Package 'Giotto'

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Title Spatial single-cell transcriptomics pipeline.

Version 0.2.0

Description Pipeline to process, analyze and visualize (spatial) single-cell expression data.

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Encoding UTF-8

LazyData true

RoxygenNote 7.0.1

Depends data.table (>= 1.12.2),
ggplot2 (>= 3.1.1),
base (>= 3.5.1),
utils (>= 3.5.1),
R (>= 3.5.1)

Imports Rtsne (>= 0.15),
uwot (>= 0.0.0.9010),
FactoMineR (>= 1.34),
factoextra (>= 1.0.5),
cowplot (>= 0.9.4),
grDevices,
RColorBrewer (>= 1.1-2),
jackstraw (>= 1.3),
dbscan (>= 1.1-3),
ggalluvial (>= 0.9.1),
scales (>= 1.0.0),
ComplexHeatmap (>= 1.20.0),
qvalue (>= 2.14.1),
lfa (>= 1.12.0),
igraph (>= 1.2.4.1),
plotly,
reticulate,
magrittr,
limma,
ggdendro,
smfishHmrf,
matrixStats (>= 0.55.0),
IRanges,
devtools,
reshape2,
ggraph,

Rcpp,
rlang (>= 0.4.3),
fitdistrplus

Suggests knitr,
rmarkdown,
MAST,
scran (>= 1.10.1),
png,
tiff,
biomaRt,
trendsceek,
multinet (>= 3.0.2)

biocViews

VignetteBuilder knitr

LinkingTo Rcpp,
RcppArmadillo

Remotes lambdamoses/smfishhmrf-r

R topics documented:

addCellMetadata *addCellMetadata*

Description

adds cell metadata to the giotto object

Usage

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

Arguments

gobject	giotto object
new_metadata	new cell metadata to use (data.table, data.frame, ...)
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

Examples

```
addCellMetadata(gobject)
```

addCellStatistics *addCellStatistics*

Description

adds cells statistics to the giotto object

Usage

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

Arguments

gobject	giotto object
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_genes: Denotes in how many genes are detected per cell
- perc_genes: Denotes what percentage of genes is detected per cell
- total_expr: Shows the total sum of gene expression per cell

Value

giotto object if return_gobject = TRUE

Examples

```
addCellStatistics(gobject)
```

---

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_cell_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

Examples

```
addGeneMetadata(gobject)
```

`addGeneStatistics` *addGeneStatistics*

Description

adds gene statistics to the giotto object

Usage

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

Arguments

`gobject`	giotto object
`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 gene metadata:

- nr_cells: Denotes in how many cells the gene is detected
- per_cells: Denotes in what percentage of cells the gene is detected
- total_expr: Shows the total sum of gene expression in all cells
- mean_expr: Average gene expression in all cells
- mean_expr_det: Average gene expression in cells with detectable levels of the gene

Value

giotto object if return_gobject = TRUE

Examples

```
addGeneStatistics(gobject)
```

---

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
name	specify a custom name

Details

Description ...

Value

giotto object

Examples

```
addHMRF(gobject)
```

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

Examples

```
addNetworkLayout(gobject)
```

addStatistics *addStatistics*

Description

adds genes and cells statistics to the giotto object

Usage

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

Arguments

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

Details

See addGeneStatistics and addCellStatistics

Value

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

Examples

```
addStatistics(gobject)
```

adjustGiottoMatrix *adjustGiottoMatrix*

Description

normalize and/or scale expresion values of Giotto object

Usage

```
adjustGiottoMatrix(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  batch_columns = NULL,
  covariate_columns = NULL,
  return_gobject = TRUE,
  update_slot = c("custom")
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
batch_columns	metadata columns that represent different batch (max = 2)
covariate_columns	metadata columns that represent covariates to regress out
return_gobject	boolean: return giotto object (default = TRUE)
update_slot	expression slot that will be updated (default = custom)

Details

This function implements the `limma::removeBatchEffect` function to remove known batch effects and to adjust expression values according to provided covariates.

Value

giotto object

Examples

```
adjustGiottoMatrix(gobject)
```

`aes_string2` *aes_string2*

Description

makes sure aes_string can also be used with names that start with numeric values

Usage

```
aes_string2(...)
```

all_plots_save_function *all_plots_save_function*

Description

Function to automatically save plots to directory of interest

Usage

```
all_plots_save_function(
  gobject,
  plot_object,
  save_dir = NULL,
  save_folder = NULL,
  save_name = NULL,
  default_save_name = "giotto_plot",
  save_format = NULL,
  show_saved_plot = F,
  ncol = 1,
  nrow = 1,
  scale = 1,
  base_width = NULL,
  base_height = NULL,
  base_aspect_ratio = NULL,
  units = NULL,
  dpi = NULL,
  limitsize = TRUE,
  ...
)
```

Arguments

gobject	giotto object
plot_object	object to plot
save_dir	directory to save to
save_folder	folder in save_dir to save to
save_name	name of plot
save_format	format (e.g. png, tiff, pdf, ...)
show_saved_plot	load & display the saved plot
ncol	number of columns
nrow	number of rows
scale	scale
base_width	width
base_height	height
base_aspect_ratio	aspect ratio

units	units
dpi	Plot resolution
limitsize	When TRUE (the default), ggsave will not save images larger than 50x50 inches, to prevent the common error of specifying dimensions in pixels.
...	additional parameters to ggplot_save_function or general_save_function

See Also

general_save_function

Examples

```
all_plots_save_function(gobject)
```

---

annotateGiotto *annotateGiotto*

Description

Converts cluster results into provided annotation.

Usage

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

Arguments

gobject	giotto object
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

```
annotateGiotto(gobject)
```

`annotateSpatialNetwork` *annotateSpatialNetwork*

Description

Annotate spatial network with cell metadata information.

Usage

```
annotateSpatialNetwork(
  gobject,
  spatial_network_name = "spatial_network",
  cluster_column
)
```

Arguments

`gobject`	giotto object
`spatial_network_name`	name of spatial network to use
`cluster_column`	name of column to use for clusters

Value

annotated network in data.table format

Examples

```
annotateSpatialNetwork(gobject)
```

`annotate_spatlocs_with_spatgrid_2D` *annotate_spatlocs_with_spatgrid_2D*

Description

annotate spatial locations with 2D spatial grid information

Usage

```
annotate_spatlocs_with_spatgrid_2D(spatloc, spatgrid)
```

Arguments

`spatloc`	spatial_locs slot from giotto object
`spatgrid`	selected spatial_grid slot from giotto object

Value

annotated spatial location data.table

Examples

```
annotate_spatlocs_with_spatgrid_2D()
```

`annotate_spatlocs_with_spatgrid_3D` *annotate_spatlocs_with_spatgrid_3D*

Description

annotate spatial locations with 3D spatial grid information

Usage

```
annotate_spatlocs_with_spatgrid_3D(spatloc, spatgrid)
```

Arguments

`spatloc`	spatial_locs slot from giotto object
`spatgrid`	selected spatial_grid slot from giotto object

Value

annotated spatial location data.table

Examples

```
annotate_spatlocs_with_spatgrid_3D()
```

`average_gene_gene_expression_in_groups` *average_gene_gene_expression_in_groups*

Description

calculate average expression per cluster

Usage

```
average_gene_gene_expression_in_groups(
  gobject,
  cluster_column = "cell_types",
  gene_set_1,
  gene_set_2
)
```

Arguments

gobject	giotto object to use
cluster_column	cluster column with cell type information
gene_set_1	first specific gene set from gene pairs
gene_set_2	second specific gene set from gene pairs

Details

Details will follow soon.

Value

data.table with average expression scores for each cluster

Examples

```
average_gene_gene_expression_in_groups(gobject)
```

---

binGetSpatialGenes *binGetSpatialGenes*

Description

Rapid computation of genes that are spatially clustered

Usage

```
binGetSpatialGenes(
  gobject,
  bin_method = c("kmeans", "rank"),
  expression_values = c("normalized", "scaled", "custom"),
  subset_genes = NULL,
  spatial_network_name = "spatial_network",
  nstart = 3,
  iter_max = 10,
  percentage_rank = 10,
  do_fisher_test = TRUE,
  calc_hub = FALSE,
  hub_min_int = 3,
  get_av_expr = TRUE,
  get_high_expr = TRUE,
  do_parallel = TRUE,
  cores = NA,
  verbose = T
)
```

Arguments

gobject	giotto object
bin_method	method to binarize gene expression
expression_values	expression values to use
subset_genes	only select a subset of genes to test
spatial_network_name	name of spatial network to use (default = 'spatial_network')
nstart	kmeans: nstart parameter
iter_max	kmeans: iter.max parameter
percentage_rank	percentage of top cells for binarization
do_fisher_test	perform fisher test
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
do_parallel	run calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
verbose	be verbose

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 k-nearest neighbor network
- 3. contingency table: A contingency table is calculated based on all pairwise cell-cell interactions (0-0, 0-1, 1-0 or 1-1)
- 4. For each gene an odds-ratio (OR) and fisher.test (optional) is calculated

Additionally 2 other statistics are provided (optional):

- Number of cells with high expression (binary = 1)
- total of high expressing cells

By selecting a subset of likely spatial genes (e.g. highly variable genes) or using multiple cores the function will be much faster.

Value

data.table with results (see details)

Examples

```
binGetSpatialGenes(gobject)
```

`binGetSpatialGenesOld` *binGetSpatialGenesOld*

Description

Rapid computation of genes that are spatially clustered

Usage

```
binGetSpatialGenesOld(
  gobject,
  bin_method = c("kmeans", "rank"),
  expression_values = c("normalized", "scaled", "custom"),
  subset_genes = NULL,
  spatial_network_name = "spatial_network",
  nstart = 3,
  iter_max = 10,
  percentage_rank = 10,
  do_fisher_test = F,
  community_expectation = 5,
  verbose = F
)
```

Arguments

`gobject`	giotto object
`bin_method`	method to binarize gene expression
`expression_values`	expression values to use
`subset_genes`	only select a subset of genes to test
`spatial_network_name`	name of spatial network to use (default = 'spatial_network')
`nstart`	kmeans: nstart parameter
`iter_max`	kmeans: iter.max parameter
`do_fisher_test`	perform fisher test
`community_expectation`	cell degree expectation in spatial communities
`verbose`	be verbose
`rank_percentage`	percentage of top cells for binarization

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 k-nearest neighbor network

- 3. contingency table: A contingency table is calculated based on all pairwise cell-cell interactions (0-0, 0-1, 1-0 or 1-1)
- 4. For each gene an odds-ratio (OR) and fisher.test (optional) is calculated

Additionally 2 other statistics are provided:

- Number of cells with high expression (binary = 1)
- total and ratio of highly connected cells: Cells with a connectivity higher than community_expectation

By selecting a subset of likely spatial genes (e.g. highly variable genes) the function will be much faster.

Value

data.table with results (see details)

Examples

```
binGetSpatialGenesOld(gobject)
```

`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

```
calculateHVG(gobject)
```

`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

```
calculateMetaTable(gobject)
```

`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

Examples

```
calculateMetaTableCells(gobject)
```

---

calculate_spatial_genes_python
calculate_spatial_genes_python

Description

Calculate spatial genes using distance matrix.

Usage

```
calculate_spatial_genes_python(
  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

Details

Description of how we compute spatial pattern genes.

Value

data.table with spatial scores

Examples

```
calculate_spatial_genes_python(gobject)
```

`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

Examples

```
cellProximityBarplot(CPscore)
```

`cellProximityEnrichment` *cellProximityEnrichment*

Description

Compute cell-cell interaction enrichment (observed vs expected)

Usage

```
cellProximityEnrichment(
  gobject,
  spatial_network_name = "spatial_network",
  cluster_column,
  number_of_simulations = 100
)
```

Arguments

`gobject`	giotto object
`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

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.

Examples

```
cellProximityEnrichment(gobject)
```

`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

Examples

```
cellProximityHeatmap(CPscore)
```

`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

Examples

```
cellProximityNetwork(CPscore)
```

---

cellProximitySpatPlot *cellProximitySpatPlot*

Description

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

Usage

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

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')

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 underlying spatial network

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_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

Examples

```
cellProximitySpatPlot(gobject)
```

`cellProximitySpatPlot2D` *cellProximitySpatPlot2D*

Description

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

Usage

```
cellProximitySpatPlot2D(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = "sdimx",
  sdimy = "sdimy",
  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 = "spatial_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,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "cellProximitySpatPlot2D"
)
```

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')
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 underlying spatial network
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_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

Examples

```
cellProximitySpatPlot2D(gobject)
```

`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 = "spatial_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 underlying spatial network
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
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

Details

Description of parameters.

Value

plotly

Examples

```
cellProximitySpatPlot3D(gobject)
```

`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 = "spatial_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_network	show underlying spatial network
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_other_border_col	border color of other points
point_other_border_stroke	stroke size of other points

Details

Description of parameters.

Value

ggplot or plotly

Examples

```
cellProximityVisPlot(gobject)
```

cellProximityVisPlot_2D_ggplot
cellProximityVisPlot_2D_ggplot

Description

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

Usage

```
cellProximityVisPlot_2D_ggplot(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = NULL,
  sdimy = 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 = "spatial_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,
  ...
)
```

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')
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 underlying spatial network

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_other_border_col
: border color of other points

point_other_border_stroke
: stroke size of other points

Details

Description of parameters.

Value

ggplot

Examples

```
cellProximityVisPlot_2D_ggplot(gobject)
```

`cellProximityVisPlot_2D_plotly` *cellProximityVisPlot_2D_plotly*

Description

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

Usage

```
cellProximityVisPlot_2D_plotly(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = NULL,
  sdimy = 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 = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  show_legend = T,
  point_size_select = 2,
  point_size_other = 1,
  point_alpha_other = 0.3,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  ...
)
```

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')
`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 underlying spatial network

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

coord_fix_ratio
: fix ratio between x and y-axis

Details

Description of parameters.

Value

plotly

Examples

```
cellProximityVisPlot_2D_plotly(gobject)
```

---

cellProximityVisPlot_3D_plotly
cellProximityVisPlot_3D_plotly

Description

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

Usage

```
cellProximityVisPlot_3D_plotly(
  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 = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  show_legend = T,
  point_size_select = 2,
  point_size_other = 1,
  point_alpha_other = 0.5,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  ...
)
```

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 underlying spatial network
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
coord_fix_ratio	fix ratio between x and y-axis

Details

Description of parameters.

Value

plotly

Examples

```
cellProximityVisPlot_3D_plotly(gobject)
```

`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

named vector with giotto instructions

Examples

```
changeGiottoInstructions()
```

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

Examples

```
clusterCells(gobject)
```

---

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

Examples

```
clusterSpatialCorGenes(gobject)
```

---

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
)
```

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

Value

combined data.table with spatial and expression communication data

Examples

```
combCCcom(gobject)
```

combineCellProximityGenes
combineCellProximityGenes

Description

Combine CPG scores in a pairwise manner.

Usage

```
combineCellProximityGenes(
  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	cell proximity 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

Examples

```
combineCellProximityGenes(gobject)
```

`combineCellProximityGenes_per_interaction` *combineCellProximityGenes_per_interaction*

Description

Combine CPG scores per interaction

Usage

```
combineCellProximityGenes_per_interaction(
  cpgObject,
  sel_int,
  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
)
```

Examples

```
combineCellProximityGenes_per_interaction()
```

`combineCPG` *combineCPG*

Description

Combine CPG scores in a pairwise manner.

Usage

```
combineCPG(
  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	cell proximity 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

Examples

```
combineCPG(gobject)
```

`combineMetadata` *combineMetadata*

Description

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

Usage

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

Arguments

gobject	Giotto object
spat_enr_names	names of spatial enrichment results to include

Value

Extended cell metadata in data.table format.

Examples

```
combineMetadata(gobject)
```

`combine_ints_f` *combine_ints_f*

Description

function to combine gene enrichment interactions

Usage

```
combine_ints_f(
  cell_int,
  all_ints,
  unif_gene_scores,
  specific_genes_1 = NULL,
  specific_genes_2 = NULL,
  min_cells = 5,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.5
)
```

Arguments

`cell_int`	selected cell interaction
`all_ints`	all interactions
`unif_gene_scores`	unif_gene_scores results
`specific_genes_1`	specific source genes (see details)
`specific_genes_2`	specific target genes (see details)
`min_cells`	min number of cells threshold
`min_spat_diff`	spatial difference threshold
`min_log2_fc`	log2 fold-change threshold
`min_pval`	p-value threshold

Value

Gene to gene scores 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

Examples

```
convertEnsemblToGeneSymbol(matrix)
```

---

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
)
```

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
dpi	resolution for raster images
height	height of plots
width	width of plots

Value

named vector with giotto instructions

Examples

```
createGiottoInstructions()
```

---

createGiottoObject *create Giotto object*

Description

Function to create a giotto object

Usage

```
createGiottoObject(
  raw_exprs,
  spatial_locs = NULL,
  norm_expr = NULL,
  norm_scaled_expr = NULL,
  custom_expr = NULL,
  cell_metadata = NULL,
  gene_metadata = 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,
  offset_file = NULL,
  instructions = NULL
)
```

Arguments

raw_exprs	matrix with raw expression counts [required]
spatial_locs	data.table or data.frame with coordinates for cell centroids
norm_expr	normalized expression values
norm_scaled_expr	scaled expression values
custom_expr	custom expression values
cell_metadata	cell annotation metadata
gene_metadata	gene annotation metadata
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)
offset_file	file used to stitch fields together (optional)
instructions	list of instructions or output result from createGiottoInstructions

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. To include spatial information about cells (or regions) you need to provide a data.table or data.frame 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 reductions
- nearest neighbours networks

Value

giotto object

Examples

```
createGiottoObject(raw_exprs, spatial_locs)
```

`createHeatmap_DT` *createHeatmap_DT*

Description

creates order for clusters

Usage

```
createHeatmap_DT(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  cluster_column = NULL,
  cluster_order = c("size", "correlation", "custom"),
  cluster_custom_order = NULL,
  cluster_cor_method = "pearson",
  cluster_hclust_method = "ward.D",
  gene_order = c("custom", "correlation"),
  gene_custom_order = NULL,
  gene_cor_method = "pearson",
  gene_hclust_method = "complete"
)
```

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_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

Details

Creates input data.tables for plotHeatmap function.

Value

list

Examples

```
createHeatmap_DT(gobject)
```

`createMetagenes` *createMetagenes*

Description

This function creates an average metagene for gene clusters.

Usage

```
createMetagenes(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  gene_clusters,
  name = "metagene",
  return_gobject = TRUE
)
```

Arguments

`gobject`	Giotto object
`expression_values`	expression values to use
`gene_clusters`	numerical vector with genes as names
`name`	name of the metagene results
`return_gobject`	return giotto object

Details

An example for the 'gene_clusters' could be like this: cluster_vector = c(1, 1, 2, 2); names(cluster_vector) = c('geneA', 'geneB', 'geneC', 'geneD')

Value

giotto object

Examples

```
createMetagenes(gobject)
```

createNearestNetwork *createNearestNetwork*

Description

create a nearest neighbour (NN) network

Usage

```
createNearestNetwork(
  gobject,
  type = c("sNN", "kNN"),
  dim_reduction_to_use = "pca",
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  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
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
genes_to_use	if dim_reduction_to_use = NULL, which genes 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

```
createNearestNetwork(gobject)
```

`createSpatialEnrich` *createSpatialEnrich*

Description

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

Usage

```
createSpatialEnrich(
  gobject,
  enrich_method = c("PAGE", "rank", "hypergeometric"),
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
  p_value = TRUE,
  n_genes = 100,
  n_times = 1000,
  top_percentage = 5,
  output_enrichment = c("original", "zscore"),
  name = "PAGE",
  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
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 = TRUE)
n_genes	(page/rank) number of randomly selected genes for each permuation
n_times	(page/rank) number of permutation iterations to calculate p-value
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
return_gobject	return giotto object

Details

For details see the individual functions:

- PAGE: PAGEEnrich
- PAGE: rankEnrich
- PAGE: hyperGeometricEnrich

Value

Giotto object or enrichment results if return_gobject = FALSE

Examples

```
createSpatialEnrich(gobject)
```

`createSpatialGrid` *createSpatialGrid*

Description

Create a spatial grid.

Usage

```
createSpatialGrid(
  gobject,
  sdimx_stepsize = NULL,
  sdimy_stepsize = NULL,
  sdimz_stepsize = NULL,
  minimum_padding = 1,
  name = "spatial_grid",
  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

Examples

```
createSpatialGrid(gobject)
```

createSpatialGrid_2D *createSpatialGrid_2D*

Description

create a spatial grid for 2D spatial data.

Usage

```
createSpatialGrid_2D(
  gobject,
  sdimx_stepsize = NULL,
  sdimy_stepsize = NULL,
  minimum_padding = 1,
  name = "spatial_grid",
  return_gobject = TRUE
)
```

Arguments

gobject	giotto object
sdimx_stepsize	stepsize along the x-axis
sdimy_stepsize	stepsize along the y-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

Examples

```
createSpatialGrid_2D(gobject)
```

createSpatialGrid_3D *createSpatialGrid_3D*

Description

Create a spatial grid for 3D spatial data.

Usage

```
createSpatialGrid_3D(
  gobject,
  sdimx_stepsize = NULL,
  sdimy_stepsize = NULL,
  sdimz_stepsize = NULL,
  minimum_padding = 1,
  name = "spatial_grid",
  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

Examples

```
createSpatialGrid_3D(gobject)
```

createSpatialNetwork *createSpatialNetwork*

Description

Create a spatial network based on cell centroid physical distances.

Usage

```
createSpatialNetwork(
  gobject,
  k = 4,
  dimensions = "all",
  maximum_distance = NULL,
  minimum_k = 0,
  name = "spatial_network",
  verbose = F,
  return_gobject = TRUE
)
```

Arguments

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

Details

Creates a spatial network connecting single-cells based on their physical distance to each other. Number of neighbors can be determined by k, 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 specifiies 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

Value

giotto object with updated spatial network slot

Examples

```
createSpatialNetwork(gobject)
```

create_average_detection_DT *create_average_detection_DT*

Description

calculates average gene detection for a cell metadata factor (e.g. cluster)

Usage

```
create_average_detection_DT(
  gobject,
  meta_data_name,
  expression_values = c("normalized", "scaled", "custom"),
  detection_threshold = 0
)
```

Arguments

gobject	giotto object
meta_data_name	name of metadata column to use
expression_values	which expression values to use
detection_threshold	detection threshold to consider a gene detected

Value

data.table with average gene epression values for each factor

create_average_DT *create_average_DT*

Description

calculates average gene expression for a cell metadata factor (e.g. cluster)

Usage

```
create_average_DT(
  gobject,
  meta_data_name,
  expression_values = c("normalized", "scaled", "custom")
)
```

Arguments

gobject	giotto object
meta_data_name	name of metadata column to use
expression_values	which expression values to use

Value

data.table with average gene epression values for each factor

---

`create_cell_type_random_cell_IDs` *create_cell_type_random_cell_IDs*

Description

creates randomized cell ids within a selection of cell types

Usage

```
create_cell_type_random_cell_IDs(
  gobject,
  cluster_column = "cell_types",
  needed_cell_types
)
```

Arguments

`gobject`	giotto object to use
`cluster_column`	cluster column with cell type information
`needed_cell_types`	vector of cell type names for which a random id will be found

Details

Details will follow.

Value

list of randomly sampled cell ids with same cell type composition

Examples

```
create_cell_type_random_cell_IDs(gobject)
```

create_cluster_matrix *create_cluster_matrix*

Description

creates aggregated matrix for a given clustering

Usage

```
create_cluster_matrix(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  gene_subset = NULL
)
```

Examples

```
create_cluster_matrix(gobject)
```

create_dimObject *create_dimObject*

Description

Creates an object that stores a dimension reduction output

Usage

```
create_dimObject(
  name = "test",
  reduction_method = NULL,
  coordinates = NULL,
  misc = NULL,
  my_rownames = NULL
)
```

Arguments

name	arbitrary name for object
reduction_method	method used to reduce dimensions
coordinates	accepts the coordinates after dimension reduction
misc	any additional information will be added to this slot

Value

number of distinct colors

`decide_cluster_order` *decide_cluster_order*

Description

creates order for clusters

Usage

```
decide_cluster_order(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  cluster_column = NULL,
  cluster_order = c("size", "correlation", "custom"),
  cluster_custom_order = NULL,
  cor_method = "pearson",
  hclust_method = "ward.D"
)
```

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
`cor_method`	method for correlation
`hclust_method`	method for hierarchical clustering

Details

Calculates order for clusters.

Value

custom

Examples

```
decide_cluster_order(gobject)
```

`detectSpatialCorGenes` *detectSpatialCorGenes*

Description

Detect genes that are spatially correlated

Usage

```
detectSpatialCorGenes(
  gobject,
  method = c("grid", "network"),
  expression_values = c("normalized", "scaled", "custom"),
  subset_genes = NULL,
  spatial_network_name = "spatial_network",
  network_smoothing = NULL,
  spatial_grid_name = "spatial_grid",
  min_cells_per_grid = 4,
  cor_method = c("pearson", "kendall", "spearman")
)
```

Arguments

`gobject`	giotto object
`method`	method to use for spatial averaging
`expression_values`	gene expression values to use
`subset_genes`	subset of genes to use
`spatial_network_name`	name of spatial network to use
`network_smoothing`	smoothing factor beteen 0 and 1 (default: automatic)
`spatial_grid_name`	name of spatial grid to use
`min_cells_per_grid`	minimum number of cells to consider a grid
`b`	smoothing factor beteen 0 and 1 (default: automatic)

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

showSpatialCorGenes

Examples

```
detectSpatialCorGenes(gobject)
```

---

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'

Examples

```
detectSpatialPatterns(gobject)
```

`dimCellPlot` *dimCellPlot*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimCellPlot(
  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_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_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 = "dimCellPlot"
)
```

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_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

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_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

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

cell_color
: color for cells (see details)

color_as_factor
: convert color column to factor

cell_color_code
: named vector with colors

title
: title for plot, defaults to cell_color parameter

Details

Description of parameters. For 3D plots see dimCellPlot2D

Value

ggplot

Examples

```
dimCellPlot(gobject)
```

`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_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_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_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
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_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

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

cell_color color for cells (see details)

color_as_factor convert color column to factor

cell_color_code named vector with colors

title title for plot, defaults to cell_color parameter

Details

Description of parameters. For 3D plots see `dimPlot3D`

Value

ggplot

Examples

```
dimCellPlot2D(gobject)
```

dimGenePlot *dimGenePlot*

Description

Visualize cells and gene expression according to dimension reduction coordinates

Usage

```
dimGenePlot(
  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,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  point_border_col = "black",
  point_border_stroke = 0.1,
  midpoint = 0,
  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 = "dimGenePlot"
)
```

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

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

`scale_alpha_with_expression`
: scale expression with ggplot alpha parameter

`point_size`
: size of point (cell)

`point_border_col`
: color of border around points

`point_border_stroke`
: stroke size of border around points

`midpoint`
: size of point (cell)

`show_legend`
: show legend

`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 from `all_plots_save_function`

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

`...`
: parameters for cowplot::save_plot()

Details

Description of parameters.

Value

ggplot

See Also

`dimGenePlot3D`

Examples

```
dimGenePlot(gobject)
```

---

dimGenePlot2D *dimGenePlot2D*

Description

Visualize cells and 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,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  point_border_col = "black",
  point_border_stroke = 0.1,
  midpoint = 0,
  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
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_border_col	color of border around points
point_border_stroke	stroke size of border around points
midpoint	size of point (cell)
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 from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for cowplot::save_plot()

Details

Description of parameters.

Value

ggplot

See Also

dimGenePlot3D

Examples

```
dimGenePlot2D(gobject)
```

---

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
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
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 from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for cowplot::save_plot()

Details

Description of parameters.

Value

ggplot

Examples

```
dimGenePlot3D(gobject)
```

dimPlot *dimPlot*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimPlot(
  gobject,
  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 = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  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,
  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_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,
  title = 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 = "dimPlot"
)
```

Arguments

gobject	giotto object
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

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_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

title
: title for plot, defaults to cell_color parameter

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 from `all_plots_save_function`

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

groub_by
: create multiple plots based on cell annotation column

Details

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

Value

ggplot

Examples

```
dimPlot(gobject)
```

dimPlot2D *dimPlot2D*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimPlot2D(
  gobject,
  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 = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  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,
  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_border_col = "black",
  point_border_stroke = 0.1,
  title = NULL,
  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 = "dimPlot2D"
)
```

Arguments

gobject	giotto object
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

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_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 from `all_plots_save_function`

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

groub_by
: create multiple plots based on cell annotation column

Details

Description of parameters. For 3D plots see `dimPlot3D`

Value

ggplot

Examples

```
dimPlot2D(gobject)
```

dimPlot2D_single *dimPlot2D_single*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
dimPlot2D_single(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  spat_enr_names = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  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,
  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_border_col = "black",
  point_border_stroke = 0.1,
  title = NULL,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  show_plot = NA,
  return_plot = NA,
```

```
  save_plot = NA,
  save_param = list(),
  default_save_name = "dimPlot2D_single"
)
```

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
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
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_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
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

Description of parameters. For 3D plots see dimPlot3D

Value

ggplot

Examples

```
dimPlot2D_single(gobject)
```

---

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,
  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
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 from `all_plots_save_function`

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

`show_legend`
: show legend

Details

Description of parameters.

Value

plotly

Examples

```
dimPlot3D(gobject)
```

direction_test_CPG *direction_test_CPG*

Description

shows direction of change

Usage

```
direction_test(x, min_fdr = 0.05)
```

Examples

```
direction_test_CPG()
```

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

```
doHclust(gobject)
```

---

doHMRF *doHMRF*

Description

Run HMRF

Usage

```
doHMRF(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  spatial_network_name = "spatial_network",
  spatial_genes = NULL,
  spatial_dimensions = c("sdimx", "sdimy", "sdimz"),
  dim_reduction_to_use = NULL,
  dim_reduction_name = "pca",
```

```
  dimensions_to_use = 1:10,
  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
name	name of HMRF run
k	number of HMRF domains
betas	betas to test for
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

Examples

```
doHMRF(gobject)
```

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

```
doKmeans(gobject)
```

`doLeidenCluster` *doLeidenCluster*

Description

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

Usage

```
doLeidenCluster(
  gobject,
  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
`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

Examples

```
doLeidenCluster(gobject)
```

---

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_variance = 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

Examples

```
doLeidenSubCluster(gobject)
```

---

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
gamma	[multinet] Resolution parameter for modularity in the generalized louvain method.
omega	[multinet] Inter-layer weight parameter in the generalized louvain method.
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

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

Examples

```
doLouvainCluster(gobject)
```

---

doLouvainCluster_community
doLouvainCluster_community

Description

cluster cells using a NN-network and the Louvain algorithm from the community module in Python

Usage

```
doLouvainCluster_community(
  gobject,
  name = "louvain_clus",
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  python_path = NULL,
  resolution = 1,
  weight_col = NULL,
  louv_random = F,
  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
python_path	specify specific path to python if required
resolution	resolution
weight_col	weight column to use for edges
louv_random	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

Details

This function is a wrapper for the Louvain algorithm implemented in Python, which can detect communities in graphs of nodes (cells). See the https://python-louvain.readthedocs.io/en/latest/index.htmlreadthedocs page for more information.

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

Value

giotto object with new clusters appended to cell metadata

Examples

```
doLouvainCluster_community(gobject)
```

doLouvainCluster_multinet *doLouvainCluster_multinet*

Description

cluster cells using a NN-network and the Louvain algorithm from the multinet package in R.

Usage

```
doLouvainCluster_multinet(
  gobject,
  name = "louvain_clus",
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  gamma = 1,
  omega = 1,
  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
gamma	Resolution parameter for modularity in the generalized louvain method.
omega	Inter-layer weight parameter in the generalized louvain method.
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

Details

See glouvain_ml from the multinet package in R for more information.

Value

giotto object with new clusters appended to cell metadata

Examples

```
doLouvainCluster_multinet(gobject)
```

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_variance = 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

Examples

```
doLouvainSubCluster(gobject)
```

doLouvainSubCluster_community
doLouvainSubCluster_community

Description

subcluster cells using a NN-network and the Louvain community detection algorithm

Usage

```
doLouvainSubCluster_community(
  gobject,
  name = "sub_louvain_comm_clus",
  cluster_column = NULL,
  selected_clusters = NULL,
  hvg_param = list(reverse_log_scale = T, difference_in_variance = 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,
  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
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 community 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 community clustering

Value

giotto object with new subclusters appended to cell metadata

See Also

doLouvainCluster_community

Examples

```
doLouvainSubCluster_community(gobject)
```

---

doLouvainSubCluster_multinet

doLouvainSubCluster_multinet

Description

subcluster cells using a NN-network and the Louvain multinet detection algorithm

Usage

```
doLouvainSubCluster_multinet(
  gobject,
  name = "sub_louvain_mult_clus",
  cluster_column = NULL,
  selected_clusters = NULL,
  hvg_param = list(reverse_log_scale = T, difference_in_variance = 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,
  gamma = 1,
  omega = 1,
  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
gamma	gamma
omega	omega
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
python_path	specify specific path to python if required

Details

This function performs subclustering using the Louvain multinet 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 multinet clustering

Value

giotto object with new subclusters appended to cell metadata

See Also

doLouvainCluster_multinet

Examples

```
doLouvainSubCluster_multinet(gobject)
```

`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

Examples

```
doRandomWalkCluster(gobject)
```

---

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

Examples

```
doSNNCluster(gobject)
```

---

do_cell_proximity_test *do_cell_proximity_test*

Description

Performs a selected differential test on subsets of a matrix

Usage

```
do_cell_proximity_test(
  expr_values,
  select_ind,
  other_ind,
  diff_test = c("permutation", "limma", "t.test", "wilcox"),
  n_perm = 100,
  adjust_method = c("bonferroni", "BH", "holm", "hochberg", "hommel", "BY", "fdr",
    "none"),
  cores = 2
)
```

Examples

```
do_cell_proximity_test()
```

`do_limmatest` *do_limmatest*

Description

Performs limma t.test on subsets of a matrix

Usage

```
do_limmatest(expr_values, select_ind, other_ind)
```

Examples

```
do_limmatest()
```

`do_multi_permuttest_random` *do_multi_permuttest_random*

Description

calculate multiple random values

Usage

```
do_multi_permuttest_random(
  expr_values,
  select_ind,
  other_ind,
  n = 100,
  cores = 2
)
```

Examples

```
do_multi_permuttest_random()
```

do_permuttest_original *do_permuttest_original*

Description

calculate original values

Usage

```
do_permuttest_original(expr_values, select_ind, other_ind, name = "orig")
```

Examples

```
do_permuttest_original()
```

do_permuttest_random *do_permuttest_random*

Description

calculate random values

Performs permutation test on subsets of a matrix

Usage

```
do_permuttest_random(expr_values, select_ind, other_ind, name = "perm_1")

do_permuttest(
  expr_values,
  select_ind,
  other_ind,
  n_perm = 100,
  adjust_method = "fdr",
  cores = 2
)
```

Examples

```
do_permuttest_random()
do_permuttest_random()
```

do_spatial_grid_averaging *do_spatial_grid_averaging*

Description

smooth gene expression over a defined spatial grid

Usage

```
do_spatial_grid_averaging(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  subset_genes = NULL,
  spatial_grid_name = "spatial_grid",
  min_cells_per_grid = 4
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
subset_genes	subset of genes to use
spatial_grid_name	name of spatial grid to use
min_cells_per_grid	minimum number of cells to consider a grid

Value

matrix with smoothened gene expression values based on spatial grid

Examples

```
do_spatial_grid_averaging(gobject)
```

do_spatial_knn_smoothing *do_spatial_knn_smoothing*

Description

smooth gene expression over a kNN spatial network

Usage

```
do_spatial_knn_smoothing(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  subset_genes = NULL,
  spatial_network_name = "spatial_network",
  b = NULL
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
subset_genes	subset of genes to use
spatial_network_name	name of spatial network to use
b	smoothing factor beteen 0 and 1 (default: automatic)

Details

This function will smoothen the gene expression values per cell according to its neighbors in the selected 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.

Value

matrix with smoothened gene expression values based on kNN spatial network

Examples

```
do_spatial_knn_smoothing(gobject)
```

---

do_ttest *do_ttest*

Description

Performs t.test on subsets of a matrix

Performs wilcoxon on subsets of a matrix

Usage

```
do_ttest(expr_values, select_ind, other_ind, adjust_method)

do_wilctest(expr_values, select_ind, other_ind, adjust_method)
```

Examples

```
do_ttest()
do_ttest()
```

`DT_removeNA` *DT_removeNA*

Description

set NA values to 0

Usage

```
DT_removeNA(DT)
```

`dt_to_matrix` *dt_to_matrix*

Description

converts data.table to matrix

Usage

```
dt_to_matrix(x)
```

Examples

```
dt_to_matrix(x)
```

`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

```
exportGiottoViewer(gobject)
```

`exprCellCellcom` *exprCellCellcom*

Description

Cell-Cell communication scores based on expression only

Usage

```
exprCellCellcom(
  gobject,
  cluster_column = "cell_types",
  random_iter = 100,
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  adjust_method = c("fdr", "bonferroni", "BH", "holm", "hochberg", "hommel", "BY",
    "none"),
  adjust_target = c("genes", "cells"),
  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
`adjust_method`	which method to adjust p-values
`adjust_target`	adjust multiple hypotheses at the cell or gene level
`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

Examples

```
exprCellCellcom(gobject)
```

extended_gini_fun *extended_gini_fun*

Description

calculate gini coefficient on a minimum length vector

Usage

```
extended_gini_fun(x, weights = rep(1, length = length(x)), minimum_length = 16)
```

Value

gini coefficient

extractNearestNetwork *extractNearestNetwork*

Description

Extracts a NN-network from a Giotto object

Usage

```
extractNearestNetwork(
  gobject,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  output = c("igraph", "data.table")
)
```

Arguments

gobject	giotto object
nn_network_to_use	kNN or sNN
network_name	name of NN network to be used
output	return a igraph or data.table object

Value

igraph or data.table object

Examples

```
extractNearestNetwork(gobject)
```

fDataDT *fDataDT*

Description

show gene metadata

Usage

```
fDataDT(gobject)
```

Arguments

gobject	giotto object

Value

data.table with gene metadata

Examples

```
pDataDT(gobject)
```

filterCellProximityGenes *filterCellProximityGenes*

Description

Filter cell proximity gene scores.

Usage

```
filterCellProximityGenes(
  cpgObject,
  min_cells = 5,
  min_int_cells = 3,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.5,
  direction = c("both", "up", "down")
)
```

Arguments

cpgObject	cell proximity gene score object
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
direction	differential expression directions to keep

Value

cpgObject that contains the filtered differential gene scores

Examples

```
filterCellProximityGenes(gobject)
```

---

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
)
```

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

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

```
filterCombinations(gobject)
```

---

filterCPG *filterCPG*

Description

Filter cell proximity gene scores.

Usage

```
filterCPG(
  cpgObject,
  min_cells = 5,
  min_int_cells = 3,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.5,
  direction = c("both", "up", "down")
)
```

Arguments

cpgObject	cell proximity gene score object
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
direction	differential expression directions to keep

Value

cpgObject that contains the filtered differential gene scores

Examples

```
filterCPG(gobject)
```

`filterCPGscores` *filterCPGscores*

Description

visualize Cell Proximity Gene enrichment scores

Usage

```
filterCPGscores(
  CPGscore,
  min_cells = 5,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.5,
  keep_int_duplicates = TRUE,
  direction = c("both", "up", "down")
)
```

Arguments

`min_cells`	min number of cells threshold
`min_fdr`	false_discovery threshold
`min_spat_diff`	spatial difference threshold
`min_log2_fc`	min log2 fold-change
`keep_int_duplicates`	keep both cell_A-cell_B and cell_B-cell_A
`direction`	expression changes to keep
`method`	visualization method

Details

This function filters the output from getCellProximityGeneScores based on false-discovery rate, minimum absolute difference, minimum log fold-change and direction of change.

Value

Gene to gene scores in data.table format

Examples

```
filterCPGscores(CPGscore)
```

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 = TRUE
)
```

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

Value

ggplot object

Examples

```
filterDistributions(gobject)
```

filterGiotto *filterGiotto*

Description

filter Giotto object based on expression threshold

Usage

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

Arguments

gobject	giotto object
expression_values	expression values to use
expression_threshold	threshold to consider a gene expressed
gene_det_in_min_cells	minimum # of cells that need to express a gene
min_det_genes_per_cell	minimum # of genes that need to be detected in a cell
verbose	verbose

Details

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

Value

giotto object

Examples

```
filterGiotto(gobject)
```

`findCellProximityGenes` *findCellProximityGenes*

Description

Identifies genes that are differentially expressed due to proximity to other cell types.

Usage

```
findCellProximityGenes(
  gobject,
  expression_values = "normalized",
  cluster_column,
  spatial_network_name = "spatial_network",
  minimum_unique_cells = 1,
  minimum_unique_int_cells = 1,
  diff_test = c("permutation", "limma", "t.test", "wilcox"),
  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
)
```

Arguments

`gobject`	giotto object
`expression_values`	expression values to use
`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
`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

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

Examples

```
findCellProximityGenes(gobject)
```

---

findCellProximityGenes_per_interaction *findCellProximityGenes_per_interaction*

Description

Identifies genes that are differentially expressed due to proximity to other cell types.

Usage

```
findCellProximityGenes_per_interaction(
  expr_values,
  cell_metadata,
  annot_spatnetwork,
  sel_int,
  minimum_unique_cells = 1,
  minimum_unique_int_cells = 1,
  exclude_selected_cells_from_test = T,
  diff_test = c("permutation", "limma", "t.test", "wilcox"),
  adjust_method = "bonferroni",
  nr_permutations = 100,
  cores = 1
)
```

Examples

```
findCellProximityGenes_per_interaction()
```

---

findCPG *findCPG*

Description

Identifies genes that are differentially expressed due to proximity to other cell types.

Usage

```
findCPG(
  gobject,
  expression_values = "normalized",
  cluster_column,
  spatial_network_name = "spatial_network",
  minimum_unique_cells = 1,
  minimum_unique_int_cells = 1,
  diff_test = c("permutation", "limma", "t.test", "wilcox"),
  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
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
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
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

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

Examples

```
findCPG(gobject)
```

---

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

```
findGiniMarkers(gobject)
```

`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

```
findGiniMarkers_one_vs_all(gobject)
```

`findMarkers` *findMarkers*

Description

Identify marker genes for selected clusters.

Usage

```
findMarkers(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  cluster_column,
  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

Examples

```
findMarkers(gobject)
```

---

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

Examples

```
findMarkers_one_vs_all(gobject)
```

`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,
  ...
)
```

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)
`...`	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.

Value

data.table with marker genes

Examples

```
findMastMarkers(gobject)
```

`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

```
findMastMarkers_one_vs_all(gobject)
```

`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,
  ...
)
```

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
`...`	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

```
findScranMarkers(gobject)
```

`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

```
findScranMarkers_one_vs_all(gobject)
```

find_grid_2D *find_grid_2D*

Description

find grid location in 2D

Usage

```
find_grid_2D(grid_DT, x_loc, y_loc)
```

find_grid_3D *find_grid_3D*

Description

find grid location in 3D

Usage

```
find_grid_3D(grid_DT, x_loc, y_loc, z_loc)
```

find_grid_x *find_grid_x*

Description

find grid location on x-axis

Usage

```
find_grid_x(grid_DT, x_loc)
```

find_grid_y *find_grid_y*

Description

find grid location on y-axis

Usage

```
find_grid_y(grid_DT, y_loc)
```

find_grid_z *find_grid_z*

Description

find grid location on z-axis

Usage

```
find_grid_z(grid_DT, z_loc)
```

fish_function *fish_function*

Description

perform fisher exact test

Usage

```
fish_function(x_to, x_from)
```

fish_function2 *fish_function2*

Description

perform fisher exact test

Usage

```
fish_function2(A, B, C, D)
```

FSV_show *FSV_show*

Description

Visualize spatial varible genes caculated by spatial_DE

Usage

```
FSV_show(
  results,
  ms_results = NULL,
  size = c(4, 2, 1),
  color = c("blue", "green", "red"),
  sig_alpha = 0.5,
  unsig_alpha = 0.5
)
```

Arguments

results	results caculated by spatial_DE
ms_results	ms_results caculated by spatial_DE
size	indicate different levels of qval
color	indicate different SV features
sig_alpha	transparency of significant genes
unsig_alpha	transparency of unsignificant genes

Details

Description of parameters.

Value

nothing

Examples

```
FSV_show(results)
```

GenePattern_show *GenePattern_show*

Description

Visualize genes distribution patterns calculated by spatial_AEH

Usage

```
GenePattern_show(
  gobject = NULL,
  AEH_results = NULL,
  sdimx = NULL,
  sdimy = NULL,
  point_size = 3,
  point_alpha = 1,
  low_color = "blue",
  mid_color = "white",
  high_color = "red",
  midpoint = 0
)
```

Arguments

gobject	giotto object
AEH_results	results from spatial_AEH
sdimx	x axis of spatial locus
sdimy	y axis of spatial locus
point_size	size of points to indicate cells
point_alpha	transparency of points to indicate cells
low_color	color to indicate low score level
mid_color	color to indicate middle score level
high_color	color to indicate high score level
midpoint	point to set mid_color

Details

Description of parameters.

Value

nothing

Examples

```
GenePattern_show(gobject,AEH_results)
```

`general_save_function` *general_save_function*

Description

Function to automatically save plots to directory of interest

Usage

```
general_save_function(
  gobject,
  plot_object,
  save_dir = NULL,
  save_folder = NULL,
  save_name = NULL,
  default_save_name = "giotto_plot",
  save_format = c("png", "tiff", "pdf", "svg"),
  show_saved_plot = F,
  base_width = NULL,
  base_height = NULL,
  base_aspect_ratio = NULL,
  units = NULL,
  dpi = NULL,
  ...
)
```

Arguments

`gobject`	giotto object
`plot_object`	non-ggplot object to plot
`save_dir`	directory to save to
`save_folder`	folder in save_dir to save to
`save_name`	name of plot
`save_format`	format (e.g. png, tiff, pdf, ...)
`show_saved_plot`	load & display the saved plot
`base_width`	width
`base_height`	height
`base_aspect_ratio`	aspect ratio
`units`	units
`dpi`	Plot resolution

Examples

```
general_save_function(gobject)
```

`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 tt 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

expression matrix from 10X

Examples

```
get10Xmatrix(10Xmatrix)
```

`getCellProximityGeneScores` *getCellProximityGeneScores*

Description

Compute cell-cell interaction enrichment (observed vs expected)

Usage

```
getCellProximityGeneScores(
  gobject,
  spatial_network_name = "spatial_network",
  cluster_column = "louvain_clus.1",
  selected_genes = NULL,
  expression_values = c("normalized", "scaled", "custom"),
  do_diff_test = TRUE,
  diff_test = c("t.test", "wilcox"),
  false_discovery_test = c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY",
    "fdr", "none"),
  false_discovery_target = c("cell_interactions", "genes"),
  minimum_unique_cells = NA,
  fold_change_addendum = 0.1,
  in_two_directions = TRUE,
  exclude_selected_cells_from_test = F,
  do_parallel = TRUE,
  cores = NA,
  verbose = T
)
```

Arguments

gobject	giotto object
spatial_network_name	name of spatial network to use
cluster_column	name of column to use for clusters
selected_genes	selection of genes to perform calculations for
expression_values	expression values to use
do_diff_test	perform differential test
diff_test	which differential expression test
false_discovery_test	test to adjust p-values for multiple hypothesis testing
false_discovery_target	adjust p-values per cell-cell pair or per gene
minimum_unique_cells	minimum number of cells needed to proceed
fold_change_addendum	constant to add when calculating log2 fold-change
in_two_directions	shows enrichment in both directions: cell1-cell2, cell2-cell1
exclude_selected_cells_from_test	exclude certain cells from test
do_parallel	run enrichment calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
verbose	verbose

Details

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

- genes: All or selected list of tested genes
- cell_expr_1: average gene expression in cell type 1 from unified_int cell-cell interaction
- cell_expr_2: average gene expression in cell type 2 from unified_int cell-cell interaction
- comb_expr: combined average gene expression in cell type 1 and 2 from unified_int cell-cell interaction
- all_cell_expr_1: average gene expression for all cells from cell type 1
- all_cell_expr_2: average gene expression for all cells from cell type 2
- all_comb_expr: combined average gene expression for all cells from cell type 1 and 2
- pval_1: p-value from test between interacting cells and all cells from cell type 1
- pval_2: p-value from test between interacting cells and all cells from cell type 2
- cell_type_1: first cell type of cell-cell interaction
- cell_type_2: second cell type of cell-cell interaction
- interaction: the cell-cell interaction, based on physical proximity
- nr_1: number of cell type 1 in the unified cell-cell interaction
- nr_2: number of cell type 2 in the unified cell-cell interaction
- all_nr_1: number of all cell type 1 in the whole dataset
- all_nr_2: number of all cell type 2 in the whole dataset
- diff_spat: difference between comb_expr and all_comb_expr
- diff_spat_1: difference between cell_expr_1 and all_cell_expr_1
- diff_spat_2: difference between cell_expr_1 and all_cell_expr_1
- log2fc_spat_1: fold-change of diff_spat_1
- log2fc_spat_2: fold-change of diff_spat_2
- log2fc_spat: fold-change of diff_spat
- type_int: type of interaction
- unified_int: interaction with alphabetically sorted cell type 1 and cell type 2
- unif_int_rank: 1 or 2
- fdr_1: fdr from test between interacting cells and all cells from cell type 1
- fdr_2: fdr from test between interacting cells and all cells from cell type 2

Value

Cell Proximity Gene scores (CPGscores) in data.table format

Examples

```
getCellProximityGeneScores(gobject)
```

`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

```
getClusterSimilarity(gobject)
```

`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

```
getDendrogramSplits(gobject)
```

---

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

`getGeneToGeneScores` *getGeneToGeneScores*

Description

Compute gene-gene enrichment scores.

Usage

```
getGeneToGeneScores(
  CPGscore,
  selected_genes = NULL,
  specific_genes_1 = NULL,
  specific_genes_2 = NULL,
  min_cells = 5,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.5,
  direction = c("both", "up", "down"),
  fold_change_addendum = 0.1,
  do_parallel = TRUE,
  cores = NA,
  verbose = TRUE
)
```

Arguments

CPGscore	CPGscore, output from getCellProximityGeneScores()
selected_genes	select subset of genes
specific_genes_1	specific source genes (see details)
specific_genes_2	specific target genes (see details)
min_cells	min number of cells threshold
min_spat_diff	spatial difference threshold
min_log2_fc	log2 fold-change threshold
direction	up or downregulation or both
fold_change_addendum	constant to add when calculating log2 fold-change
do_parallel	run enrichment calculations in parallel with mclapply
cores	number of cores to use if do_parallel = TRUE
verbose	verbose
min_pval	p-value threshold

Details

This converts the single gene cell proximityscores into pairwise combinations of genes, which allows you to determine if 2 genes are differentially expressed in interacting cell types.

Value

Gene to gene scores in data.table format

Examples

```
getGeneToGeneScores(CPGscore)
```

---

get_cell_to_cell_sorted_name_conversion

get_cell_to_cell_sorted_name_conversion

Description

creates unified cell-cell interaction names

Usage

```
get_cell_to_cell_sorted_name_conversion(all_cell_types)
```

Examples

```
get_cell_to_cell_sorted_name_conversion()
```

---

get_interaction_gene_enrichment

get_interaction_gene_enrichment

Description

Computes gene enrichment between all interactions

Usage

```
get_interaction_gene_enrichment(
  spatial_network,
  unified_int_col = "unified_int",
  source_col = "source_clus",
  source_IDs = "from",
  neighb_col = "neighb_clus",
  neighb_IDs = "to",
  expression_matrix,
  cell_annotation,
  annotation_ID = "uniq_ID",
  cell_type_col,
  do_diff_test = T,
```

```
  diff_test = c("t.test", "wilcox"),
  minimum_unique_cells = NA,
  exclude_selected_cells_from_test = T,
  do_parallel = TRUE,
  cores = NA,
  verbose = T
)
```

Examples

```
get_interaction_gene_enrichment()
```

`get_specific_interaction_gene_enrichment` *get_specific_interaction_gene_enrichment*

Description

Computes gene enrichment between specified interaction

Usage

```
get_specific_interaction_gene_enrichment(
  sub_spatial_network,
  source_col = "source_clus",
  source_IDs = "from",
  neighb_col = "neighb_clus",
  neighb_IDs = "to",
  expression_matrix,
  interaction_name = "to_specify",
  cell_annotation,
  annotation_ID = "uniq_ID",
  cell_type_col,
  do_diff_test = T,
  diff_test = c("t.test", "wilcox"),
  minimum_unique_cells = NA,
  exclude_selected_cells_from_test = T
)
```

Examples

```
get_specific_interaction_gene_enrichment()
```

ggplot_save_function *ggplot_save_function*

Description

Function to automatically save plots to directory of interest

Usage

```
ggplot_save_function(
  gobject,
  plot_object,
  save_dir = NULL,
  save_folder = NULL,
  save_name = NULL,
  default_save_name = "giotto_plot",
  save_format = NULL,
  show_saved_plot = F,
  ncol = 1,
  nrow = 1,
  scale = 1,
  base_width = NULL,
  base_height = NULL,
  base_aspect_ratio = NULL,
  units = NULL,
  dpi = NULL,
  limitsize = TRUE,
  ...
)
```

Arguments

gobject	giotto object
plot_object	ggplot object to plot
save_dir	directory to save to
save_folder	folder in save_dir to save to
save_name	name of plot
save_format	format (e.g. png, tiff, pdf, ...)
show_saved_plot	load & display the saved plot
ncol	number of columns
nrow	number of rows
scale	scale
base_width	width
base_height	height
base_aspect_ratio	aspect ratio

units	units
dpi	Plot resolution
limitsize	When TRUE (the default), ggsave will not save images larger than 50x50 inches, to prevent the common error of specifying dimensions in pixels.

See Also

cowplot::save_plot

Examples

```
ggplot_save_function(gobject)
```

---

giotto-class *S4 giotto Class*

Description

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

Slots

raw_exprs raw expression counts

norm_expr normalized expression counts

norm_scaled_expr normalized and scaled expression counts

custom_expr custom normalized counts

spatial_locs spatial location coordinates for cells

cell_metadata metadata for cells

gene_metadata metadata for genes

cell_ID unique cell IDs

gene_ID unique gene IDs

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

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

dimension_reduction slot to save dimension reduction coordinates

nn_network nearest neighbor network in igraph format

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

heatmSpatialCorGenes *heatmSpatialCorGenes*

Description

Create heatmap of spatially correlated genes

Usage

```
heatmSpatialCorGenes(
  gobject,
  spatCorObject,
  use_clus_name = NULL,
  show_cluster_annot = TRUE,
  show_row_dend = T,
  show_column_dend = F,
  show_row_names = F,
  show_column_names = F,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "heatmSpatialCorGenes",
  ...
)
```

Arguments

gobject	giotto object
spatCorObject	spatial correlation object
use_clus_name	name of clusters to visualize (from clusterSpatialCorGenes())
show_cluster_annot	show cluster annotation on top of heatmap
show_row_dend	show row dendrogram
show_column_dend	show column dendrogram
show_row_names	show row names
show_column_names	show column names
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 parameters to the Heatmap function from ComplexHeatmap

Value

Heatmap generated by ComplexHeatmap

Examples

```
heatmSpatialCorGenes(gobject)
```

`hyperGeometricEnrich` *hyperGeometricEnrich*

Description

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

Usage

```
hyperGeometricEnrich(
  gobject,
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
  top_percentage = 5,
  output_enrichment = c("original", "zscore")
)
```

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

Details

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

Value

data.table with enrichment results

Examples

```
hyperGeometricEnrich(gobject)
```

`kmeans_binarize` *kmeans_binarize*

Description

create binarized scores using kmeans

Usage

```
kmeans_binarize(x, nstart = 3, iter.max = 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

Examples

```
loadHMRF(gobject)
```

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

Examples

```
makeSignMatrixPAGE()
```

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, gobject = NULL)
```

Arguments

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

Value

matrix

See Also

rankEnrich

Examples

```
makeSignMatrixRank()
```

---

make_simulated_network *make_simulated_network*

Description

Simulate random network.

Usage

```
make_simulated_network(
  gobject,
  spatial_network_name = "spatial_network",
  cluster_column,
  number_of_simulations = 100
)
```

Examples

```
make_simulated_network(gobject)
```

---

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,
```

```
  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)
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.
A giotto object is returned by default, if FALSE then the merging vector will be returned.

Value

Giotto object

Examples

```
mergeClusters(gobject)
```

`mygini_fun` *mygini_fun*

Description

calculate gini coefficient

Usage

```
mygini_fun(x, weights = rep(1, length(x)))
```

Value

gini coefficient

nnDT_to_kNN *nnDT_to_kNN*

Description

Convert a nearest network data.table to a kNN object

Usage

```
nnDT_to_kNN(nnDT)
```

Arguments

nnDT	nearest neighbor network in data.table format

Value

kNN object

node_clusters *node_clusters*

Description

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

Usage

```
node_clusters(hclus_obj, verbose = TRUE)
```

Arguments

hclus_obj	hclus object
verbose	be verbose

Value

list of splitted dendrogram nodes from high to low node height

Examples

```
node_clusters(hclus_obj)
```

normalizeGiotto *normalizeGiotto*

Description

fast normalize and/or scale expresion values of Giotto object

Usage

```
normalizeGiotto(
  gobject,
  norm_methods = c("standard", "osmFISH"),
  library_size_norm = TRUE,
  scalefactor = 6000,
  log_norm = TRUE,
  log_offset = 1,
  logbase = 2,
  scale_genes = T,
  scale_cells = T,
  scale_order = c("first_genes", "first_cells"),
  verbose = F
)
```

Arguments

gobject	giotto object
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_genes	z-score genes over all cells
scale_cells	z-score cells over all genes
scale_order	order to scale genes 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

```
normalizeGiotto(gobject)
```

`normalizeGiottoOld` *normalizeGiotto*

Description

normalize and/or scale expresion values of Giotto object

Usage

```
normalizeGiottoOld(
  gobject,
  norm_methods = c("standard", "osmFISH"),
  library_size_norm = TRUE,
  scalefactor = 6000,
  log_norm = TRUE,
  logbase = 2,
  scale_genes = T,
  scale_cells = T,
  scale_order = c("first_genes", "first_cells"),
  verbose = F
)
```

Arguments

`gobject`	giotto object
`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
`logbase`	log base to use to log normalize expression values
`scale_genes`	z-score genes over all cells
`scale_cells`	z-score cells over all genes
`scale_order`	order to scale genes 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

```
normalizeGiotto(gobject)
```

`OR_function2` *OR_function2*

Description

calculate odds-ratio

Usage

```
OR_function2(A, B, C, D)
```

PAGEEnrich *PAGEEnrich*

Description

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

Usage

```
PAGEEnrich(
  gobject,
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
  output_enrichment = c("original", "zscore")
)
```

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

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

Examples

```
PAGEEnrich(gobject)
```

pagePermutation *pagePermutation*

Description

creates permutation for the PAGEEnrich test

Usage

```
pagePermutation(sc_gene, gene_number, n)
```

Examples

```
pagePermutation()
```

pDataDT *pDataDT*

Description

show cell metadata

Usage

```
pDataDT(gobject)
```

Arguments

gobject	giotto object

Value

data.table with cell metadata

Examples

```
pDataDT(gobject)
```

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
show	values to show on heatmap

Value

ggplot

Examples

```
plotCCcomDotplot(CPGscores)
```

`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

Examples

```
plotCCcomHeatmap(CPGscores)
```

---

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 = 5,
  min_int_cells = 3,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.5,
  direction = c("both", "up", "down"),
  cell_color_code = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "showCPGscores"
)
```

Arguments

gobject	giotto object
cpgObject	cell proximity gene score object
method	plotting method to use
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#' @param facet_scales ggplot facet scales paramter
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

Examples

```
plotCPG(CPGscores)
```

---

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

Examples

```
plotCombineCCcom(CPGscores)
```

---

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

Examples

```
plotCombineCellCellCommunication(CPGscores)
```

plotCombineCellProximityGenes
plotCombineCellProximityGenes

Description

Create visualization for combined (pairwise) cell proximity gene scores

Usage

```
plotCombineCellProximityGenes(
  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 = "plotCombineCPG"
)
```

Arguments

gobject	giotto object
combCpgObject	CPGscores, output from combineCellProximityGenes()
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

Examples

```
plotCombineCellProximityGenes(CPGscores)
```

---

plotCombineCPG *plotCombineCPG*

Description

Create visualization for combined (pairwise) cell proximity gene scores

Usage

```
plotCombineCPG(
  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 = "plotCombineCPG"
)
```

Arguments

gobject	giotto object
combCpgObject	CPGscores, output from combineCellProximityGenes()
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

Examples

```
plotCombineCPG(CPGscores)
```

---

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_int_cells = 3,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.2,
  direction = c("both", "up", "down"),
  cell_color_code = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "showCPGscores"
)
```

Arguments

gobject	giotto object
cpgObject	cell proximity gene score object
method	plotting method to use
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#' @param facet_scales ggplot facet scales paramter
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

Examples

```
plotCPG(CPGscores)
```

---

plotCPGscores *plotCPGscores*

Description

Create heatmap from cell-cell proximity scores

Usage

```
plotCPGscores(
  CPGscores,
  selected_interactions = NULL,
  selected_genes = NULL,
  detail_plot = T,
  simple_plot = F,
  simple_plot_facet = c("interaction", "genes"),
  facet_scales = "fixed",
  facet_ncol = length(selected_genes),
  facet_nrow = length(selected_interactions),
  show_plot = F
)
```

Arguments

CPGscores	CPGscores, output from getCellProximityGeneScores()
selected_interactions	interactions to show
selected_genes	genes 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
show_plot	show plot

Details

Give more details ...

Value

ggplot barplot

Examples

```
plotCPGscores(CPGscores)
```

---

plotGTGscores *plotGTGscores*

Description

Create heatmap from cell-cell proximity scores

Usage

```
plotGTGscores(
  gobject,
  GTGscore,
  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("blue", "red"),
  show_plot = NA,
  return_plot = NA,
```

```
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotGTGscores"
)
```

Arguments

gobject	giotto object
GTGscore	GTGscore, output from getGeneToGeneScores()
selected_interactions	interactions 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 2 colors to represent respectively all and selected cells
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
selected_genes	genes to show

Details

Give more details ...

Value

ggplot barplot

Examples

```
plotGTGscores(GTGscore)
```

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("custom", "correlation"),
  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 from `all_plots_save_function`

`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

```
plotHeatmap(gobject)
```

plotly_axis_scale_2D *plotly_axis_scale_2D*

Description

adjust the axis scale in 3D plotly plot

Usage

```
plotly_axis_scale_2D(
  cell_locations,
  sdimx = NULL,
  sdimy = NULL,
  mode = c("cube", "real", "custom"),
  custom_ratio = NULL
)
```

Arguments

cell_locations	spatial_loc in giotto object
sdimx	x axis of cell spatial location
sdimy	y axis of cell spatial location
mode	axis adjustment mode
custom_ratio	set the ratio artificially

Value

edges in spatial grid as data.table()

Examples

```
plotly_axis_scale_2D(gobject)
```

plotly_axis_scale_3D *plotly_axis_scale_3D*

Description

adjust the axis scale in 3D plotly plot

Usage

```
plotly_axis_scale_3D(
  cell_locations,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  mode = c("cube", "real", "custom"),
  custom_ratio = NULL
)
```

Arguments

cell_locations	spatial_loc in giotto object
sdimx	x axis of cell spatial location
sdimy	y axis of cell spatial location
sdimz	z axis of cell spatial location
mode	axis adjustment mode
custom_ratio	set the ratio artificially

Value

edges in spatial grid as data.table()

Examples

```
plotly_axis_scale_3D(gobject)
```

---

plotly_grid *plotly_grid*

Description

provide grid segment to draw in plot_ly()

Usage

```
plotly_grid(
  spatial_grid,
  x_start = "x_start",
  y_start = "y_start",
  x_end = "x_end",
  y_end = "y_end"
)
```

Arguments

spatial_grid	spatial_grid in giotto object

Value

edges in spatial grid as data.table()

Examples

```
plotly_grid(gobject)
```

plotly_network *plotly_network*

Description

provide network segment to draw in 3D plot_ly()

Usage

```
plotly_network(
  network,
  x = "sdimx_begin",
  y = "sdimy_begin",
  z = "sdimz_begin",
  x_end = "sdimx_end",
  y_end = "sdimy_end",
  z_end = "sdimz_end"
)
```

Arguments

gobject	network in giotto object

Value

edges in network as data.table()

Examples

```
plotly_network(gobject)
```

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
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 from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param
custom_gene_order	custom gene order (default = NULL)

gene_cor_method
: correlation method for genes

gene_cluster_method
: hierarchical cluster method for the genes

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.

Examples

```
plotMetaDataCellsHeatmap(gobject)
```

---

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",
  midpoint = 0,
  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
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 from all_plots_save_function
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

```
plotMetaDataHeatmap(gobject)
```

---

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

`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_border_col`
: color of border around points

`point_border_stroke`
: stroke size of border around points

`show_legend`
: show legend

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

`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 from `all_plots_save_function`

Details

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

Value

ggplot

Examples

```
plotPCA(gobject)
```

`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	dimension reduction name
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_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

`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_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 from `all_plots_save_function`

Details

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

Value

ggplot

Examples

```
plotPCA_2D(gobject)
```

`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	pca dimension reduction name
default_save_name	default save name for saving, ideally change save_name in save_param
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
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_legend	show legend
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

Details

Description of parameters.

Value

plotly

Examples

```
plotPCA_3D(gobject)
```

---

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

Examples

```
plotRankSpatvsExpr(CPGscores)
```

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

Examples

```
plotRecovery(CPGscores)
```

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

Examples

```
plotRecovery_sub(CPGscores)
```

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

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_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 from all_plots_save_function

Details

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

Value

ggplot

Examples

```
plotTSNE(gobject)
```

---

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

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_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 from `all_plots_save_function`

Details

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

Value

ggplot

Examples

```
plotTSNE_2D(gobject)
```

`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	tsne dimension reduction name
default_save_name	default save name for saving, don't change, change save_name in save_param
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
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_legend	show legend
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

Details

Description of parameters.

Value

plotly

Examples

```
plotTSNE_3D(gobject)
```

---

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

`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_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 from `all_plots_save_function`

Details

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

Value

ggplot

Examples

```
plotUMAP(gobject)
```

`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`	dimension reduction name
`default_save_name`	default save name for saving, don't change, change save_name in save_param
`groub_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

`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_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 from `all_plots_save_function`

Details

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

Value

ggplot

Examples

```
plotUMAP_2D(gobject)
```

---

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	umap dimension reduction name
default_save_name	default save name for saving, don't change, change save_name in save_param
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
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_legend	show legend
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

Details

Description of parameters.

Value

plotly

Examples

```
plotUMAP_3D(gobject)
```

`plot_network_layer_ggplot` *plot_network_layer_ggplot*

Description

Visualize cells in network layer according to dimension reduction coordinates

Usage

```
plot_network_layer_ggplot(
  ggobject,
  annotated_network_DT,
  edge_alpha = NULL,
  show_legend = T
)
```

Arguments

annotated_network_DT	annotated network data.table of selected cells
edge_alpha	alpha of network edges
show_legend	show legend
gobject	giotto object

Details

Description of parameters.

Value

ggplot

Examples

```
plot_network_layer_ggplot(gobject)
```

---

plot_point_layer_ggplot *plot_point_layer_ggplot*

Description

Visualize cells in point layer according to dimension reduction coordinates

Usage

```
plot_point_layer_ggplot(
  ggobject,
  annotated_DT_selected,
  annotated_DT_other,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = 0,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_size = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  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,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_legend = T
)
```

Arguments

annotated_DT_selected	annotated data.table of selected cells
annotated_DT_other	annotated data.table 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
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_size	size of point (cell)
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
label_size	size of labels
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_legend	show legend
gobject	giotto object

Details

Description of parameters.

Value

ggplot

Examples

```
plot_point_layer_ggplot(gobject)
```

---

plot_point_layer_ggplot_noFILL *plot_point_layer_ggplot_noFILL*

Description

Visualize cells in point layer according to dimension reduction coordinates without borders

Usage

```
plot_point_layer_ggplot_noFILL(
  ggobject,
  annotated_DT_selected,
  annotated_DT_other,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = 0,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_size = 1,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 4,
  label_fontface = "bold",
  edge_alpha = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_legend = T
)
```

Arguments

annotated_DT_selected
: annotated data.table of selected cells

annotated_DT_other
: annotated data.table 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

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_size
: size of point (cell)

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

label_fontface
: font of labels

edge_alpha
: column to use for alpha of the edges

show_other_cells
: display not selected cells

other_cell_color
: color of not selected cells

other_point_size
: size of not selected cells

show_legend
: show legend

gobject
: giotto object

Details

Description of parameters.

Value

ggplot

Examples

```
plot_point_layer_ggplot_noFILL(gobject)
```

plot_spat_point_layer_ggplot *plot_spat_point_layer_ggplot*

Description

creat ggplot point layer for spatial coordinates

Usage

```
plot_spat_point_layer_ggplot(
  ggobject,
  sdimx = NULL,
  sdimy = NULL,
  cell_locations_metadata_selected,
  cell_locations_metadata_other,
  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_size = 2,
  point_border_col = "lightgrey",
  point_border_stroke = 0.1,
  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",
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1,
  show_legend = TRUE
)
```

Arguments

sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
cell_locations_metadata_selected	annotated location from selected cells
cell_locations_metadata_other	annotated location from non-selected cells
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_size
: size of point (cell)

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

label_size
: size of labels

label_fontface
: font of labels

show_other_cells
: display not selected cells

other_cell_color
: color for not selected cells

other_point_size
: point size for not selected cells

show_legend
: show legend

gobject
: giotto object

Details

Description of parameters.

Value

ggplot

Examples

```
plot_spat_point_layer_ggplot(gobject)
```

plot_spat_point_layer_ggplot_noFILL
plot_spat_point_layer_ggplot_noFILL

Description

creat ggplot point layer for spatial coordinates without borders

Usage

```
plot_spat_point_layer_ggplot_noFILL(
  ggobject,
  sdimx = NULL,
  sdimy = NULL,
  cell_locations_metadata_selected,
  cell_locations_metadata_other,
  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_size = 2,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 4,
  label_fontface = "bold",
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1,
  show_legend = TRUE
)
```

Arguments

sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
cell_locations_metadata_selected	annotated location from selected cells
cell_locations_metadata_other	annotated location from non-selected cells
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_size`
: size of point (cell)

`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

`label_fontface`
: font of labels

`show_other_cells`
: display not selected cells

`other_cell_color`
: color for not selected cells

`other_point_size`
: point size for not selected cells

`show_legend`
: show legend

`gobject`
: giotto object

Details

Description of parameters.

Value

ggplot

Examples

```
plot_spat_point_layer_ggplot_noFILL(gobject)
```

`print.giotto` *print method for giotto class*

Description

print method for giotto class. Prints the chosen number of genes (rows) and cells (columns) from the raw count matrix. Also print the spatial locations for the chosen number of cells.

Usage

```
print.giotto(object, ...)
```

Arguments

nr_genes	number of genes (rows) to print
nr_cells	number of cells (columns) to print

---

rankEnrich *rankEnrich*

Description

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

Usage

```
rankEnrich(
  gobject,
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
  output_enrichment = c("original", "zscore")
)
```

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

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

Examples

```
rankEnrich(gobject)
```

`rankPermutation` *rankPermutation*

Description

creates permutation for the rankEnrich test

Usage

```
rankPermutation(sc_gene, n)
```

Examples

```
rankPermutation()
```

`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 from all_plots_save_function
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

Examples

```
rankSpatialCorGroups(gobject)
```

---

rank_binarize *rank_binarize*

Description

create binarized scores using arbitrary rank of top genes

Usage

```
rank_binarize(x, max_rank = 200)
```

---

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

Examples

```
readGiottoInstrunctions()
```

`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

```
removeCellAnnotation(gobject)
```

`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

```
removeGeneAnnotation(gobject)
```

---

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

named vector with giotto instructions

Examples

```
replaceGiottoInstructions()
```

runPCA *runPCA*

Description

runs a Principal Component Analysis

Usage

```
runPCA(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "genes"),
  name = "pca",
  genes_to_use = NULL,
  return_gobject = TRUE,
  scale_unit = F,
  ncp = 200,
  ...
)
```

Arguments

gobject	giotto object
expression_values	expression values to use
reduction	cells or genes
name	arbitrary name for PCA run
genes_to_use	subset of genes to use for PCA
return_gobject	boolean: return giotto object (default = TRUE)
scale_unit	scale features before PCA
ncp	number of principal components to calculate
...	additional parameters for PCA (see details)

Details

See PCA for more information about other parameters.

Value

giotto object with updated PCA dimension recuction

Examples

```
runPCA(gobject)
```

runtSNE *runtSNE*

Description

run tSNE

Usage

```
runtSNE(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "genes"),
  dim_reduction_to_use = "pca",
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  name = "tsne",
  genes_to_use = NULL,
  return_gobject = TRUE,
  dims = 2,
  perplexity = 30,
  theta = 0.5,
  do_PCA_first = F,
  set_seed = T,
  seed_number = 1234,
  ...
)
```

Arguments

gobject	giotto object
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
genes_to_use	if dim_reduction_to_use = NULL, which genes 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
...	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
- multiple tSNE results can be stored by changing the *name* of the analysis

Value

giotto object with updated tSNE dimension recuction

Examples

```
runtSNE(gobject)
```

---

runUMAP *runUMAP*

Description

run UMAP

Usage

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

Arguments

gobject	giotto object
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
genes_to_use	if dim_reduction_to_use = NULL, which genes 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 to use
spread	UMAP param: spread
set_seed	use of seed
seed_number	seed number to use
...	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
- multiple UMAP results can be stored by changing the *name* of the analysis

Value

giotto object with updated UMAP dimension recuction

Examples

```
runUMAP(gobject)
```

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.

Details

Description.

Value

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

Examples

```
selectPatternGenes(gobject)
```

select_expression_values *select_expression_values*

Description

helper function to select expression values

Usage

```
select_expression_values(gobject, values)
```

Arguments

gobject	giotto object
values	expression values to extract

Value

expression matrix

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

Description

show method for giotto class

Usage

```
## S4 method for signature 'giotto'
show(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 from all_plots_save_function
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

```
showClusterDendrogram(gobject)
```

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 from all_plots_save_function
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

```
showClusterHeatmap(gobject)
```

---

showCPGscores *showCPGscores*

Description

visualize Cell Proximity Gene enrichment scores

Usage

```
showCPGscores(
  gobject,
  CPGscore,
  method = c("volcano", "cell_barplot", "cell-cell", "cell_sankey", "heatmap",
    "dotplot"),
  min_cells = 5,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.5,
  keep_int_duplicates = TRUE,
  direction = c("both", "up", "down"),
  cell_color_code = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "showCPGscores"
)
```

Arguments

CPGscore	CPGscore, output from getCellProximityGeneScores()
method	visualization method
min_cells	min number of cells threshold
min_fdr	fdr threshold
min_spat_diff	spatial difference threshold
min_log2_fc	min log2 fold-change
keep_int_duplicates	keep both cell_A-cell_B and cell_B-cell_A
direction	up or downregulation or both
cell_color_code	color code for cell types
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

Different ways to visualize how many genes are differentially regulated within a source cell type due to the proximity of another neighboring cell type.

Value

Gene to gene scores in data.table format

Examples

```
showCPGscores(CPGscore)
```

`showGeneExpressionProximityScore` *showGeneExpressionProximityScore*

Description

Create heatmap from cell-cell proximity scores

Usage

```
showGeneExpressionProximityScore(
  scores,
  selected_gene,
  sort_column = "diff_spat"
)
```

Arguments

`scores`	CPscore, output from getAverageCellProximityGeneScores()
`selected_gene`	gene to show
`sort_column`	column name to use for sorting

Details

Give more details ...

Value

ggplot barplot

Examples

```
showGeneExpressionProximityScore(scores)
```

showGiottoInstructions *showGiottoInstructions*

Description

Function to display all instructions from giotto object

Usage

```
showGiottoInstructions(gobject)
```

Arguments

gobject	giotto object

Value

named vector with giotto instructions

Examples

```
showGiottoInstructions()
```

showGTGscores *showGTGscores*

Description

visualize Cell Proximity Gene enrichment scores

Usage

```
showGTGscores(
  GTGscore,
  method = c("cell_barplot", "cell-cell", "cell_sankey"),
  min_cells = 5,
  min_pval = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.5,
  direction = c("both", "up", "down"),
  cell_color_code = NULL,
  show_plot = T,
  specific_genes_1 = NULL,
  specific_genes_2 = NULL,
  first_cell_name = "ligand cell",
  second_cell_name = "receptor cell",
  return_DT = F
)
```

Arguments

method	visualization method
min_cells	min number of cells threshold
min_pval	p-value threshold
min_spat_diff	spatial difference threshold
min_log2_fc	log2 fold-change threshold
direction	up or downregulation or both
cell_color_code	color code for cell types
show_plot	print plot
specific_genes_1	subset of genes, matched with specific_genes_2
specific_genes_2	subset of genes, matched with specific_genes_1
first_cell_name	name for first cells
second_cell_name	name for second cells
CPGscore	CPGscore, output from getCellProximityGeneScores()

Details

Give more details ...

Value

ggplot

Examples

```
showGTGscores(CPGscore)
```

---

showIntExpressionProximityScore *showIntExpressionProximityScore*

Description

Create heatmap from cell-cell proximity scores

Usage

```
showIntExpressionProximityScore(
  scores,
  selected_interaction,
  sort_column = "diff_spat",
  show_enriched_n = 5,
  show_depleted_n = 5
)
```

Arguments

scores	scores, output from getAverageCellProximityGeneScores()
selected_interaction	interaction to show
sort_column	column name to use for sorting
show_enriched_n	show top enriched interactions
show_depleted_n	show top depleted interactions

Details

Give more details ...

Value

ggplot barplot

Examples

```
showIntExpressionProximityScore(scores)
```

---

showPattern *showPattern*

Description

show patterns for 2D spatial data

Usage

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

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
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

See Also

showPattern2D

Examples

```
showPattern(gobject)
```

---

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
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

Examples

```
showPattern2D(gobject)
```

---

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 from all_plots_save_function

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

Value

plotly

Examples

```
showPattern3D(gobject)
```

---

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 from all_plots_save_function()
default_save_name	default save name for saving, don't change, change save_name in save_param

Value

ggplot

Examples

```
showPatternGenes(gobject)
```

---

showProcessingSteps *showProcessingSteps*

Description

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

Usage

```
showProcessingSteps(gobject)
```

Arguments

gobject	giotto object

Value

list of processing steps and names

Examples

```
showProcessingSteps(gobject)
```

showSpatialCorGenes *showSpatialCorGenes*

Description

Shows and filters spatially correlated genes

Usage

```
showSpatialCorGenes(
  spatCorObject,
  use_clus_name = NULL,
  selected_clusters = NULL,
  genes = NULL,
  min_spat_cor = 0.5,
  min_expr_cor = NULL,
  min_cor_diff = NULL,
  min_rank_diff = NULL,
  show_top_genes = NULL
)
```

Arguments

spatCorObject	spatial correlation object
use_clus_name	cluster information to show
selected_clusters	subset of clusters to show
genes	subset of genes to show
min_spat_cor	filter on minimum spatial correlation
min_expr_cor	filter on minimum single-cell expression correlation
min_cor_diff	filter on minimum correlation difference (spatial vs expression)
min_rank_diff	filter on minimum correlation rank difference (spatial vs expression)
show_top_genes	show top genes per gene

Value

data.table with filtered information

Examples

```
showSpatialCorGenes(gobject)
```

showTopGeneToGene *showTopGeneToGene*

Description

Show enriched/depleted gene-gene enrichments

Usage

```
showTopGeneToGene(
  GTGscore,
  top_interactions = 10,
  direction = c("increased", "decreased"),
  complement_data = T,
  subset_cell_ints = NULL,
  subset_genes = NULL
)
```

Arguments

GTGscore	GTGscore, output from getGeneToGeneScores()
top_interactions	number of top gene-gene enrichments to show
direction	show top increased or decreased gene-gene enrichments
complement_data	include non-enriched gene-gene scores from other cell-cell interactions
subset_cell_ints	subset cell-cell interactions to show
subset_genes	subset genes to show

Details

Give more details ...

Value

ggplot barplot

Examples

```
showTopGeneToGene(scores)
```

signPCA *signPCA*

Description

identify significant prinicipal components (PCs)

Usage

```
signPCA(
  gobject,
  method = c("screeplot", "jackstraw"),
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "genes"),
  genes_to_use = NULL,
  scale_unit = T,
  ncp = 50,
  scree_labels = T,
  scree_ylim = c(0, 10),
  jack_iter = 10,
  jack_threshold = 0.01,
  jack_verbose = T,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "signPCA",
  ...
)
```

Arguments

gobject	giotto object
method	method to use to identify significant PCs
expression_values	expression values to use
reduction	cells or genes
genes_to_use	subset of genes to use for PCA
scale_unit	scale features before PCA
ncp	number of principal components to calculate
scree_labels	show labels on scree plot
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_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
...	additional parameters for PCA

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 does not show a significant contribution anymore (= 'elbow method').
2. The Jackstraw method uses the permutationPA function. By systematically permuting genes it identifies robust, and thus significant, PCs.
multiple PCA results can be stored by changing the *name* parameter

Value

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

Examples

```
signPCA(gobject)
```

---

sort_combine_two_DT_columns
sort_combine_two_DT_columns

Description

fast sorting and pasting of 2 character columns

Usage

```
sort_combine_two_DT_columns(DT, column1, column2, myname = "unif_gene_gene")
```

Examples

```
sort_combine_two_DT_columns()
```

spatCellCellcom *spatCellCellcom*

Description

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

Usage

```
spatCellCellcom(
  gobject,
  spatial_network_name = "spatial_network",
  cluster_column = "cell_types",
  random_iter = 100,
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  min_observations = 2,
  adjust_method = c("fdr", "bonferroni", "BH", "holm", "hochberg", "hommel", "BY",
    "none"),
  adjust_target = c("genes", "cells"),
  do_parallel = TRUE,
  cores = NA,
  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
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
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.. More details will follow soon.

Value

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

Examples

```
spatCellCellcom(gobject)
```

---

spatCellPlot *spatCellPlot*

Description

Visualize cells according to spatial coordinates

Usage

```
spatCellPlot(
  gobject,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spat_enr_names = NULL,
  cell_annotation_values = 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"),
  point_size = 3,
  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 = "spatial_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,
  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 = "spatCellPlot"
)
```

Arguments

gobject	giotto object
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	point with border or not (border or no_border)
point_size	size of point (cell)
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
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

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 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

Examples

```
spatCellPlot(gobject)
```

spatCellPlot2D *spatCellPlot2D*

Description

Visualize cells according to spatial coordinates

Usage

```
spatCellPlot2D(
  gobject,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spat_enr_names = NULL,
  cell_annotation_values = 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"),
  point_size = 3,
  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 = "spatial_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,
  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 = "spatCellPlot2D"
)
```

Arguments

gobject	giotto object
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	point with border or not (border or no_border)
point_size	size of point (cell)
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
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

`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 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

Examples

```
spatCellPlot2D(gobject)
```

spatDimCellPlot *spatDimCellPlot*

Description

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

Usage

```
spatDimCellPlot(
  gobject,
  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_border_col = "black",
  dim_point_border_stroke = 0.1,
  spat_point_shape = c("border", "no_border"),
  spat_point_size = 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 = "spatial_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,
  coord_fix_ratio = NULL,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  dim_background_color = "white",
  spat_background_color = "white",
  axis_text = 8,
  axis_title = 8,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatDimCellPlot"
)
```

Arguments

gobject	giotto object
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
: spatial points with border or not (border or no_border)

dim_point_size
: size of points 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
: spatial points with border or not (border or no_border)

spat_point_size
: size 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_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_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

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 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

Examples

```
spatDimCellPlot(gobject)
```

`spatDimCellPlot2D` *spatDimCellPlot2D*

Description

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

Usage

```
spatDimCellPlot2D(
  gobject,
  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_border_col = "black",
  dim_point_border_stroke = 0.1,
  spat_point_shape = c("border", "no_border"),
  spat_point_size = 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 = "spatial_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",
  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
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_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
: spatial points with border or not (border or no_border)

spat_point_size
: size 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_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_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

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 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

Examples

```
spatDimCellPlot2D(gobject)
```

---

spatDimGenePlot *spatDimGenePlot*

Description

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

Usage

```
spatDimGenePlot(
  gobject,
  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_border_col = "black",
  dim_point_border_stroke = 0.1,
  show_NN_network = F,
  show_spatial_network = F,
  show_spatial_grid = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  edge_alpha_dim = NULL,
```

```
  scale_alpha_with_expression = FALSE,
  spatial_network_name = "spatial_network",
  spatial_grid_name = "spatial_grid",
  spat_point_shape = c("border", "no_border"),
  spat_point_size = 1,
  spat_point_border_col = "black",
  spat_point_border_stroke = 0.1,
  midpoint = 0,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  show_legend = T,
  legend_text = 8,
  dim_background_color = "white",
  spat_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 = "spatDimGenePlot"
)
```

Arguments

gobject	giotto object
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	dimension points with border or not (border or no_border)
dim_point_size	dim reduction plot: point size
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

`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

`edge_alpha_dim`
: dim reduction plot: column to use for alpha of the edges

`scale_alpha_with_expression`
: scale expression with ggplot alpha parameter

`spatial_network_name`
: name of spatial network to use

`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_border_col`
: color of border around points

`spat_point_border_stroke`
: stroke size of border around points

`midpoint`
: size of point (cell)

`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

`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 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

spatDimGenePlot3D

Examples

```
spatDimGenePlot(gobject)
```

`spatDimGenePlot2D` *spatDimGenePlot2D*

Description

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

Usage

```
spatDimGenePlot2D(
  gobject,
  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_border_col = "black",
  dim_point_border_stroke = 0.1,
  show_NN_network = F,
  show_spatial_network = F,
  show_spatial_grid = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  edge_alpha_dim = NULL,
  scale_alpha_with_expression = FALSE,
  spatial_network_name = "spatial_network",
  spatial_grid_name = "spatial_grid",
  spat_point_shape = c("border", "no_border"),
  spat_point_size = 1,
  spat_point_border_col = "black",
  spat_point_border_stroke = 0.1,
  midpoint = 0,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  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",
  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
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_border_col	color of border around points
dim_point_border_stroke	stroke size of border around points
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
edge_alpha_dim	dim reduction plot: column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
spatial_network_name	name of spatial network to use
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_border_col`
: color of border around points

`spat_point_border_stroke`
: stroke size of border around points

`midpoint`
: size of point (cell)

`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

`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 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

`spatDimGenePlot3D`

Examples

```
spatDimGenePlot2D(gobject)
```

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 = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  label_size = 16,
  genes_low_color = "blue",
  genes_mid_color = "white",
  genes_high_color = "red",
  dim_point_size = 3,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  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,
  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
genes	genes to show
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
dim_point_size	dim reduction plot: point size
spatial_network_name	name of spatial network to use
spatial_grid_name	name of spatial grid to use
spatial_point_size	spatial plot: point size
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
edge_alpha_dim	dim reduction plot: column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_size	size of point (cell)
show_legend	show legend

Details

Description of parameters.

Value

plotly

Examples

```
spatDimGenePlot3D(gobject)
```

`spatDimPlot` *spatDimPlot*

Description

Visualize cells according to spatial AND dimension reduction coordinates 2D

Usage

```
spatDimPlot(
  gobject,
  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_border_col = "black",
  dim_point_border_stroke = 0.1,
  spat_point_shape = c("border", "no_border"),
  spat_point_size = 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_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 = "spatial_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",
  axis_text = 8,
  axis_title = 8,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatDimPlot"
)
```

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

`spat_point_size`
size 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_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

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

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 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

spatDimPlot2D and spatDimPlot3D for 3D visualization.

Examples

```
spatDimPlot(gobject)
```

---

spatDimPlot2D *spatDimPlot2D*

Description

Visualize cells according to spatial AND dimension reduction coordinates 2D

Usage

```
spatDimPlot2D(
  gobject,
  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_border_col = "black",
  dim_point_border_stroke = 0.1,
  spat_point_shape = c("border", "no_border"),
  spat_point_size = 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_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 = "spatial_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",
  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
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_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
: point with border or not (border or no_border)

spat_point_size
: size 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_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

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

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 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

spatDimPlot3D

Examples

```
spatDimPlot2D(gobject)
```

---

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",
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  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,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  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
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

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

nn_network_alpha
column to use for alpha of the edges

show_spatial_network
show spatial network

spatial_network_name
name of spatial network to use

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_point_size
size of spatial points

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

dim_point_border_col
border color of points in dim. reduction space

dim_point_border_stroke
: border stroke of points in dim. reduction space

spatial_network_color
: color of spatial network

spatial_other_point_size
: size of not selected spatial points

spatial_other_cells_alpha
: alpha of not selected spatial points

dim_other_point_size
: size of not selected dim. reduction points

show_legend
: show legend

Details

Description of parameters.

Value

plotly

Examples

```
spatDimPlot3D(gobject)
```

---

spatGenePlot *spatGenePlot*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
spatGenePlot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  genes_high_color = "darkred",
  genes_mid_color = "white",
  genes_low_color = "darkblue",
  show_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_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"),
  point_size = 1,
```

```
  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 = "spatGenePlot"
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
genes	genes to show
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_network	show underlying spatial network
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
midpoint	expression midpoint
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_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 from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for cowplot::save_plot()

Details

Description of parameters.

Value

ggplot

See Also

spatGenePlot3D and spatGenePlot2D

Examples

```
spatGenePlot(gobject)
```

---

spatGenePlot2D *spatGenePlot2D*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
spatGenePlot2D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  genes_high_color = "darkred",
  genes_mid_color = "white",
  genes_low_color = "darkblue",
  show_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_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"),
  point_size = 1,
  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 = "spatGenePlot2D"
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
genes	genes to show
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_network	show underlying spatial network
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

midpoint
: expression midpoint

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_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 from `all_plots_save_function`

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

...
: parameters for cowplot::save_plot()

Details

Description of parameters.

Value

ggplot

See Also

`spatGenePlot3D`

Examples

```
spatGenePlot2D(gobject)
```

spatGenePlot3D *spatGenePlot3D*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
spatGenePlot3D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  show_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_network",
  edge_alpha = NULL,
  show_grid = F,
  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",
  spatial_grid_name = "spatial_grid",
  point_size = 2,
  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 = "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

show_grid
: show spatial grid

genes_high_color
: color represents high gene expression

genes_mid_color
: color represents middle gene expression

genes_low_color
: color represents low gene expression

spatial_grid_name
: name of spatial grid to use

point_size
: size of point (cell)

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 from all_plots_save_function

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

grid_color
: color of spatial grid

midpoint
: expression midpoint

scale_alpha_with_expression
: scale expression with ggplot alpha parameter

...
: parameters for cowplot::save_plot()

Details

Description of parameters.

Value

ggplot

Examples

```
spatGenePlot3D(gobject)
```

---

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

Examples

```
spatialAEH(gobject)
```

---

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 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 is a wrapper for the SpatialDE method implemented in the ...

Value

a list of data.frames with results and plot (optional)

Examples

```
spatialDE(gobject)
```

Spatial_AEH *Spatial_AEH*

Description

calculate automatic expression histology with spatialDE method

Usage

```
Spatial_AEH(
  gobject = NULL,
  results = NULL,
  pattern_num = 5,
  l = 1.05,
  show_AEH = T,
  sdimx = NULL,
  sdimy = NULL,
  point_size = 3,
  point_alpha = 1,
  low_color = "blue",
  mid_color = "white",
  high_color = "red",
  midpoint = 0,
  python_path = NULL
)
```

Arguments

gobject	Giotto object
results	output from spatial_DE
pattern_num	the number of gene expression patterns
show_AEH	show AEH plot
python_path	specify specific path to python if required

Details

Description.

Value

a list or a dataframe of SVs

Examples

```
Spatial_AEH(gobject)
```

Spatial_DE *Spatial_DE*

Description

calculate spatial varible genes with spatialDE method

Usage

```
Spatial_DE(
  gobject = NULL,
  show_plot = T,
  size = c(4, 2, 1),
  color = c("blue", "green", "red"),
  sig_alpha = 0.5,
  unsig_alpha = 0.5,
  python_path = NULL
)
```

Arguments

gobject	Giotto object
show_plot	show FSV plot
python_path	specify specific path to python if required

Details

Description.

Value

a list or a dataframe of SVs

Examples

```
Spatial_DE(gobject)
```

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

Examples

```
spatNetwDistributionsDistance(gobject)
```

`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

Examples

```
spatNetwDistributionsDistance(gobject)
```

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

Examples

```
spatNetwDistributionsKneighbors(gobject)
```

spatPlot *spatPlot*

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot(
  gobject,
  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"),
  point_size = 3,
  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 = "spatial_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",
  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 = "spatPlot"
)
```

Arguments

gobject	giotto object
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	point with border or not (border or no_border)
point_size	size of point (cell)
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

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

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 from all_plots_save_function

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

groub_by create multiple plots based on cell annotation column

Details

Description of parameters.

Value

ggplot

See Also

spatPlot3D

Examples

```
spatPlot(gobject)
```

---

spatPlot2D *spatPlot2D*

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot2D(
  gobject,
  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"),
  point_size = 3,
  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 = "spatial_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",
  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
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	point with border or not (border or no_border)
point_size	size of point (cell)

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

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

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 from all_plots_save_function
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_by	create multiple plots based on cell annotation column

Details

Description of parameters.

Value

ggplot

See Also

spatPlot3D

Examples

```
spatPlot2D(gobject)
```

---

spatPlot2D_single *spatPlot2D_single*

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot2D_single(
  gobject,
  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"),
  point_size = 3,
  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 = "spatial_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",
  axis_text = 8,
  axis_title = 8,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatPlot2D_single"
)
```

Arguments

gobject	giotto object
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 point with border or not (border or no_border)

point_size size of point (cell)

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

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

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 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

spatPlot3D

Examples

```
spatPlot2D_single(gobject)
```

---

spatPlot3D *spatPlot3D*

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot3D(
  gobject,
  sdimx = "sdimx",
  sdimy = "sdimy",
  sdimz = "sdimz",
  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,
  show_network = F,
  network_color = NULL,
  network_alpha = 1,
  other_cell_alpha = 0.5,
  spatial_network_name = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  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')
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
show_network	show underlying spatial network
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
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 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

Examples

```
spatPlot3D(gobject)
```

`spat_fish_func` *spat_fish_func*

Description

performs fisher exact test

Usage

```
spat_fish_func(gene, bin_matrix, spat_mat, calc_hub = F, hub_min_int = 3)
```

`spat_OR_func` *spat_OR_func*

Description

calculate odds-ratio

Usage

```
spat_OR_func(gene, bin_matrix, spat_mat, calc_hub = F, hub_min_int = 3)
```

specificCellCellcommunicationScores
specificCellCellcommunicationScores

Description

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

Usage

```
specificCellCellcommunicationScores(
  gobject,
  spatial_network_name = "spatial_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,
  adjust_method = c("fdr", "bonferroni", "BH", "holm", "hochberg", "hommel", "BY",
    "none"),
  adjust_target = c("genes", "cells"),
  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
adjust_method	which method to adjust p-values
adjust_target	adjust multiple hypotheses at the cell or gene level
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.. More details will follow soon.

Value

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

Examples

```
specificCellCellcommunicationScores(gobject)
```

`split_dendrogram_in_two`

split_dendrogram_in_two

Description

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

Usage

```
split_dendrogram_in_two(dend)
```

Arguments

dend	dendrogram object

Value

list of two dendrograms and height of node

Examples

```
split_dendrogram_in_two(dend)
```

`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

Examples

```
stitchFieldCoordinates(gobject)
```

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

Details

...

Examples

```
stitchTileCoordinates(gobject)
```

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_variance = 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,
```

```
  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
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

Examples

```
subClusterCells(gobject)
```

---

subsetGiotto *subsetGiotto*

Description

subsets Giotto object including previous analyses.

Usage

```
subsetGiotto(gobject, cell_ids = NULL, gene_ids = NULL, verbose = FALSE)
```

Arguments

gobject	giotto object
cell_ids	cell IDs to keep
gene_ids	gene IDs to keep
verbose	be verbose

Value

giotto object

Examples

```
subsetGiotto(gobject)
```

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

Details

if return_gobject = FALSE, then a filtered combined metadata data.table will be returned

Value

giotto object

Examples

```
subsetGiottoLocs(gobject)
```

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

Examples

```
trendSceek(gobject)
```

viewHMRFresults *viewHMRFresults*

Description

View results from doHMRF.

Usage

```
viewHMRFresults(
  gobject,
  HMRFoutput,
  k = NULL,
  betas_to_view = NULL,
  third_dim = 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
...	paramters to visPlot()

Details

Description ...

Value

spatial plots with HMRF domains

See Also

visPlot

Examples

```
viewHMRFresults(gobject)
```

`viewHMRFresults2D` *viewHMRFresults2D*

Description

View results from doHMRF.

Usage

```
viewHMRFresults2D(
  gobject,
  HMRFoutput,
  k = NULL,
  betas_to_view = NULL,
  third_dim = 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
`...`	paramters to visPlot()

Details

Description ...

Value

spatial plots with HMRF domains

See Also

`spatPlot2D`

Examples

```
viewHMRFresults2D(gobject)
```

viewHMRFresults3D *viewHMRFresults3D*

Description

View results from doHMRF.

Usage

```
viewHMRFresults3D(
  gobject,
  HMRFoutput,
  k = NULL,
  betas_to_view = NULL,
  third_dim = 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
...	paramters to visPlot()

Details

Description ...

Value

spatial plots with HMRF domains

See Also

spatPlot3D

Examples

```
viewHMRFresults3D(gobject)
```

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

Value

ggplot

Examples

```
violinPlot(gobject)
```

---

visDimGenePlot *visDimGenePlot*

Description

Visualize cells and gene expression according to dimension reduction coordinates

Usage

```
visDimGenePlot(
  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 = NULL,
  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_size = 1,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  point_border_col = "black",
  point_border_stroke = 0.1,
  midpoint = 0,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_legend = T,
  plot_method = c("ggplot", "plotly"),
  show_plots = F
)
```

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
edge_alpha	column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
midpoint	size of point (cell)
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
show_plots	show plots

Details

Description of parameters.

Value

ggplot

Examples

```
visDimGenePlot(gobject)
```

visDimGenePlot_2D_ggplot *visDimGenePlot_2D_ggplot*

Description

Visualize cells and gene expression according to dimension reduction coordinates

Usage

```
visDimGenePlot_2D_ggplot(
  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_size = 1,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  point_border_col = "black",
  point_border_stroke = 0.1,
  midpoint = 0,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_legend = T,
  show_plots = F
)
```

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
edge_alpha	column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
midpoint	size of point (cell)
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
show_plots	show plots

Details

Description of parameters.

Value

ggplot

Examples

```
visDimGenePlot_2D_ggplot(gobject)
```

---

visDimGenePlot_3D_plotly

visDimGenePlot_3D_plotly

Description

Visualize cells and gene expression according to dimension reduction coordinates

Usage

```
visDimGenePlot_3D_plotly(
  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",
  edge_alpha = NULL,
  point_size = 1,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  show_legend = T,
  show_plots = F
)
```

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
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
show_legend	show legend
show_plots	show plots

Details

Description of parameters.

Value

ggplot

Examples

```
visDimGenePlot_3D_plotly(gobject)
```

`visDimPlot` *visDimPlot*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
visDimPlot(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = 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_size = 3,
  point_border_col = "black",
  point_border_stroke = 0.1,
  plot_method = c("ggplot", "plotly"),
  show_legend = T,
  show_plot = F,
  return_plot = TRUE,
  save_plot = F,
  save_dir = NULL,
```

```
  save_folder = NULL,
  save_name = NULL,
  save_format = NULL,
  show_saved_plot = F,
  ...
)
```

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
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
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
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_dir	directory to save the plot

save_folder	(optional) folder in directory to save the plot
save_name	name of plot
save_format	format of plot (e.g. tiff, png, pdf, ...)
show_saved_plot	load & display the saved plot

Details

Description of parameters.

Value

ggplot or plotly

Examples

```
visDimPlot(gobject)
```

---

visDimPlot_2D_ggplot *visDimPlot_2D_ggplot*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
visDimPlot_2D_ggplot(
  gobject,
  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",
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = 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_size = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  show_plot = F,
  return_plot = TRUE,
  save_plot = F,
  save_dir = NULL,
  save_folder = NULL,
  save_name = NULL,
  save_format = NULL,
  show_saved_plot = F,
  ...
)
```

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
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
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend

Details

Description of parameters.

Value

ggplot

Examples

```
visDimPlot_2D_ggplot(gobject)
```

---

visDimPlot_2D_plotly *visDimPlot_2D_plotly*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
visDimPlot_2D_plotly(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  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 = 5
)
```

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
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)

Details

Description of parameters.

Value

plotly

Examples

```
visDimPlot_2D_plotly(gobject)
```

visDimPlot_3D_plotly *visDimPlot_3D_plotly*

Description

Visualize cells according to dimension reduction coordinates

Usage

```
visDimPlot_3D_plotly(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = 3,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  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 = 1
)
```

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
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)

Details

Description of parameters.

Value

plotly

Examples

```
visDimPlot_3D_plotly(gobject)
```

---

visForceLayoutPlot *visForceLayoutPlot*

Description

Visualize cells according to forced layout algorithm coordinates

Usage

```
visForceLayoutPlot(
  gobject,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  layout_name = "layout",
  dim1_to_use = 1,
  dim2_to_use = 2,
  show_NN_network = T,
  cell_color = NULL,
  color_as_factor = TRUE,
  cell_color_code = NULL,
  edge_alpha = NULL,
  point_size = 1,
```

```
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  show_plot = F,
  return_plot = TRUE,
  save_plot = F,
  save_dir = NULL,
  save_folder = NULL,
  save_name = NULL,
  save_format = NULL,
  show_saved_plot = F,
  ...
)
```

Arguments

gobject	giotto object
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	NN network to use
layout_name	name of layout to use
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
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_dir	directory to save the plot
save_folder	(optional) folder in directory to save the plot
save_name	name of plot
save_format	format of plot (e.g. tiff, png, pdf, ...)
show_saved_plot	load & display the saved plot

Details

Description of parameters.

Value

ggplot

Examples

```
visForceLayoutPlot(gobject)
```

`visGenePlot` *visGenePlot*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
visGenePlot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  show_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_network",
  edge_alpha = NULL,
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  midpoint = 0,
  scale_alpha_with_expression = FALSE,
  point_size = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  plot_method = c("ggplot", "plotly"),
  show_plots = F
)
```

Arguments

gobject	giotto object
expression_values	gene expression values to use
genes	genes to show
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_network	show underlying spatial network
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
midpoint	expression midpoint
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
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
axis_scale	three mode to adjust axis scale
x_ticks	number of ticks on x axis
y_ticks	number of ticks on y axis
z_ticks	number of ticks on z axis
plot_method	two methods of plot
show_plots	show plots

Details

Description of parameters.

Value

ggplot or plotly

Examples

```
visGenePlot(gobject)
```

`visGenePlot_2D_ggplot` *visGenePlot_2D_ggplot*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
visGenePlot_2D_ggplot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  genes_high_color = "darkred",
  genes_mid_color = "white",
  genes_low_color = "darkblue",
  show_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_network",
  edge_alpha = NULL,
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  midpoint = 0,
  scale_alpha_with_expression = FALSE,
  point_size = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plots = F
)
```

Arguments

`gobject`	giotto object
`expression_values`	gene expression values to use
`genes`	genes to show
`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_network
: show underlying spatial network

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

midpoint
: expression midpoint

scale_alpha_with_expression
: scale expression with ggplot alpha parameter

point_size
: size of point (cell)

point_border_col
: color of border around points

point_border_stroke
: stroke size of border around points

show_legend
: show legend

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_plots
: show plots

Details

Description of parameters.

Value

ggplot

Examples

```
visGenePlot_2D_ggplot(gobject)
```

`visGenePlot_3D_plotly` *visGenePlot_3D_plotly*

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
visGenePlot_3D_plotly(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  show_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_network",
  edge_alpha = NULL,
  show_grid = F,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  spatial_grid_name = "spatial_grid",
  point_size = 1,
  show_legend = T,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plots = F
)
```

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
show_grid	show spatial grid
genes_high_color	color represents high gene expression
genes_mid_color	color represents middle gene expression
genes_low_color	color represents low gene expression
spatial_grid_name	name of spatial grid to use
point_size	size of point (cell)
show_legend	show legend
axis_scale	three mode to adjust axis scale
x_ticks	number of ticks on x axis
y_ticks	number of ticks on y axis

z_ticks	number of ticks on z axis
show_plots	show plots
grid_color	color of spatial grid
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

Details

Description of parameters.

Value

plotly

Examples

```
visGenePlot_3D_plotly(gobject)
```

---

visPlot *visPlot*

Description

Visualize cells according to spatial coordinates

Usage

```
visPlot(
  gobject,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  point_size = 3,
  point_border_col = "black",
  point_border_stroke = 0.1,
  cell_color = NULL,
  cell_color_code = NULL,
  color_as_factor = T,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  show_network = F,
  network_color = NULL,
  network_alpha = 1,
  other_cell_alpha = 0.1,
  spatial_network_name = "spatial_network",
  show_grid = F,
```

```
  grid_color = NULL,
  grid_alpha = 1,
  spatial_grid_name = "spatial_grid",
  coord_fix_ratio = 0.6,
  title = "",
  show_legend = T,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  plot_method = c("ggplot", "plotly"),
  show_plot = F,
  return_plot = TRUE,
  save_plot = F,
  save_dir = NULL,
  save_folder = NULL,
  save_name = NULL,
  save_format = NULL,
  show_saved_plot = F,
  ...
)
```

Arguments

gobject	giotto object
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimz')
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
cell_color	color for cells (see details)
cell_color_code	named vector with colors
color_as_factor	convert color column to factor
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
show_network	show underlying spatial network
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
title	title of plot
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_dir	directory to save the plot
save_folder	(optional) folder in directory to save the plot
save_name	name of plot
save_format	format of plot (e.g. tiff, png, pdf, ...)
show_saved_plot	load & display the saved plot

Details

Description of parameters.

Value

ggplot

Examples

```
visPlot(gobject)
```

`visPlot_2D_ggplot` *visPlot_2D_ggplot*

Description

Visualize cells according to spatial coordinates

Usage

```
visPlot_2D_ggplot(
  gobject,
  sdimx = NULL,
  sdimy = NULL,
  point_size = 3,
  point_border_col = "black",
  point_border_stroke = 0.1,
  cell_color = NULL,
  cell_color_code = NULL,
```

```
  color_as_factor = T,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  show_network = F,
  network_color = NULL,
  network_alpha = 1,
  other_cells_alpha = 0.1,
  spatial_network_name = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  coord_fix_ratio = 0.6,
  title = "",
  show_legend = T,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = F,
  return_plot = TRUE,
  save_plot = F,
  save_dir = NULL,
  save_folder = NULL,
  save_name = NULL,
  save_format = NULL,
  show_saved_plot = F,
  ...
)
```

Arguments

gobject	giotto object
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
cell_color	color for cells (see details)
cell_color_code	named vector with colors
color_as_factor	convert color column to factor
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

show_network
: show underlying spatial network

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

title
: title of plot

show_legend
: show legend

show_plot
: show plot

return_plot
: return ggplot object

save_plot
: directly save the plot [boolean]

save_dir
: directory to save the plot

save_folder
: (optional) folder in directory to save the plot

save_name
: name of plot

save_format
: format of plot (e.g. tiff, png, pdf, ...)

show_saved_plot
: load & display the saved plot

Details

Description of parameters.

Value

ggplot

Examples

```
visPlot_2D_ggplot(gobject)
```

visPlot_2D_plotly *visPlot_2D_plotly*

Description

Visualize cells according to spatial coordinates

Usage

```
visPlot_2D_plotly(
  gobject,
  sdimx = NULL,
  sdimy = NULL,
  point_size = 3,
  cell_color = NULL,
  cell_color_code = NULL,
  color_as_factor = T,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_network = F,
  network_color = "lightgray",
  network_alpha = 1,
  other_cell_alpha = 0.5,
  spatial_network_name = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  grid_alpha = 1,
  spatial_grid_name = "spatial_grid",
  show_legend = T,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  show_plot = F
)
```

Arguments

gobject	giotto object
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
point_size	size of point (cell)
cell_color	color for cells (see details)
cell_color_code	named vector with colors
color_as_factor	convert color column to factor

select_cell_groups
: select a subset of the groups from cell_color

show_network
: show underlying spatial network

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

grid_alpha
: alpha of spatial grid

spatial_grid_name
: name of spatial grid to use

show_legend
: show legend

show_plot
: show plot

Details

Description of parameters.

Value

plotly

Examples

```
visPlot_2D_plotly(gobject)
```

`visPlot_3D_plotly` *visPlot_3D_plotly*

Description

Visualize cells according to spatial coordinates

Usage

```
visPlot_3D_plotly(
  gobject,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = 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,
  show_network = F,
```

```
  network_color = NULL,
  network_alpha = 1,
  other_cell_alpha = 0.5,
  spatial_network_name = "spatial_network",
  spatial_grid_name = "spatial_grid",
  title = "",
  show_legend = T,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = F
)
```

Arguments

gobject	giotto object
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimz')
point_size	size of point (cell)
cell_color	color for cells (see details)
cell_color_code	named vector with colors
select_cell_groups	select a subset of the groups from cell_color
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
spatial_grid_name	name of spatial grid to use
title	title of plot
show_legend	show legend
show_plot	show plot
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
color_as_factor	convert color column to factor
show_grid	show spatial grid
grid_color	color of spatial grid
coord_fix_ratio	fix ratio between x and y-axis

Details

Description of parameters.

Value

ggplot

Examples

```
visPlot_3D_plotly(gobject)
```

`visSpatDimGenePlot` *visSpatDimGenePlot*

Description

integration of visSpatDimGenePlot_2D(ggplot) and visSpatDimGenePlot_3D(plotly)

Usage

```
visSpatDimGenePlot(
  gobject,
  plot_method = c("ggplot", "plotly"),
  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 = NULL,
  sdimy = NULL,
  sdimz = NULL,
  genes,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  edge_alpha_dim = NULL,
  scale_alpha_with_expression = FALSE,
  label_size = 16,
  genes_low_color = "blue",
  genes_mid_color = "white",
  genes_high_color = "red",
  dim_point_size = 3,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  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,
  spatial_point_border_col = "black",
  spatial_point_border_stroke = 0.1,
  legend_text_size = 12,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  midpoint = 0,
  point_size = 1,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_legend = T,
  show_plots = F
)
```

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	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimz')
genes	genes to show
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
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

edge_alpha_dim dim reduction plot: column to use for alpha of the edges

scale_alpha_with_expression
: scale expression with ggplot alpha parameter

label_size size for the label

genes_low_color
: color to represent low expression of gene

genes_high_color
: color to represent high expression of gene

dim_point_size dim reduction plot: point size

spatial_network_name
: name of spatial network to use

spatial_grid_name
: name of spatial grid to use

spatial_point_size
: spatial plot: point size

spatial_point_border_col
: color of border around points

spatial_point_border_stroke
: stroke size of border around points

legend_text_size
: the size of the text in legend

axis_scale three modes to adjust axis scale ratio

custom_ratio set the axis scale ratio on custom

x_ticks number of ticks on x axis

y_ticks number of ticks on y axis

z_ticks number of ticks on z axis

midpoint size of point (cell)

point_size size of point (cell)

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

show_plot show plot

Details

Description of parameters.

Value

ggplot or plotly

Examples

```
visSpatDimGenePlot(gobject)
```

visSpatDimGenePlot_2D *visSpatDimGenePlot_2D*

Description

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

Usage

```
visSpatDimGenePlot_2D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  plot_alignment = c("horizontal", "vertical"),
  genes,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  point_size = 1,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  show_NN_network = F,
  show_spatial_network = F,
  show_spatial_grid = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  edge_alpha_dim = NULL,
  scale_alpha_with_expression = FALSE,
  spatial_network_name = "spatial_network",
  spatial_grid_name = "spatial_grid",
  spatial_point_size = 1,
  spatial_point_border_col = "black",
  spatial_point_border_stroke = 0.1,
  midpoint = 0,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  show_legend = T,
  show_plots = F
)
```

Arguments

gobject	giotto object

`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

`point_size`
: size of point (cell)

`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

`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

`edge_alpha_dim`
: dim reduction plot: column to use for alpha of the edges

`scale_alpha_with_expression`
: scale expression with ggplot alpha parameter

`spatial_network_name`
: name of spatial network to use

`spatial_grid_name`
: name of spatial grid to use

`spatial_point_size`
: spatial plot: point size

`spatial_point_border_col`
: color of border around points

`spatial_point_border_stroke`
: stroke size of border around points

`midpoint`
: size of point (cell)

`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

`dim_point_size`
: dim reduction plot: point size

`show_plot`
: show plot

Details

Description of parameters.

Value

ggplot

Examples

```
visSpatDimGenePlot_2D(gobject)
```

`visSpatDimGenePlot_3D` *visSpatDimGenePlot_3D*

Description

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

Usage

```
visSpatDimGenePlot_3D(
  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 = NULL,
  sdimy = NULL,
  sdimz = NULL,
  genes,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  label_size = 16,
  genes_low_color = "blue",
  genes_mid_color = "white",
  genes_high_color = "red",
  dim_point_size = 3,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  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,
  legend_text_size = 12,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
```

```
  y_ticks = NULL,
  z_ticks = NULL
)
```

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
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
genes_low_color	color represent high gene expression (see details)
genes_high_color	color represent high gene expression (see details)
nn_network_alpha	column to use for alpha of the edges
show_spatial_network	show spatial network
spatial_network_name	name of spatial network to use
network_color	color of spatial/nn 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
legend_text_size	text size of legend
show_legend	show legend
show_plot	show plot

Details

Description of parameters.

Value

plotly

Examples

```
visSpatDimPlot_3D(gobject)
```

`visSpatDimPlot` *visSpatDimPlot*

Description

integration of visSpatDimPlot_2D and visSpatDimPlot_3D

Usage

```
visSpatDimPlot(
  gobject,
  plot_method = c("ggplot", "plotly"),
  plot_alignment = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = NULL,
  label_fontface = "bold",
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  dim_point_size = 3,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  nn_network_alpha = NULL,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  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,
  legend_text_size = 12,
  spatial_point_border_col = "black",
  spatial_point_border_stroke = 0.1,
  show_legend = T,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = F
)
```

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
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
nn_network_alpha	column to use for alpha of the edges
show_spatial_network	show spatial network

spatial_network_name
: name of spatial network to use

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

legend_text_size
: text size of legend

show_legend
: show legend

show_plot
: show plot

plot_mode
: choose the mode to draw plot : ggplot or plotly

spatial_network_color
: color of spatial network

Details

Description of parameters.

Value

ggplot or plotly

Examples

```
visSpatDimPlot(gobject)
```

---

visSpatDimPlot_2D *visSpatDimPlot_2D*

Description

Visualize cells according to spatial AND dimension reduction coordinates in ggplot2 mode

Usage

```
visSpatDimPlot_2D(
  gobject,
  plot_alignment = c("vertical", "horizontal"),
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  sdimx = NULL,
  sdimy = NULL,
```

```
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 4,
  label_fontface = "bold",
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  dim_plot_mode = NULL,
  dim_point_size = 1,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  nn_network_alpha = 0.05,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  spatial_network_color = NULL,
  show_spatial_grid = F,
  spatial_grid_name = "spatial_grid",
  spatial_grid_color = NULL,
  spatial_point_size = 1,
  spatial_point_border_col = "black",
  spatial_point_border_stroke = 0.1,
  show_legend = T,
  show_plot = F,
  plot_method = "ggplot"
)
```

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
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

nn_network_alpha
: column to use for alpha of the edges

show_spatial_network
: show spatial network

spatial_network_name
: name of spatial network to use

spatial_network_color
: color 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

show_legend
: show legend

show_plot
: show plot

return_plot
: return ggplot object

save_plot
: directly save the plot [boolean]

save_dir
: directory to save the plot

save_folder
: (optional) folder in directory to save the plot

save_name
: name of plot

save_format
: format of plot (e.g. tiff, png, pdf, ...)

show_saved_plot
: load & display the saved plot

Details

Description of parameters.

Value

ggplot

Examples

```
visSpatDimPlot_2D(gobject)
```

visSpatDimPlot_3D *visSpatDimPlot_3D*

Description

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

Usage

```
visSpatDimPlot_3D(
  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 = NULL,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 16,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  dim_point_size = 3,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  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
)
```

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

`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

`nn_network_alpha`
column to use for alpha of the edges

`show_spatial_network`
show spatial network

`spatial_network_name`
name of spatial network to use

`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

`legend_text_size`
text size of legend

`spatial_network_color`
color of spatial network

`show_legend` show legend

`show_plot` show plot

Details

Description of parameters.

Value

plotly

Examples

```
visSpatDimPlot_3D(gobject)
```

---

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

Examples

```
writeHMRFresults(gobject)
```

---

write_giotto_viewer_annotation *write_giotto_viewer_annotation*

Description

write out factor-like annotation data from a giotto object for the Viewer

Usage

```
write_giotto_viewer_annotation(
  annotation,
  annot_name = "test",
  output_directory = getwd()
)
```

Arguments

annotation	annotation from the data.table from giotto object
annot_name	name of the annotation
output_directory	directory where to save the files

Value

write a .txt and .annot file for the selection annotation

---

write_giotto_viewer_dim_reduction *write_giotto_viewer_dim_reduction*

Description

write out dimensional reduction data from a giotto object for the Viewer

Usage

```
write_giotto_viewer_dim_reduction(
  dim_reduction_cell,
  dim_red = NULL,
  dim_red_name = NULL,
  dim_red_rounding = NULL,
  dim_red_rescale = c(-20, 20),
  output_directory = getwd()
)
```

Arguments

dim_reduction_cell	dimension reduction slot from giotto object
dim_red	high level name of dimension reduction
dim_red_name	specific name of dimension reduction to use
dim_red_rounding	numerical indicating how to round the coordinates
dim_red_rescale	numericals to rescale the coordinates
output_directory	directory where to save the files

Value

write a .txt and .annot file for the selection annotation

`write_giotto_viewer_numeric_annotation` *write_giotto_viewer_numeric_annotation*

Description

write out numeric annotation data from a giotto object for the Viewer

Usage

```
write_giotto_viewer_numeric_annotation(
  annotation,
  annot_name = "test",
  output_directory = getwd()
)
```

Arguments

`annotation`	annotation from the data.table from giotto object
`annot_name`	name of the annotation
`output_directory`	directory where to save the files

Value

write a .txt and .annot file for the selection annotation

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