for each cluster

`spat_center_point_size`
size of the spatial center points

`spat_center_point_border_col`
border color of the spatial center points

`spat_center_point_border_stroke`
stroke size of the spatial center points

`spat_label_size`
size of the center label

`spat_label_fontface`
font of the center label

`show_NN_network`
show underlying NN network

nn_network_to_use
: type of NN network to use (kNN vs sNN)

nn_network_name
: name of NN network to use, if show_NN_network = TRUE

dim_edge_alpha
: column to use for alpha of the edges

spat_show_network
: show spatial network

spatial_network_name
: name of spatial network to use

spat_network_color
: color of spatial network

spat_network_alpha
: alpha of spatial network

spat_show_grid
: show spatial grid

spatial_grid_name
: name of spatial grid to use

spat_grid_color
: color of spatial grid

show_other_cells
: display not selected cells

other_cell_color
: color of not selected cells

dim_other_point_size
: size of not selected dim cells

spat_other_point_size
: size of not selected spat cells

spat_other_cells_alpha
: alpha of not selected spat cells

show_legend
: show legend

legend_text
: size of legend text

legend_symbol_size
: size of legend symbols

dim_background_color
: background color of points in dim. reduction space

spat_background_color
: background color of spatial points

vor_border_color
: border colorr for voronoi plot

vor_max_radius
: maximum radius for voronoi 'cells'

vor_alpha
: transparancy of voronoi 'cells'

axis_text
: size of axis text

axis_title
: size of axis title

coord_fix_ratio
: ratio for coordinates

cow_n_col
: cowplot param: how many columns

cow_rel_h
: cowplot param: relative height

cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

Other spatial and dimension reduction cell annotation visualizations: spatDimCellPlot()

Examples

```
data(mini_giotto_single_cell)

# combine all metadata
combineMetadata(mini_giotto_single_cell, spat_enr_names = 'cluster_metagene')

# visualize total expression information
spatDimCellPlot2D(mini_giotto_single_cell, cell_annotation_values = 'total_expr')

# visualize enrichment results
spatDimCellPlot2D(mini_giotto_single_cell,
                  spat_enr_names = 'cluster_metagene',
                  cell_annotation_values = c('1','2'))
```

---

spatDimGenePlot *spatDimGenePlot*

Description

Visualize cells according to spatial AND dimension reduction coordinates in ggplot mode

Usage

```
spatDimGenePlot(...)
```

Arguments

...	Arguments passed on to spatDimGenePlot2D gobject giotto object show_image show a tissue background image gimage a giotto image image_name name of a giotto image expression_values gene expression values to use plot_alignment direction to align plot genes genes to show dim_reduction_to_use dimension reduction to use dim_reduction_name dimension reduction name dim1_to_use dimension to use on x-axis dim2_to_use dimension to use on y-axis dim_point_shape dim reduction points with border or not (border or no_border) dim_point_size dim reduction plot: point size dim_point_alpha transparancy of dim. reduction points dim_point_border_col color of border around points dim_point_border_stroke stroke size of border around points show_NN_network show underlying NN network show_spatial_network show underlying spatial netwok nn_network_to_use type of NN network to use (kNN vs sNN) network_name name of NN network to use, if show_NN_network = TRUE dim_network_color color of NN network dim_edge_alpha dim reduction plot: column to use for alpha of the edges scale_alpha_with_expression scale expression with ggplot alpha parameter sdimx spatial x-axis dimension name (default = 'sdimx') sdimy spatial y-axis dimension name (default = 'sdimy') spatial_network_name name of spatial network to use spatial_network_color color of spatial network show_spatial_grid show spatial grid grid_color color of spatial grid spatial_grid_name name of spatial grid to use spat_point_shape spatial points with border or not (border or no_border) spat_point_size spatial plot: point size spat_point_alpha transparancy of spatial points spat_point_border_col color of border around points spat_point_border_stroke stroke size of border around points spat_edge_alpha edge alpha cell_color_gradient vector with 3 colors for numeric data gradient_midpoint midpoint for color gradient gradient_limits vector with lower and upper limits show_legend show legend legend_text size of legend text dim_background_color color of plot background for dimension plot spat_background_color color of plot background for spatial plot

vor_border_color border colorr for voronoi plot

vor_max_radius maximum radius for voronoi 'cells'

vor_alpha transparancy of voronoi 'cells'

axis_text size of axis text

axis_title size of axis title

cow_n_col cowplot param: how many columns

cow_rel_h cowplot param: relative height

cow_rel_w cowplot param: relative width

cow_align cowplot param: how to align

show_plot show plots

return_plot return ggplot object

save_plot directly save the plot [boolean]

save_param list of saving parameters, see showSaveParameters

default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

spatDimGenePlot3D

Other spatial and dimension reduction gene expression visualizations: spatDimGenePlot2D(), spatDimGenePlot3D()

Examples

```
data(mini_giotto_single_cell)

all_genes = slot(mini_giotto_single_cell, 'gene_ID')
selected_genes = all_genes[1]
spatDimGenePlot(mini_giotto_single_cell, genes = selected_genes,
                dim_point_size = 3, spat_point_size = 3,
                cow_n_col = 1, plot_alignment = 'horizontal')
```

---

spatDimGenePlot2D *spatDimGenePlot2D*

Description

Visualize cells according to spatial AND dimension reduction coordinates in ggplot mode

Usage

```
spatDimGenePlot2D(
  gobject,
  show_image = F,
  gimage = NULL,
  image_name = "image",
  expression_values = c("normalized", "scaled", "custom"),
  plot_alignment = c("vertical", "horizontal"),
  genes,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim_point_shape = c("border", "no_border"),
  dim_point_size = 1,
  dim_point_alpha = 1,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  show_NN_network = F,
  show_spatial_network = F,
  dim_network_color = "gray",
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  dim_edge_alpha = NULL,
  scale_alpha_with_expression = FALSE,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spatial_network_name = "Delaunay_network",
  spatial_network_color = NULL,
  show_spatial_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  spat_point_shape = c("border", "no_border", "voronoi"),
  spat_point_size = 1,
  spat_point_alpha = 1,
  spat_point_border_col = "black",
  spat_point_border_stroke = 0.1,
  spat_edge_alpha = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_legend = T,
  legend_text = 8,
  dim_background_color = "white",
  spat_background_color = "white",
  vor_border_color = "white",
  vor_max_radius = 200,
  vor_alpha = 1,
```

```
  axis_text = 8,
  axis_title = 8,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatDimGenePlot2D"
)
```

Arguments

gobject	giotto object
show_image	show a tissue background image
gimage	a giotto image
image_name	name of a giotto image
expression_values	gene expression values to use
plot_alignment	direction to align plot
genes	genes to show
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim_point_shape	dim reduction points with border or not (border or no_border)
dim_point_size	dim reduction plot: point size
dim_point_alpha	transparancy of dim. reduction points
dim_point_border_col	color of border around points
dim_point_border_stroke	stroke size of border around points
show_NN_network	show underlying NN network
show_spatial_network	show underlying spatial netwok
dim_network_color	color of NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
dim_edge_alpha	dim reduction plot: column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
sdimx	spatial x-axis dimension name (default = 'sdimx')

sdimy spatial y-axis dimension name (default = 'sdimy')

spatial_network_name
name of spatial network to use

spatial_network_color
color of spatial network

show_spatial_grid
show spatial grid

grid_color color of spatial grid

spatial_grid_name
name of spatial grid to use

spat_point_shape
spatial points with border or not (border or no_border)

spat_point_size
spatial plot: point size

spat_point_alpha
transparancy of spatial points

spat_point_border_col
color of border around points

spat_point_border_stroke
stroke size of border around points

spat_edge_alpha
edge alpha

cell_color_gradient
vector with 3 colors for numeric data

gradient_midpoint
midpoint for color gradient

gradient_limits
vector with lower and upper limits

cow_n_col cowplot param: how many columns

cow_rel_h cowplot param: relative height

cow_rel_w cowplot param: relative width

cow_align cowplot param: how to align

show_legend show legend

legend_text size of legend text

dim_background_color
color of plot background for dimension plot

spat_background_color
color of plot background for spatial plot

vor_border_color
border colorr for voronoi plot

vor_max_radius maximum radius for voronoi 'cells'

vor_alpha transparancy of voronoi 'cells'

axis_text size of axis text

axis_title size of axis title

show_plot show plots

return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

spatDimGenePlot3D

Other spatial and dimension reduction gene expression visualizations: spatDimGenePlot3D(), spatDimGenePlot()

Examples

```
data(mini_giotto_single_cell)

all_genes = slot(mini_giotto_single_cell, 'gene_ID')
selected_genes = all_genes[1]
spatDimGenePlot2D(mini_giotto_single_cell, genes = selected_genes,
                  dim_point_size = 3, spat_point_size = 3,
                  cow_n_col = 1, plot_alignment = 'horizontal')
```

---

spatDimGenePlot3D *spatDimGenePlot3D*

Description

Visualize cells according to spatial AND dimension reduction coordinates in ggplot mode

Usage

```
spatDimGenePlot3D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  plot_alignment = c("horizontal", "vertical"),
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  sdimx = "sdimx",
  sdimy = "sdimy",
```

```
  sdimz = "sdimz",
  genes,
  cluster_column = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1.5,
  show_NN_network = FALSE,
  nn_network_to_use = "sNN",
  nn_network_color = "lightgrey",
  nn_network_alpha = 0.5,
  network_name = "sNN.pca",
  label_size = 16,
  genes_low_color = "blue",
  genes_mid_color = "white",
  genes_high_color = "red",
  dim_point_size = 3,
  show_spatial_network = FALSE,
  spatial_network_name = "Delaunay_network",
  spatial_network_color = "lightgray",
  spatial_network_alpha = 0.5,
  show_spatial_grid = FALSE,
  spatial_grid_name = "spatial_grid",
  spatial_grid_color = NULL,
  spatial_grid_alpha = 0.5,
  spatial_point_size = 3,
  legend_text_size = 12,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatDimGenePlot3D"
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
plot_alignment	direction to align plot
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis

dim3_to_use dimension to use on z-axis

sdimx spatial dimension to use on x-axis

sdimy spatial dimension to use on y-axis

sdimz spatial dimension to use on z-axis

genes genes to show

cluster_column cluster column to select groups

select_cell_groups
: select subset of cells/clusters based on cell_color parameter

select_cells select subset of cells based on cell IDs

show_other_cells
: display not selected cells

other_cell_color
: color of not selected cells

other_point_size
: size of not selected cells

show_NN_network
: show underlying NN network

nn_network_to_use
: type of NN network to use (kNN vs sNN)

nn_network_color
: color of NN network

nn_network_alpha
: alpha of NN network

network_name name of NN network to use, if show_NN_network = TRUE

label_size size of labels

genes_low_color
: color for low expression levels

genes_mid_color
: color for medium expression levels

genes_high_color
: color for high expression levels

dim_point_size dim reduction plot: point size

show_spatial_network
: show spatial network (boolean)

spatial_network_name
: name of spatial network to use

spatial_network_color
: color of spatial network

spatial_network_alpha
: alpha of spatial network

show_spatial_grid
: show spatial grid (boolean)

spatial_grid_name
: name of spatial grid to use

spatial_grid_color
: color of spatial grid

`spatial_grid_alpha`
: alpha of spatial grid

`spatial_point_size`
: spatial plot: point size

`legend_text_size`
: size of legend

`axis_scale`
: the way to scale the axis

`custom_ratio`
: customize the scale of the plot

`x_ticks`
: set the number of ticks on the x-axis

`y_ticks`
: set the number of ticks on the y-axis

`z_ticks`
: set the number of ticks on the z-axis

`show_plot`
: show plots

`return_plot`
: return plotly object

`save_plot`
: directly save the plot [boolean]

`save_param`
: list of saving parameters, see `showSaveParameters`

`default_save_name`
: default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

plotly

See Also

Other spatial and dimension reduction gene expression visualizations: `spatDimGenePlot2D()`, `spatDimGenePlot()`

`spatDimPlot` *spatDimPlot*

Description

Visualize cells according to spatial AND dimension reduction coordinates 2D

Usage

```
spatDimPlot(...)
```

Arguments

...	Arguments passed on to spatDimPlot2D gobject giotto object feat_type feature type show_image show a tissue background image gimage a giotto image image_name name of a giotto image plot_alignment direction to align plot dim_reduction_to_use dimension reduction to use dim_reduction_name dimension reduction name dim1_to_use dimension to use on x-axis dim2_to_use dimension to use on y-axis sdimx = spatial dimension to use on x-axis sdimy = spatial dimension to use on y-axis spat_enr_names names of spatial enrichment results to include cell_color color for cells (see details) color_as_factor convert color column to factor cell_color_code named vector with colors cell_color_gradient vector with 3 colors for numeric data gradient_midpoint midpoint for color gradient gradient_limits vector with lower and upper limits select_cell_groups select subset of cells/clusters based on cell_color parameter select_cells select subset of cells based on cell IDs dim_point_shape point with border or not (border or no_border) dim_point_size size of points in dim. reduction space dim_point_alpha transparancy of point in dim. reduction space dim_point_border_col border color of points in dim. reduction space dim_point_border_stroke border stroke of points in dim. reduction space spat_point_shape shape of points (border, no_border or voronoi) spat_point_size size of spatial points spat_point_alpha transparancy of spatial points spat_point_border_col border color of spatial points spat_point_border_stroke border stroke of spatial points dim_show_cluster_center show the center of each cluster dim_show_center_label provide a label for each cluster dim_center_point_size size of the center point dim_center_point_border_col border color of center point dim_center_point_border_stroke stroke size of center point dim_label_size size of the center label dim_label_fontface font of the center label spat_show_cluster_center show the center of each cluster spat_show_center_label provide a label for each cluster spat_center_point_size size of the center point spat_center_point_border_col border color of spatial center points

spat_center_point_border_stroke border strike size of spatial center points
spat_label_size size of the center label
spat_label_fontface font of the center label
show_NN_network show underlying NN network
nn_network_to_use type of NN network to use (kNN vs sNN)
network_name name of NN network to use, if show_NN_network = TRUE
nn_network_alpha column to use for alpha of the edges
show_spatial_network show spatial network
spat_network_name name of spatial network to use
spat_network_color color of spatial network
spat_network_alpha alpha of spatial network
show_spatial_grid show spatial grid
spat_grid_name name of spatial grid to use
spat_grid_color color of spatial grid
show_other_cells display not selected cells
other_cell_color color of not selected cells
dim_other_point_size size of not selected dim cells
spat_other_point_size size of not selected spat cells
spat_other_cells_alpha alpha of not selected spat cells
dim_show_legend show legend of dimension reduction plot
spat_show_legend show legend of spatial plot
legend_text size of legend text
legend_symbol_size size of legend symbols
dim_background_color background color of points in dim. reduction space
spat_background_color background color of spatial points
vor_border_color border colorr for voronoi plot
vor_max_radius maximum radius for voronoi 'cells'
vor_alpha transparancy of voronoi 'cells'
axis_text size of axis text
axis_title size of axis title
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters
default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

spatDimPlot2D and spatDimPlot3D for 3D visualization.

Other spatial and dimension reduction visualizations: spatDimPlot2D(), spatDimPlot3D()

Examples

```
data(mini_giotto_single_cell)

spatDimPlot(mini_giotto_single_cell)
spatDimPlot(mini_giotto_single_cell, cell_color = 'cell_types',
            spat_point_size = 3, dim_point_size = 3)
```

---

spatDimPlot2D *spatDimPlot2D*

Description

Visualize cells according to spatial AND dimension reduction coordinates 2D

Usage

```
spatDimPlot2D(
  gobject,
  feat_type = NULL,
  show_image = F,
  gimage = NULL,
  image_name = "image",
  plot_alignment = c("vertical", "horizontal"),
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spat_enr_names = NULL,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  dim_point_shape = c("border", "no_border"),
  dim_point_size = 1,
  dim_point_alpha = 1,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  spat_point_shape = c("border", "no_border", "voronoi"),
  spat_point_size = 1,
  spat_point_alpha = 1,
  spat_point_border_col = "black",
  spat_point_border_stroke = 0.1,
  dim_show_cluster_center = F,
  dim_show_center_label = T,
```

```
  dim_center_point_size = 4,
  dim_center_point_border_col = "black",
  dim_center_point_border_stroke = 0.1,
  dim_label_size = 4,
  dim_label_fontface = "bold",
  spat_show_cluster_center = F,
  spat_show_center_label = F,
  spat_center_point_size = 4,
  spat_center_point_border_col = "blue",
  spat_center_point_border_stroke = 0.1,
  spat_label_size = 4,
  spat_label_fontface = "bold",
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  nn_network_alpha = 0.05,
  show_spatial_network = F,
  spat_network_name = "Delaunay_network",
  spat_network_color = "blue",
  spat_network_alpha = 0.5,
  show_spatial_grid = F,
  spat_grid_name = "spatial_grid",
  spat_grid_color = "blue",
  show_other_cells = T,
  other_cell_color = "lightgrey",
  dim_other_point_size = 1,
  spat_other_point_size = 1,
  spat_other_cells_alpha = 0.5,
  dim_show_legend = F,
  spat_show_legend = F,
  legend_text = 8,
  legend_symbol_size = 1,
  dim_background_color = "white",
  spat_background_color = "white",
  vor_border_color = "white",
  vor_max_radius = 200,
  vor_alpha = 1,
  axis_text = 8,
  axis_title = 8,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatDimPlot2D"
)
```

Arguments

gobject	giotto object
feat_type	feature type
show_image	show a tissue background image
gimage	a giotto image

image_name name of a giotto image

plot_alignment direction to align plot

dim_reduction_to_use
: dimension reduction to use

dim_reduction_name
: dimension reduction name

dim1_to_use dimension to use on x-axis

dim2_to_use dimension to use on y-axis

sdimx = spatial dimension to use on x-axis

sdimy = spatial dimension to use on y-axis

spat_enr_names names of spatial enrichment results to include

cell_color color for cells (see details)

color_as_factor
: convert color column to factor

cell_color_code
: named vector with colors

cell_color_gradient
: vector with 3 colors for numeric data

gradient_midpoint
: midpoint for color gradient

gradient_limits
: vector with lower and upper limits

select_cell_groups
: select subset of cells/clusters based on cell_color parameter

select_cells select subset of cells based on cell IDs

dim_point_shape
: point with border or not (border or no_border)

dim_point_size size of points in dim. reduction space

dim_point_alpha
: transparancy of point in dim. reduction space

dim_point_border_col
: border color of points in dim. reduction space

dim_point_border_stroke
: border stroke of points in dim. reduction space

spat_point_shape
: shape of points (border, no_border or voronoi)

spat_point_size
: size of spatial points

spat_point_alpha
: transparancy of spatial points

spat_point_border_col
: border color of spatial points

spat_point_border_stroke
: border stroke of spatial points

dim_show_cluster_center
: show the center of each cluster

`dim_show_center_label`
: provide a label for each cluster

`dim_center_point_size`
: size of the center point

`dim_center_point_border_col`
: border color of center point

`dim_center_point_border_stroke`
: stroke size of center point

`dim_label_size` size of the center label

`dim_label_fontface`
: font of the center label

`spat_show_cluster_center`
: show the center of each cluster

`spat_show_center_label`
: provide a label for each cluster

`spat_center_point_size`
: size of the center point

`spat_center_point_border_col`
: border color of spatial center points

`spat_center_point_border_stroke`
: border strike size of spatial center points

`spat_label_size`
: size of the center label

`spat_label_fontface`
: font of the center label

`show_NN_network`
: show underlying NN network

`nn_network_to_use`
: type of NN network to use (kNN vs sNN)

`network_name` name of NN network to use, if show_NN_network = TRUE

`nn_network_alpha`
: column to use for alpha of the edges

`show_spatial_network`
: show spatial network

`spat_network_name`
: name of spatial network to use

`spat_network_color`
: color of spatial network

`spat_network_alpha`
: alpha of spatial network

`show_spatial_grid`
: show spatial grid

`spat_grid_name` name of spatial grid to use

`spat_grid_color`
: color of spatial grid

`show_other_cells`
: display not selected cells

`other_cell_color`
: color of not selected cells

`dim_other_point_size`
: size of not selected dim cells

`spat_other_point_size`
: size of not selected spat cells

`spat_other_cells_alpha`
: alpha of not selected spat cells

`dim_show_legend`
: show legend of dimension reduction plot

`spat_show_legend`
: show legend of spatial plot

`legend_text`
: size of legend text

`legend_symbol_size`
: size of legend symbols

`dim_background_color`
: background color of points in dim. reduction space

`spat_background_color`
: background color of spatial points

`vor_border_color`
: border colorr for voronoi plot

`vor_max_radius`
: maximum radius for voronoi 'cells'

`vor_alpha`
: transparancy of voronoi 'cells'

`axis_text`
: size of axis text

`axis_title`
: size of axis title

`show_plot`
: show plot

`return_plot`
: return ggplot object

`save_plot`
: directly save the plot [boolean]

`save_param`
: list of saving parameters, see `showSaveParameters`

`default_save_name`
: default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

`spatDimPlot3D`

Other spatial and dimension reduction visualizations: `spatDimPlot3D()`, `spatDimPlot()`

Examples

```
data(mini_giotto_single_cell)

spatDimPlot2D(mini_giotto_single_cell)
spatDimPlot2D(mini_giotto_single_cell, cell_color = 'cell_types',
              spat_point_size = 3, dim_point_size = 3)
```

spatDimPlot3D *spatDimPlot3D*

Description

Visualize cells according to spatial AND dimension reduction coordinates in plotly mode

Usage

```
spatDimPlot3D(
  gobject,
  plot_alignment = c("horizontal", "vertical"),
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = 3,
  sdimx = "sdimx",
  sdimy = "sdimy",
  sdimz = "sdimz",
  spat_enr_names = NULL,
  show_NN_network = FALSE,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  nn_network_color = "lightgray",
  nn_network_alpha = 0.5,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 16,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1.5,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  dim_point_size = 3,
  show_spatial_network = F,
  spatial_network_name = "Delaunay_network",
  spatial_network_color = "lightgray",
  spatial_network_alpha = 0.5,
  show_spatial_grid = F,
  spatial_grid_name = "spatial_grid",
  spatial_grid_color = NULL,
  spatial_grid_alpha = 0.5,
  spatial_point_size = 3,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
```

```
  y_ticks = NULL,
  z_ticks = NULL,
  legend_text_size = 12,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatDimPlot3D"
)
```

Arguments

gobject	giotto object
plot_alignment	direction to align plot
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim3_to_use	dimension to use on z-axis
sdimx	= spatial dimension to use on x-axis
sdimy	= spatial dimension to use on y-axis
sdimz	= spatial dimension to use on z-axis
spat_enr_names	names of spatial enrichment results to include
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
nn_network_color	color of nn network
nn_network_alpha	column to use for alpha of the edges
show_cluster_center	show the center of each cluster
show_center_label	provide a label for each cluster
center_point_size	size of the center point
label_size	size of the center label
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells

other_point_size
: size of not selected cells

cell_color
: color for cells (see details)

color_as_factor
: convert color column to factor

cell_color_code
: named vector with colors

dim_point_size
: size of points in dim. reduction space

show_spatial_network
: show spatial network

spatial_network_name
: name of spatial network to use

spatial_network_color
: color of spatial network

spatial_network_alpha
: alpha of spatial network

show_spatial_grid
: show spatial grid

spatial_grid_name
: name of spatial grid to use

spatial_grid_color
: color of spatial grid

spatial_grid_alpha
: alpha of spatial grid

spatial_point_size
: size of spatial points

axis_scale
: the way to scale the axis

custom_ratio
: customize the scale of the plot

x_ticks
: set the number of ticks on the x-axis

y_ticks
: set the number of ticks on the y-axis

z_ticks
: set the number of ticks on the z-axis

legend_text_size
: size of legend

show_plot
: show plot

return_plot
: return ggplot object

save_plot
: directly save the plot [boolean]

save_param
: list of saving parameters, see showSaveParameters

default_save_name
: default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

plotly

See Also

Other spatial and dimension reduction visualizations: spatDimPlot2D(), spatDimPlot()

---

spatGenePlot *spatGenePlot*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
spatGenePlot(...)
```

Arguments

...	Arguments passed on to spatGenePlot2D
	gobject giotto object
	show_image show a tissue background image
	gimage a giotto image
	image_name name of a giotto image
	sdimx x-axis dimension name (default = 'sdimx')
	sdimy y-axis dimension name (default = 'sdimy')
	expression_values gene expression values to use
	genes genes to show
	cell_color_gradient vector with 3 colors for numeric data
	gradient_midpoint midpoint for color gradient
	gradient_limits vector with lower and upper limits
	show_network show underlying spatial network
	network_color color of spatial network
	spatial_network_name name of spatial network to use
	edge_alpha alpha of edge
	show_grid show spatial grid
	grid_color color of spatial grid
	spatial_grid_name name of spatial grid to use
	midpoint expression midpoint
	scale_alpha_with_expression scale expression with ggplot alpha parameter
	point_shape shape of points (border, no_border or voronoi)
	point_size size of point (cell)
	point_alpha transparancy of points
	point_border_col color of border around points
	point_border_stroke stroke size of border around points
	cow_n_col cowplot param: how many columns
	cow_rel_h cowplot param: relative height
	cow_rel_w cowplot param: relative width
	cow_align cowplot param: how to align

show_legend show legend

legend_text size of legend text

background_color color of plot background

vor_border_color border colorr for voronoi plot

vor_max_radius maximum radius for voronoi 'cells'

vor_alpha transparancy of voronoi 'cells'

axis_text size of axis text

axis_title size of axis title

show_plot show plots

return_plot return ggplot object

save_plot directly save the plot [boolean]

save_param list of saving parameters, see showSaveParameters

default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

spatGenePlot3D and spatGenePlot2D

Other spatial gene expression visualizations: spatGenePlot2D(), spatGenePlot3D()

Examples

```
data(mini_giotto_single_cell)

all_genes = slot(mini_giotto_single_cell, 'gene_ID')
selected_genes = all_genes[1:2]
spatGenePlot(mini_giotto_single_cell, genes = selected_genes, point_size = 3)
```

---

spatGenePlot2D *spatGenePlot2D*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
spatGenePlot2D(
  gobject,
  show_image = F,
  gimage = NULL,
  image_name = "image",
  sdimx = "sdimx",
  sdimy = "sdimy",
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  show_network = F,
  network_color = NULL,
  spatial_network_name = "Delaunay_network",
  edge_alpha = NULL,
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  midpoint = 0,
  scale_alpha_with_expression = FALSE,
  point_shape = c("border", "no_border", "voronoi"),
  point_size = 1,
  point_alpha = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  legend_text = 8,
  background_color = "white",
  vor_border_color = "white",
  vor_alpha = 1,
  vor_max_radius = 200,
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatGenePlot2D"
)
```

Arguments

gobject	giotto object
show_image	show a tissue background image
gimage	a giotto image

image_name	name of a giotto image
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
expression_values	gene expression values to use
genes	genes to show
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
edge_alpha	alpha of edge
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
midpoint	expression midpoint
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_shape	shape of points (border, no_border or voronoi)
point_size	size of point (cell)
point_alpha	transparancy of points
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
legend_text	size of legend text
background_color	color of plot background
vor_border_color	border colorr for voronoi plot
vor_alpha	transparancy of voronoi 'cells'
vor_max_radius	maximum radius for voronoi 'cells'
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width

cow_align	cowplot param: how to align
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

spatGenePlot3D

Other spatial gene expression visualizations: spatGenePlot3D(), spatGenePlot()

Examples

```
data(mini_giotto_single_cell)

all_genes = slot(mini_giotto_single_cell, 'gene_ID')
selected_genes = all_genes[1:2]
spatGenePlot2D(mini_giotto_single_cell, genes = selected_genes, point_size = 3)
```

---

spatGenePlot3D *spatGenePlot3D*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
spatGenePlot3D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  show_network = FALSE,
  network_color = NULL,
  spatial_network_name = "Delaunay_network",
  edge_alpha = NULL,
  cluster_column = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
```

```
  other_cell_color = "lightgrey",
  other_point_size = 1,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  show_grid = FALSE,
  spatial_grid_name = "spatial_grid",
  point_size = 2,
  show_legend = TRUE,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatGenePlot3D"
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
genes	genes to show
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
edge_alpha	alpha of edges
cluster_column	cluster column to select groups
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
genes_high_color	color represents high gene expression
genes_mid_color	color represents middle gene expression
genes_low_color	color represents low gene expression
show_grid	show spatial grid

spatial_grid_name
: name of spatial grid to use

point_size
: size of point (cell)

show_legend
: show legend

axis_scale
: the way to scale the axis

custom_ratio
: customize the scale of the plot

x_ticks
: set the number of ticks on the x-axis

y_ticks
: set the number of ticks on the y-axis

z_ticks
: set the number of ticks on the z-axis

show_plot
: show plots

return_plot
: return ggplot object

save_plot
: directly save the plot [boolean]

save_param
: list of saving parameters, see showSaveParameters

default_save_name
: default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

Other spatial gene expression visualizations: spatGenePlot2D(), spatGenePlot()

---

spatialAEH *spatialAEH*

Description

Compute spatial variable genes with spatialDE method

Usage

```
spatialAEH(
  gobject = NULL,
  SpatialDE_results = NULL,
  name_pattern = "AEH_patterns",
  expression_values = c("raw", "normalized", "scaled", "custom"),
  pattern_num = 6,
  l = 1.05,
  python_path = NULL,
  return_gobject = TRUE
)
```

Arguments

gobject	Giotto object
SpatialDE_results	results of spatialDE function
name_pattern	name for the computed spatial patterns
expression_values	gene expression values to use
pattern_num	number of spatial patterns to look for
l	lengthscale
python_path	specify specific path to python if required
return_gobject	show plot

Details

This function is a wrapper for the SpatialAEH method implemented in the ...

Value

An updated giotto object

---

spatialDE *spatialDE*

Description

Compute spatial variable genes with spatialDE method

Usage

```
spatialDE(
  gobject = NULL,
  expression_values = c("raw", "normalized", "scaled", "custom"),
  size = c(4, 2, 1),
  color = c("blue", "green", "red"),
  sig_alpha = 0.5,
  unsig_alpha = 0.5,
  python_path = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "SpatialDE"
)
```

Arguments

gobject	Giotto object
expression_values	gene expression values to use
size	size of plot
color	low/medium/high color scheme for plot
sig_alpha	alpha value for significance
unsig_alpha	alpha value for unsignificance
python_path	specify specific path to python if required
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

This function is a wrapper for the SpatialDE method implemented in the ...

Value

a list of data.frames with results and plot (optional)

---

spatNetwDistributions *spatNetwDistributionsDistance*

Description

This function return histograms displaying the distance distribution for each spatial k-neighbor

Usage

```
spatNetwDistributions(
  gobject,
  spatial_network_name = "spatial_network",
  distribution = c("distance", "k_neighbors"),
  hist_bins = 30,
  test_distance_limit = NULL,
  ncol = 1,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatNetwDistributions"
)
```

Arguments

gobject	Giotto object
spatial_network_name	name of spatial network
distribution	show the distribution of cell-to-cell distance or number of k neighbors
hist_bins	number of binds to use for the histogram
test_distance_limit	effect of different distance threshold on k-neighbors
ncol	number of columns to visualize the histograms in
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, alternatively change save_name in save_param

Details

The **distance** option shows the spatial distance distribution for each nearest neighbor rank (1st, 2nd, 3th, ... neigbor). With this option the user can also test the effect of a distance limit on the spatial network. This distance limit can be used to remove neigbor cells that are considered to far away. The **k_neighbors** option shows the number of k neighbors distribution over all cells.

Value

ggplot plot

---

spatNetwDistributionsDistance

spatNetwDistributionsDistance

Description

This function return histograms displaying the distance distribution for each spatial k-neighbor

Usage

```
spatNetwDistributionsDistance(
  gobject,
  spatial_network_name = "spatial_network",
  hist_bins = 30,
  test_distance_limit = NULL,
  ncol = 1,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatNetwDistributionsDistance"
)
```

Arguments

gobject	Giotto object
spatial_network_name	name of spatial network
hist_bins	number of binds to use for the histogram
test_distance_limit	effect of different distance threshold on k-neighbors
ncol	number of columns to visualize the histograms in
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, alternatively change save_name in save_param

Value

ggplot plot

---

spatNetwDistributionsKneighbors *spatNetwDistributionsKneighbors*

Description

This function returns a histogram displaying the number of k-neighbors distribution for each cell

Usage

```
spatNetwDistributionsKneighbors(
  gobject,
  spatial_network_name = "spatial_network",
  hist_bins = 30,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatNetwDistributionsKneighbors"
)
```

Arguments

gobject	Giotto object
spatial_network_name	name of spatial network
hist_bins	number of binds to use for the histogram
show_plot	show plot

return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function
default_save_name	default save name for saving, alternatively change save_name in save_param

Value

ggplot plot

---

spatPlot *spatPlot*

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot(...)
```

Arguments

...	Arguments passed on to spatPlot2D
	gobject giotto object
	feat_type feature type
	show_image show a tissue background image
	gimage a giotto image
	image_name name of a giotto image
	group_by create multiple plots based on cell annotation column
	group_by_subset subset the group_by factor column
	sdimx x-axis dimension name (default = 'sdimx')
	sdimy y-axis dimension name (default = 'sdimy')
	spat_enr_names names of spatial enrichment results to include
	cell_color color for cells (see details)
	color_as_factor convert color column to factor
	cell_color_code named vector with colors
	cell_color_gradient vector with 3 colors for numeric data
	gradient_midpoint midpoint for color gradient
	gradient_limits vector with lower and upper limits
	select_cell_groups select subset of cells/clusters based on cell_color parameter
	select_cells select subset of cells based on cell IDs
	point_shape shape of points (border, no_border or voronoi)
	point_size size of point (cell)
	point_alpha transparancy of point
	point_border_col color of border around points

point_border_stroke stroke size of border around points
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
center_point_border_col border color of center points
center_point_border_stroke border stroke size of center points
label_size size of labels
label_fontface font of labels
show_network show underlying spatial network
spatial_network_name name of spatial network to use
network_color color of spatial network
network_alpha alpha of spatial network
show_grid show spatial grid
spatial_grid_name name of spatial grid to use
grid_color color of spatial grid
show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size point size of not selected cells
other_cells_alpha alpha of not selected cells
coord_fix_ratio fix ratio between x and y-axis
title title of plot
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
background_color color of plot background
vor_border_color border colorr for voronoi plot
vor_max_radius maximum radius for voronoi 'cells'
vor_alpha transparancy of voronoi 'cells'
axis_text size of axis text
axis_title size of axis title
cow_n_col cowplot param: how many columns
cow_rel_h cowplot param: relative height
cow_rel_w cowplot param: relative width
cow_align cowplot param: how to align
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see showSaveParameters
default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

spatPlot3D

Other spatial visualizations: spatPlot2D(), spatPlot3D()

Examples

```
data(mini_giotto_single_cell)

spatPlot(mini_giotto_single_cell)
spatPlot(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

---

spatPlot2D *spatPlot2D*

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot2D(
  gobject,
  feat_type = NULL,
  show_image = F,
  gimage = NULL,
  image_name = "image",
  group_by = NULL,
  group_by_subset = NULL,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spat_enr_names = NULL,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_shape = c("border", "no_border", "voronoi"),
  point_size = 3,
  point_alpha = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_cluster_center = F,
  show_center_label = F,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
```

```
  label_fontface = "bold",
  show_network = F,
  spatial_network_name = "Delaunay_network",
  network_color = NULL,
  network_alpha = 1,
  show_grid = F,
  spatial_grid_name = "spatial_grid",
  grid_color = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1,
  other_cells_alpha = 0.1,
  coord_fix_ratio = NULL,
  title = NULL,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  background_color = "white",
  vor_border_color = "white",
  vor_max_radius = 200,
  vor_alpha = 1,
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatPlot2D"
)
```

Arguments

gobject	giotto object
feat_type	feature type
show_image	show a tissue background image
gimage	a giotto image
image_name	name of a giotto image
group_by	create multiple plots based on cell annotation column
group_by_subset	subset the group_by factor column
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
spat_enr_names	names of spatial enrichment results to include
cell_color	color for cells (see details)
color_as_factor	convert color column to factor

cell_color_code
: named vector with colors

cell_color_gradient
: vector with 3 colors for numeric data

gradient_midpoint
: midpoint for color gradient

gradient_limits
: vector with lower and upper limits

select_cell_groups
: select subset of cells/clusters based on cell_color parameter

select_cells
: select subset of cells based on cell IDs

point_shape
: shape of points (border, no_border or voronoi)

point_size
: size of point (cell)

point_alpha
: transparancy of point

point_border_col
: color of border around points

point_border_stroke
: stroke size of border around points

show_cluster_center
: plot center of selected clusters

show_center_label
: plot label of selected clusters

center_point_size
: size of center points

center_point_border_col
: border color of center points

center_point_border_stroke
: border stroke size of center points

label_size
: size of labels

label_fontface
: font of labels

show_network
: show underlying spatial network

spatial_network_name
: name of spatial network to use

network_color
: color of spatial network

network_alpha
: alpha of spatial network

show_grid
: show spatial grid

spatial_grid_name
: name of spatial grid to use

grid_color
: color of spatial grid

show_other_cells
: display not selected cells

other_cell_color
: color of not selected cells

other_point_size
: point size of not selected cells

other_cells_alpha
: alpha of not selected cells

coord_fix_ratio
: fix ratio between x and y-axis

title
: title of plot

show_legend
: show legend

legend_text
: size of legend text

legend_symbol_size
: size of legend symbols

background_color
: color of plot background

vor_border_color
: border colorr for voronoi plot

vor_max_radius
: maximum radius for voronoi 'cells'

vor_alpha
: transparancy of voronoi 'cells'

axis_text
: size of axis text

axis_title
: size of axis title

cow_n_col
: cowplot param: how many columns

cow_rel_h
: cowplot param: relative height

cow_rel_w
: cowplot param: relative width

cow_align
: cowplot param: how to align

show_plot
: show plot

return_plot
: return ggplot object

save_plot
: directly save the plot [boolean]

save_param
: list of saving parameters, see showSaveParameters

default_save_name
: default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

spatPlot3D

Other spatial visualizations: spatPlot3D(), spatPlot()

Examples

```
data(mini_giotto_single_cell)

spatPlot2D(mini_giotto_single_cell)
spatPlot2D(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 3)
```

spatPlot3D *spatPlot3D*

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot3D(
  gobject,
  sdimx = "sdimx",
  sdimy = "sdimy",
  sdimz = "sdimz",
  spat_enr_names = NULL,
  point_size = 3,
  cell_color = NULL,
  cell_color_code = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  other_cell_alpha = 0.5,
  show_network = F,
  spatial_network_name = "Delaunay_network",
  network_color = NULL,
  network_alpha = 1,
  show_grid = F,
  spatial_grid_name = "spatial_grid",
  grid_color = NULL,
  grid_alpha = 1,
  title = "",
  show_legend = T,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spat3D"
)
```

Arguments

gobject	giotto object
sdimx	x-axis dimension name (default = 'sdimx')

sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimy')
spat_enr_names	names of spatial enrichment results to include
point_size	size of point (cell)
cell_color	color for cells (see details)
cell_color_code	named vector with colors
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
other_cell_alpha	alpha of not selected cells
show_network	show underlying spatial network
spatial_network_name	name of spatial network to use
network_color	color of spatial network
network_alpha	opacity of spatial network
show_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
grid_color	color of spatial grid
grid_alpha	opacity of spatial grid
title	title of plot
show_legend	show legend
axis_scale	the way to scale the axis
custom_ratio	customize the scale of the plot
x_ticks	set the number of ticks on the x-axis
y_ticks	set the number of ticks on the y-axis
z_ticks	set the number of ticks on the z-axis
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

See Also

Other spatial visualizations: spatPlot2D(), spatPlot()

specificCellCellcommunicationScores
specificCellCellcommunicationScores

Description

Specific Cell-Cell communication scores based on spatial expression of interacting cells

Usage

```
specificCellCellcommunicationScores(
  gobject,
  spatial_network_name = "Delaunay_network",
  cluster_column = "cell_types",
  random_iter = 100,
  cell_type_1 = "astrocyte",
  cell_type_2 = "endothelial",
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  min_observations = 2,
  detailed = FALSE,
  adjust_method = c("fdr", "bonferroni", "BH", "holm", "hochberg", "hommel", "BY",
    "none"),
  adjust_target = c("genes", "cells"),
  set_seed = FALSE,
  seed_number = 1234,
  verbose = T
)
```

Arguments

gobject	giotto object to use
spatial_network_name	spatial network to use for identifying interacting cells
cluster_column	cluster column with cell type information
random_iter	number of iterations
cell_type_1	first cell type
cell_type_2	second cell type
gene_set_1	first specific gene set from gene pairs
gene_set_2	second specific gene set from gene pairs
log2FC_addendum	addendum to add when calculating log2FC
min_observations	minimum number of interactions needed to be considered
detailed	provide more detailed information (random variance and z-score)
adjust_method	which method to adjust p-values

adjust_target	adjust multiple hypotheses at the cell or gene level
set_seed	set a seed for reproducibility
seed_number	seed number
verbose	verbose

Details

Statistical framework to identify if pairs of genes (such as ligand-receptor combinations) are expressed at higher levels than expected based on a reshuffled null distribution of gene expression values in cells that are spatially in proximity to eachother.

- LR_comb:Pair of ligand and receptor
- lig_cell_type: cell type to assess expression level of ligand
- lig_expr: average expression of ligand in lig_cell_type
- ligand: ligand name
- rec_cell_type: cell type to assess expression level of receptor
- rec_expr: average expression of receptor in rec_cell_type
- receptor: receptor name
- LR_expr: combined average ligand and receptor expression
- lig_nr: total number of cells from lig_cell_type that spatially interact with cells from rec_cell_type
- rec_nr: total number of cells from rec_cell_type that spatially interact with cells from lig_cell_type
- rand_expr: average combined ligand and receptor expression from random spatial permutations
- av_diff: average difference between LR_expr and rand_expr over all random spatial permutations
- sd_diff: (optional) standard deviation of the difference between LR_expr and rand_expr over all random spatial permutations
- z_score: (optinal) z-score
- log2fc: log2 fold-change (LR_expr/rand_expr)
- pvalue: p-value
- LR_cell_comb: cell type pair combination
- p.adj: adjusted p-value
- PI: significanc score: log2fc * -log10(p.adj)

Value

Cell-Cell communication scores for gene pairs based on spatial interaction

`stitchFieldCoordinates` *stitchFieldCoordinates*

Description

Helper function to stitch field coordinates together to form one complete picture

Usage

```
stitchFieldCoordinates(
  location_file,
  offset_file,
  cumulate_offset_x = F,
  cumulate_offset_y = F,
  field_col = "Field of View",
  X_coord_col = "X",
  Y_coord_col = "Y",
  reverse_final_x = F,
  reverse_final_y = T
)
```

Arguments

`location_file`	location dataframe with X and Y coordinates
`offset_file`	dataframe that describes the offset for each field (see details)
`cumulate_offset_x`	(boolean) Do the x-axis offset values need to be cumulated?
`cumulate_offset_y`	(boolean) Do the y-axis offset values need to be cumulated?
`field_col`	column that indicates the field within the location_file
`X_coord_col`	column that indicates the x coordinates
`Y_coord_col`	column that indicates the x coordinates
`reverse_final_x`	(boolean) Do the final x coordinates need to be reversed?
`reverse_final_y`	(boolean) Do the final y coordinates need to be reversed?

Details

Stitching of fields:

- 1. have cell locations: at least 3 columns: field, X, Y
- 2. create offset file: offset file has 3 columns: field, x_offset, y_offset
- 3. create new cell location file by stitching original cell locations with stitchFieldCoordinates
- 4. provide new cell location file to `createGiottoObject`

Value

Updated location dataframe with new X ['X_final'] and Y ['Y_final'] coordinates

`stitchTileCoordinates` *stitchTileCoordinates*

Description

Helper function to stitch tile coordinates together to form one complete picture

Usage

```
stitchTileCoordinates(location_file, Xtilespan, Ytilespan)
```

Arguments

`location_file`	location dataframe with X and Y coordinates
`Xtilespan`	numerical value specifying the width of each tile
`Ytilespan`	numerical value specifying the height of each tile

`subClusterCells` *subClusterCells*

Description

subcluster cells

Usage

```
subClusterCells(
  gobject,
  name = "sub_clus",
  cluster_method = c("leiden", "louvain_community", "louvain_multinet"),
  cluster_column = NULL,
  selected_clusters = NULL,
 hvg_param = list(reverse_log_scale = T, difference_in_cov = 1, expression_values =
    "normalized"),
  hvg_min_perc_cells = 5,
  hvg_mean_expr_det = 1,
  use_all_genes_as_hvg = FALSE,
  min_nr_of_hvg = 5,
  pca_param = list(expression_values = "normalized", scale_unit = T),
  nn_param = list(dimensions_to_use = 1:20),
  k_neighbors = 10,
  resolution = 1,
  n_iterations = 1000,
  gamma = 1,
  omega = 1,
  python_path = NULL,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  return_gobject = TRUE,
  verbose = T
)
```

Arguments

gobject	giotto object
name	name for new clustering result
cluster_method	clustering method to use
cluster_column	cluster column to subcluster
selected_clusters	only do subclustering on these clusters
hvg_param	parameters for calculateHVG
hvg_min_perc_cells	threshold for detection in min percentage of cells
hvg_mean_expr_det	threshold for mean expression level in cells with detection
use_all_genes_as_hvg	forces all genes to be HVG and to be used as input for PCA
min_nr_of_hvg	minimum number of HVG, or all genes will be used as input for PCA
pca_param	parameters for runPCA
nn_param	parameters for parameters for createNearestNetwork
k_neighbors	number of k for createNearestNetwork
resolution	resolution
n_iterations	number of interations to run the Leiden algorithm.
gamma	gamma
omega	omega
python_path	specify specific path to python if required
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
return_gobject	boolean: return giotto object (default = TRUE)
verbose	verbose

Details

This function performs subclustering on selected clusters. The systematic steps are:

- 1. subset Giotto object
- 2. identify highly variable genes
- 3. run PCA
- 4. create nearest neighbouring network
- 5. do clustering

Value

giotto object with new subclusters appended to cell metadata

See Also

doLouvainCluster_multinet, doLouvainCluster_community and @seealso doLeidenCluster

subsetGiotto *subsetGiotto*

Description

subsets Giotto object including previous analyses.

Usage

```
subsetGiotto(
  gobject,
  cell_ids = NULL,
  feat_type = NULL,
  feat_ids = NULL,
  verbose = FALSE
)
```

Arguments

gobject	giotto object
cell_ids	cell IDs to keep
feat_type	feature type to use
feat_ids	feature IDs to keep
verbose	be verbose

Value

giotto object

Examples

```
data(mini_giotto_single_cell)

random_cells = sample(slot(mini_giotto_single_cell, 'cell_ID'), 10)
random_genes = sample(slot(mini_giotto_single_cell, 'gene_ID'), 10)

subset_obj = subsetGiotto(mini_giotto_single_cell,
                          cell_ids = random_cells,
                          feat_ids = random_genes)
```

subsetGiottoLocs *subsetGiottoLocs*

Description

subsets Giotto object based on spatial locations

Usage

```
subsetGiottoLocs(
  gobject,
  x_max = NULL,
  x_min = NULL,
  y_max = NULL,
  y_min = NULL,
  z_max = NULL,
  z_min = NULL,
  return_gobject = T,
  verbose = FALSE
)
```

Arguments

gobject	giotto object
x_max	maximum x-coordinate
x_min	minimum x-coordinate
y_max	maximum y-coordinate
y_min	minimum y-coordinate
z_max	maximum z-coordinate
z_min	minimum z-coordinate
return_gobject	return Giotto object
verbose	be verbose

Details

if return_gobject = FALSE, then a filtered combined metadata data.table will be returned

Value

giotto object

Examples

```
data(mini_giotto_single_cell)

# spatial plot
spatPlot(mini_giotto_single_cell)

# subset giotto object based on spatial locations
```

```
subset_obj = subsetGiottoLocs(mini_giotto_single_cell,
x_max = 1500, x_min = 1000,
y_max = -500, y_min = -1000)

# spatial plot of subset giotto object
spatPlot(subset_obj)
```

`trendSceek` *trendSceek*

Description

Compute spatial variable genes with trendsceek method

Usage

```
trendSceek(
  gobject,
  expression_values = c("normalized", "raw"),
  subset_genes = NULL,
  nrand = 100,
  ncores = 8,
  ...
)
```

Arguments

`gobject`	Giotto object
`expression_values`	gene expression values to use
`subset_genes`	subset of genes to run trendsceek on
`nrand`	An integer specifying the number of random resamplings of the mark distribution as to create the null-distribution.
`ncores`	An integer specifying the number of cores to be used by BiocParallel
`...`	Additional parameters to the `trendsceek_test` function

Details

This function is a wrapper for the trendsceek_test method implemented in the trendsceek package

Value

data.frame with trendsceek spatial genes results

t_giotto *t_giotto*

Description

t function that works with multiple matrix representations

Usage

```
t_giotto(mymatrix)
```

Arguments

mymatrix	matrix object

Value

transposed matrix

updateGiottoImage *updateGiottoImage*

Description

Updates the boundaries of a giotto image attached to a giotto object

Usage

```
updateGiottoImage(
  gobject,
  image_name,
  xmax_adj = 0,
  xmin_adj = 0,
  ymax_adj = 0,
  ymin_adj = 0,
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
image_name	spatial locations
xmax_adj	adjustment of the maximum x-value to align the image
xmin_adj	adjustment of the minimum x-value to align the image
ymax_adj	adjustment of the maximum y-value to align the image
ymin_adj	adjustment of the minimum y-value to align the image
return_gobject	return a giotto object

Value

a giotto object or an updated giotto image if return_gobject = F

`viewHMRFresults` *viewHMRFresults*

Description

View results from doHMRF.

Usage

```
viewHMRFresults(
  gobject,
  HMRFoutput,
  k = NULL,
  betas_to_view = NULL,
  third_dim = FALSE,
  ...
)
```

Arguments

`gobject`	giotto object
`HMRFoutput`	HMRF output from doHMRF
`k`	number of HMRF domains
`betas_to_view`	results from different betas that you want to view
`third_dim`	3D data (boolean)
`...`	additional paramters (see details)

Value

spatial plots with HMRF domains

See Also

`spatPlot2D` and `spatPlot3D`

`viewHMRFresults2D` *viewHMRFresults2D*

Description

View results from doHMRF.

Usage

```
viewHMRFresults2D(gobject, HMRFoutput, k = NULL, betas_to_view = NULL, ...)
```

Arguments

gobject	giotto object
HMRFoutput	HMRF output from doHMRF
k	number of HMRF domains
betas_to_view	results from different betas that you want to view
...	additional parameters to spatPlot2D()

Value

spatial plots with HMRF domains

See Also

spatPlot2D

---

viewHMRFresults3D *viewHMRFresults3D*

Description

View results from doHMRF.

Usage

```
viewHMRFresults3D(gobject, HMRFoutput, k = NULL, betas_to_view = NULL, ...)
```

Arguments

gobject	giotto object
HMRFoutput	HMRF output from doHMRF
k	number of HMRF domains
betas_to_view	results from different betas that you want to view
...	additional parameters to spatPlot3D()

Value

spatial plots with HMRF domains

See Also

spatPlot3D

violinPlot *violinPlot*

Description

Creates violinplot for selected clusters

Usage

```
violinPlot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  cluster_column,
  cluster_custom_order = NULL,
  color_violin = c("genes", "cluster"),
  cluster_color_code = NULL,
  strip_position = c("top", "right", "left", "bottom"),
  strip_text = 7,
  axis_text_x_size = 10,
  axis_text_y_size = 6,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "violinPlot"
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
genes	genes to plot
cluster_column	name of column to use for clusters
cluster_custom_order	custom order of clusters
color_violin	color violin according to genes or clusters
cluster_color_code	color code for clusters
strip_position	position of gene labels
strip_text	size of strip text
axis_text_x_size	size of x-axis text
axis_text_y_size	size of y-axis text
show_plot	show plot
return_plot	return ggplot object

save_plot	directly save the plot [boolean]
save_param	list of saving parameters, see showSaveParameters
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

Examples

```
## Not run:

data(mini_giotto_single_cell)

# get all genes
all_genes = slot(mini_giotto_single_cell, 'gene_ID')

# look at cell metadata
cell_metadata = pDataDT(mini_giotto_single_cell)

# plot violinplot with selected genes and stratified for identified cell types
violinPlot(mini_giotto_single_cell,
           genes = all_genes[1:10],
           cluster_column = 'cell_types')


## End(Not run)
```

---

writeHMRFresults *writeHMRFresults*

Description

write results from doHMRF to a data.table.

Usage

```
writeHMRFresults(
  gobject,
  HMRFoutput,
  k = NULL,
  betas_to_view = NULL,
  print_command = F
)
```

Arguments

gobject	giotto object
HMRFoutput	HMRF output from doHMRF
k	k to write results for
betas_to_view	results from different betas that you want to view
print_command	see the python command

Value

data.table with HMRF results for each b and the selected k

Index