

Package ‘Giotto’

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

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

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Imports data.table (>= 1.12.2),
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matrixStats (>= 0.55.0),
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ClusterR,
grDevices,
graphics,
RColorBrewer (>= 1.1-2),
dbscan (>= 1.1-3),
farver (>= 2.0.3),
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scales (>= 1.0.0),
ComplexHeatmap (>= 1.20.0),
qvalue (>= 2.14.1),
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igraph (>= 1.2.4.1),
irlba,
plotly,
parallel,

reticulate (≥ 1.14),
 magrittr,
 limma,
 ggdendro,
 smfishHmrf,
 devtools,
 reshape2,
 ggraph,
 Rcpp,
 Rfast,
 Rtsne (≥ 0.15),
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 R.utils,
 fitdistrplus,
 quadprog

Suggests knitr,
 rmarkdown,
 MAST,
 scan ($\geq 1.10.1$),
 png,
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 tiff,
 biomaRt,
 trendsseek,
 multinet ($\geq 3.0.2$),
 RTriangle ($\geq 1.6-0.10$)

biocViews

VignetteBuilder knitr

LinkingTo Rcpp,
 RcppArmadillo

Remotes lambdamoses/smfishhmr-r

R topics documented:

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| | |
|--------------------|---------------------------|
| addCellIntMetadata | <i>addCellIntMetadata</i> |
|--------------------|---------------------------|

Description

Creates an additional metadata column with information about interacting and non-interacting cell types of the selected cell-cell interaction.

Usage

```
addCellIntMetadata(  
  gobject,  
  spatial_network = "spatial_network",  
  cluster_column,  
  cell_interaction,  
  name = "select_int",  
  return_gobject = TRUE  
)
```

Arguments

| | |
|------------------|----------------------------------|
| gobject | giotto object |
| spatial_network | name of spatial network to use |
| cluster_column | column of cell types |
| cell_interaction | cell-cell interaction to use |
| name | name for the new metadata column |
| return_gobject | return an updated giotto object |

Details

This function will create an additional metadata column which selects interacting cell types for a specific cell-cell interaction. For example, if you want to color interacting astrocytes and oligodendrocytes it will create a new metadata column with the values "select_astrocytes", "select_oligodendrocytes", "other_astrocytes", "other_oligodendrocytes" and "other". Where "other" is all other cell types found within the selected cell type column.

Value

Giotto object

Examples

```
addCellIntMetadata(gobject)
```

| | |
|-----------------|------------------------|
| addCellMetadata | <i>addCellMetadata</i> |
|-----------------|------------------------|

Description

adds cell metadata to the giotto object

Usage

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

Arguments

| | |
|-----------------------------|---|
| <code>gobject</code> | giotto object |
| <code>new_metadata</code> | new cell metadata to use (data.table, data.frame, ...) |
| <code>vector_name</code> | (optional) custom name if you provide a single vector |
| <code>by_column</code> | merge metadata based on cell_ID column in pDataDT (default = FALSE) |
| <code>column_cell_ID</code> | 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 specify 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 | <i>addCellStatistics</i> |
|-------------------|--------------------------|

Description

adds cells statistics to the giotto object

Usage

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

Arguments

| | |
|----------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>detection_threshold</code> | detection threshold to consider a gene detected |
| <code>return_gobject</code> | 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 | <i>addGeneMetadata</i> |
|-----------------|------------------------|

Description

adds gene metadata to the giotto object

Usage

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

Arguments

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

Details

You can add additional gene metadata in two manners: 1. Provide a data.table or data.frame with gene annotations in the same order as the gene_ID column in fDataDT(gobject) 2. Provide a data.table or data.frame with gene annotations and specify 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)
```

| | |
|--------------|---------------------|
| addGenesPerc | <i>addGenesPerc</i> |
|--------------|---------------------|

Description

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

Usage

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

Arguments

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

Value

giotto object if return_gobject = TRUE, else a vector with

Examples

```
addGenesPerc(gobject)
```

| | |
|-------------------|--------------------------|
| addGeneStatistics | <i>addGeneStatistics</i> |
|-------------------|--------------------------|

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)
```

```
addGiottoImage
```

```
addGiottoImage
```

Description

Adds giotto image objects to your giotto object

Usage

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

Arguments

gobject giotto object

images list of giotto image objects, see [createGiottoImage](#)

Value

an updated Giotto object with access to the list of images

Examples

```
addGiottoImage(mg_object)
```

```
addGiottoImageToSpatPlot
```

```
addGiottoImageToSpatPlot
```

Description

Add a giotto image to a spatial ggplot object post creation

Usage

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

Arguments

spatpl a spatial ggplot object

gimage a giotto image, see [createGiottoImage](#)

Value

an updated spatial ggplot object

Examples

```
addGiottoImageToSpatPlot(mg_object)
```

| | |
|---------|----------------|
| addHMRF | <i>addHMRF</i> |
|---------|----------------|

Description

Add selected results from doHMRF to the giotto object

Usage

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

Arguments

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

Value

giotto object

Examples

```
addHMRF(gobject)
```

| | |
|------------------|-------------------------|
| addNetworkLayout | <i>addNetworkLayout</i> |
|------------------|-------------------------|

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

| | |
|--------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>nn_network_to_use</code> | kNN or sNN |
| <code>network_name</code> | name of NN network to be used |
| <code>layout_type</code> | layout algorithm to use |
| <code>options_list</code> | list of options for selected layout |
| <code>layout_name</code> | name for layout |
| <code>return_gobject</code> | 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

| | |
|----------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>detection_threshold</code> | detection threshold to consider a gene detected |
| <code>return_gobject</code> | 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 | <i>adjustGiottoMatrix</i> |
|--------------------|---------------------------|

Description

normalize and/or scale expression 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 [removeBatchEffect](#) function to remove known batch effects and to adjust expression values according to provided covariates.

Value

giotto object

Examples

```
adjustGiottoMatrix(gobject)
```

| | |
|-----------------|------------------------|
| anndataToGiotto | <i>anndataToGiotto</i> |
|-----------------|------------------------|

Description

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

Usage

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

Arguments

| | |
|---------------|-----------------------------|
| anndata_path | path to the .h5ad file |
| metadata_cols | metadata columns to include |
| instructions | giotto instructions |

Details

Function in beta.

Value

Giotto object

| | |
|----------------|-----------------------|
| annotateGiotto | <i>annotateGiotto</i> |
|----------------|-----------------------|

Description

Converts cluster results into provided annotation.

Usage

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


Arguments

| | |
|--------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>annotation_vector</code> | named annotation vector (names = cluster ids) |
| <code>cluster_column</code> | cluster column to convert to annotation names |
| <code>name</code> | new name for annotation column |

Details

You need to specify 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)
```

`annotateSpatialGrid` *annotateSpatialGrid*

Description

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

Usage

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

Arguments

| | |
|--------------------------------|---|
| <code>gobject</code> | Giotto object |
| <code>spatial_grid_name</code> | name of spatial grid, see showGrids |
| <code>cluster_columns</code> | names of cell metadata, see pDataDT |

Value

annotated spatial grid data.table

Examples

```
annotateSpatialGrid()
```

```
annotateSpatialNetwork
```

```
annotateSpatialNetwork
```

Description

Annotate spatial network with cell metadata information.

Usage

```
annotateSpatialNetwork(
  gobject,
  spatial_network_name = "Delaunay_network",
  cluster_column,
  create_full_network = F
)
```

Arguments

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

Value

annotated network in data.table format

Examples

```
annotateSpatialNetwork(gobject)
```

```
binSpect
```

```
binSpect
```

Description

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

Usage

```

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

```

Arguments

| | |
|-----------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>bin_method</code> | method to binarize gene expression |
| <code>expression_values</code> | expression values to use |
| <code>subset_genes</code> | only select a subset of genes to test |
| <code>spatial_network_name</code> | name of spatial network to use (default = 'spatial_network') |
| <code>spatial_network_k</code> | different k's for a spatial kNN to evaluate |
| <code>reduce_network</code> | default uses the full network |
| <code>kmeans_algo</code> | kmeans algorithm to use (kmeans, kmeans_arma, kmeans_arma_subset) |
| <code>nstart</code> | kmeans: nstart parameter |
| <code>iter_max</code> | kmeans: iter.max parameter |
| <code>extreme_nr</code> | number of top and bottom cells (see details) |
| <code>sample_nr</code> | total number of cells to sample (see details) |

| | |
|-----------------|--|
| percentage_rank | percentage of top cells for binarization |
| do_fisher_test | perform fisher test |
| adjust_method | p-value adjusted method to use (see p.adjust) |
| calc_hub | calculate the number of hub cells |
| hub_min_int | minimum number of cell-cell interactions for a hub cell |
| get_av_expr | calculate the average expression per gene of the high expressing cells |
| get_high_expr | calculate the number of high expressing cells per gene |
| implementation | enrichment implementation (data.table, simple, matrix) |
| group_size | number of genes to process together with data.table implementation (default = automatic) |
| do_parallel | run calculations in parallel with mclapply |
| cores | number of cores to use if do_parallel = TRUE |
| verbose | be verbose |
| set.seed | set a seed before kmeans binarization |
| bin_matrix | a binarized matrix, when provided it will skip the binarization process |
| summarize | summarize the p-values or adjusted p-values |

Details

We provide two ways to identify spatial genes based on gene expression binarization. Both methods are identical 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: All cells are connected through a spatial network based on the physical coordinates
- 3. contingency table: A contingency table is calculated based on all edges of neighboring cells and the binarized expression (0-0, 0-1, 1-0 or 1-1)
- 4. For each gene an odds-ratio (OR) and fisher.test (optional) is calculated

Three different kmeans algorithms have been implemented:

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

Other statistics are provided (optional):

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

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

Value

data.table with results (see details)

Examples

```
binSpect(gobject)
```

| | |
|---------------|----------------------|
| binSpectMulti | <i>binSpectMulti</i> |
|---------------|----------------------|

Description

binSpect for multiple spatial kNN networks

Usage

```
binSpectMulti(
  gobject,
  bin_method = c("kmeans", "rank"),
  expression_values = c("normalized", "scaled", "custom"),
  subset_genes = NULL,
  spatial_network_k = c(5, 10, 20),
  reduce_network = FALSE,
  kmeans_algo = c("kmeans", "kmeans_arma", "kmeans_arma_subset"),
  nstart = 3,
  iter_max = 10,
  extreme_nr = 50,
  sample_nr = 50,
  percentage_rank = c(10, 30),
  do_fisher_test = TRUE,
  adjust_method = "fdr",
  calc_hub = FALSE,
  hub_min_int = 3,
  get_av_expr = TRUE,
  get_high_expr = TRUE,
  implementation = c("data.table", "simple", "matrix"),
  group_size = "automatic",
  do_parallel = TRUE,
  cores = NA,
  verbose = T,
  knn_params = NULL,
  set.seed = NULL,
  summarize = c("p.value", "adj.p.value")
)
```

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

Details

We provide two ways to identify spatial genes based on gene expression binarization. Both methods are identical 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: All cells are connected through a spatial network based on the physical coordinates
- 3. contingency table: A contingency table is calculated based on all edges of neighboring cells and the binarized expression (0-0, 0-1, 1-0 or 1-1)
- 4. For each gene an odds-ratio (OR) and fisher.test (optional) is calculated

Three different kmeans algorithms have been implemented:

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

Other statistics are provided (optional):

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

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

Value

data.table with results (see details)

Examples

```
binSpectMulti(gobject)
```

| | |
|----------------|-----------------------|
| binSpectSingle | <i>binSpectSingle</i> |
|----------------|-----------------------|

Description

binSpect for a single spatial network

Usage

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

```

    verbose = T,
    set.seed = NULL,
    bin_matrix = NULL
  )

```

Arguments

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

Details

We provide two ways to identify spatial genes based on gene expression binarization. Both methods are identical 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**: All cells are connected through a spatial network based on the physical coordinates

- 3. contingency table: A contingency table is calculated based on all edges of neighboring cells and the binarized expression (0-0, 0-1, 1-0 or 1-1)
- 4. For each gene an odds-ratio (OR) and fisher.test (optional) is calculated

Three different kmeans algorithms have been implemented:

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

Other statistics are provided (optional):

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

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

Value

data.table with results (see details)

Examples

```
binSpectSingle(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

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>method</code> | method to calculate highly variable genes |
| <code>reverse_log_scale</code> | reverse log-scale of expression values (default = FALSE) |
| <code>logbase</code> | if <code>reverse_log_scale</code> is TRUE, which log base was used? |
| <code>expression_threshold</code> | expression threshold to consider a gene detected |
| <code>nr_expression_groups</code> | number of expression groups for <code>cov_groups</code> |
| <code>zscore_threshold</code> | zscore to select hvg for <code>cov_groups</code> |
| <code>HVGname</code> | name for highly variable genes in cell metadata |
| <code>difference_in_cov</code> | minimum difference in coefficient of variance required |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters from all_plots_save_function |
| <code>default_save_name</code> | default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code> |
| <code>return_gobject</code> | 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 ($COV \sim \log(\text{mean expression})$). Genes that show a higher than predicted COV (*difference_in_cov*) are considered highly variable.

Value

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

Examples

```

data(mini_giotto_single_cell) # loads existing Giotto object

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

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

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

```

| | |
|--------------------|---------------------------|
| calculateMetaTable | <i>calculateMetaTable</i> |
|--------------------|---------------------------|

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

| | |
|--------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>metadata_cols</code> | annotation columns found in <code>pDataDT(gobject)</code> |
| <code>selected_genes</code> | 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)
```

```
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

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

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 = "Delaunay_network",
  cluster_column,
  number_of_simulations = 1000,
  adjust_method = c("none", "fdr", "bonferroni", "BH", "holm", "hochberg", "hommel",
    "BY")
)

```

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
adjust_method method to adjust p.values

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

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

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

| | |
|---|--|
| <code>gobject</code> | giotto object |
| <code>CPscore</code> | CPscore, output from <code>cellProximityEnrichment()</code> |
| <code>remove_self_edges</code> | remove enrichment/depletion edges with itself |
| <code>self_loop_strength</code> | size of self-loops |
| <code>color_depletion</code> | color for depleted cell-cell interactions |
| <code>color_enrichment</code> | color for enriched cell-cell interactions |
| <code>rescale_edge_weights</code> | rescale edge weights (boolean) |
| <code>edge_weight_range_depletion</code> | numerical vector of length 2 to rescale depleted edge weights |
| <code>edge_weight_range_enrichment</code> | numerical vector of length 2 to rescale enriched edge weights |
| <code>layout</code> | layout algorithm to use to draw nodes and edges |
| <code>only_show_enrichment_edges</code> | show only the enriched pairwise scores |
| <code>edge_width_range</code> | range of edge width |
| <code>node_size</code> | size of nodes |
| <code>node_text_size</code> | size of node labels |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters from all_plots_save_function |
| <code>default_save_name</code> | default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code> |

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

| | |
|----------------------|--|
| <code>gobject</code> | giotto object |
| <code>...</code> | Arguments passed on to cellProximitySpatPlot2D |
| | <code>interaction_name</code> cell-cell interaction name |
| | <code>cluster_column</code> cluster column with cell clusters |
| | <code>sdimx</code> x-axis dimension name (default = 'sdimx') |
| | <code>sdimy</code> y-axis dimension name (default = 'sdimy') |
| | <code>cell_color</code> color for cells (see details) |
| | <code>cell_color_code</code> named vector with colors |
| | <code>color_as_factor</code> convert color column to factor |
| | <code>show_other_cells</code> decide if show cells not in network |
| | <code>show_network</code> show spatial network of selected cells |
| | <code>show_other_network</code> show spatial network of not selected cells |
| | <code>network_color</code> color of spatial network |
| | <code>spatial_network_name</code> name of spatial network to use |
| | <code>show_grid</code> show spatial grid |
| | <code>grid_color</code> color of spatial grid |
| | <code>spatial_grid_name</code> name of spatial grid to use |
| | <code>coord_fix_ratio</code> fix ratio between x and y-axis |
| | <code>show_legend</code> show legend |
| | <code>point_size_select</code> size of selected points |
| | <code>point_select_border_col</code> border color of selected points |
| | <code>point_select_border_stroke</code> stroke size of selected points |
| | <code>point_size_other</code> size of other points |
| | <code>point_alpha_other</code> opacity of other points |
| | <code>point_other_border_col</code> border color of other points |
| | <code>point_other_border_stroke</code> stroke size of other points |
| | <code>show_plot</code> 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 = "Delaunay_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  coord_fix_ratio = 1,
  show_legend = T,

```

```

    point_size_select = 2,
    point_select_border_col = "black",
    point_select_border_stroke = 0.05,
    point_size_other = 1,
    point_alpha_other = 0.3,
    point_other_border_col = "lightgrey",
    point_other_border_stroke = 0.01,
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "cellProximitySpatPlot2D"
)

```

Arguments

| | |
|---|--|
| <code>gobject</code> | giotto object |
| <code>interaction_name</code> | cell-cell interaction name |
| <code>cluster_column</code> | cluster column with cell clusters |
| <code>sdimx</code> | x-axis dimension name (default = 'sdimx') |
| <code>sdimy</code> | y-axis dimension name (default = 'sdimy') |
| <code>cell_color</code> | color for cells (see details) |
| <code>cell_color_code</code> | named vector with colors |
| <code>color_as_factor</code> | convert color column to factor |
| <code>show_other_cells</code> | decide if show cells not in network |
| <code>show_network</code> | show spatial network of selected cells |
| <code>show_other_network</code> | show spatial network of not selected cells |
| <code>network_color</code> | color of spatial network |
| <code>spatial_network_name</code> | name of spatial network to use |
| <code>show_grid</code> | show spatial grid |
| <code>grid_color</code> | color of spatial grid |
| <code>spatial_grid_name</code> | name of spatial grid to use |
| <code>coord_fix_ratio</code> | fix ratio between x and y-axis |
| <code>show_legend</code> | show legend |
| <code>point_size_select</code> | size of selected points |
| <code>point_select_border_col</code> | border color of selected points |
| <code>point_select_border_stroke</code> | stroke size of selected points |

| | |
|---------------------------|--|
| point_size_other | size of other points |
| point_alpha_other | opacity of other points |
| point_other_border_col | border color of other points |
| point_other_border_stroke | stroke size of other points |
| show_plot | show plots |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters from all_plots_save_function |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

ggplot

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 = "Delaunay_network",
    show_grid = F,
    grid_color = NULL,
    spatial_grid_name = "spatial_grid",
    show_legend = T,
    point_size_select = 4,
    point_size_other = 2,
    point_alpha_other = 0.5,
    axis_scale = c("cube", "real", "custom"),
    custom_ratio = NULL,
    x_ticks = NULL,
    y_ticks = NULL,
    z_ticks = NULL,
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "cellProximitySpatPlot3D",
    ...
)

```

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>interaction_name</code> | cell-cell interaction name |
| <code>cluster_column</code> | cluster column with cell clusters |
| <code>sdimx</code> | x-axis dimension name (default = 'sdimx') |
| <code>sdimy</code> | y-axis dimension name (default = 'sdimy') |
| <code>sdimz</code> | z-axis dimension name (default = 'sdimz') |
| <code>cell_color</code> | color for cells (see details) |
| <code>cell_color_code</code> | named vector with colors |
| <code>color_as_factor</code> | convert color column to factor |
| <code>show_other_cells</code> | decide if show cells not in network |
| <code>show_network</code> | show spatial network of selected cells |
| <code>show_other_network</code> | show spatial network of not selected cells |
| <code>network_color</code> | color of spatial network |
| <code>spatial_network_name</code> | name of spatial network to use |
| <code>show_grid</code> | show spatial grid |
| <code>grid_color</code> | color of spatial grid |
| <code>spatial_grid_name</code> | name of spatial grid to use |
| <code>show_legend</code> | show legend |

| | |
|-------------------|--|
| point_size_select | size of selected points |
| point_size_other | size of other points |
| point_alpha_other | opacity of other points |
| axis_scale | scale of axis |
| custom_ratio | custom ratio of axes |
| x_ticks | ticks on x-axis |
| y_ticks | ticks on y-axis |
| z_ticks | ticks on z-axis |
| show_plot | show plots |
| return_plot | return plotly object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters from all_plots_save_function |
| default_save_name | default save name for saving, don't change, change save_name in save_param |
| ... | additional parameters |

Details

Description of parameters.

Value

plotly

Examples

```
cellProximitySpatPlot3D(gobject)
```

| | |
|----------------------|-----------------------------|
| cellProximityVisPlot | <i>cellProximityVisPlot</i> |
|----------------------|-----------------------------|

Description

Visualize cell-cell interactions according to spatial coordinates

Usage

```
cellProximityVisPlot(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  cell_color = NULL,
```

```

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

```

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>interaction_name</code> | cell-cell interaction name |
| <code>cluster_column</code> | cluster column with cell clusters |
| <code>sdimx</code> | x-axis dimension name (default = 'sdimx') |
| <code>sdimy</code> | y-axis dimension name (default = 'sdimy') |
| <code>sdimz</code> | z-axis dimension name (default = 'sdimz') |
| <code>cell_color</code> | color for cells (see details) |
| <code>cell_color_code</code> | named vector with colors |
| <code>color_as_factor</code> | convert color column to factor |
| <code>show_other_cells</code> | show not selected cells |
| <code>show_network</code> | show underlying spatial network |
| <code>show_other_network</code> | show underlying spatial network of other cells |
| <code>network_color</code> | color of spatial network |
| <code>spatial_network_name</code> | name of spatial network to use |

| | |
|----------------------------|---------------------------------|
| show_grid | show spatial grid |
| grid_color | color of spatial grid |
| spatial_grid_name | name of spatial grid to use |
| coord_fix_ratio | fix ratio between x and y-axis |
| show_legend | show legend |
| point_size_select | size of selected points |
| point_select_border_col | border color of selected points |
| point_select_border_stroke | stroke size of selected points |
| point_size_other | size of other points |
| point_alpha_other | alpha of other points |
| point_other_border_col | border color of other points |
| point_other_border_stroke | stroke size of other points |
| axis_scale | scale of axis |
| custom_ratio | custom ratio of scales |
| x_ticks | x ticks |
| y_ticks | y ticks |
| z_ticks | z ticks |
| plot_method | method to plot |
| ... | additional parameters |

Details

Description of parameters.

Value

ggplot or plotly

Examples

```
cellProximityVisPlot(gobject)
```

| | |
|--------------------------|---------------------------------|
| changeGiottoInstructions | <i>changeGiottoInstructions</i> |
|--------------------------|---------------------------------|

Description

Function to change one or more instructions from giotto object

Usage

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

Arguments

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

Value

giotto object with one or more changed instructions

Examples

```
changeGiottoInstructions()
```

| | |
|---------------|----------------------|
| changeImageBg | <i>changeImageBg</i> |
|---------------|----------------------|

Description

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

Usage

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

Arguments

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

Value

magick image or giotto image object with updated background color

Examples

```
changeImageBg(mg_object)
```

| | |
|--------------|---------------------|
| clusterCells | <i>clusterCells</i> |
|--------------|---------------------|

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

| | |
|-----------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>cluster_method</code> | community cluster method to use |
| <code>name</code> | name for new clustering result |
| <code>nn_network_to_use</code> | type of NN network to use (kNN vs sNN) |
| <code>network_name</code> | name of NN network to use |
| <code>pyth_leid_resolution</code> | resolution for leiden |
| <code>pyth_leid_weight_col</code> | column to use for weights |
| <code>pyth_leid_part_type</code> | partition type to use |
| <code>pyth_leid_init_memb</code> | initial membership |
| <code>pyth_leid_iterations</code> | number of iterations |
| <code>pyth_louv_resolution</code> | resolution for louvain |
| <code>pyth_louv_weight_col</code> | python louvain param: weight column |
| <code>python_louv_random</code> | python louvain param: random |
| <code>python_path</code> | specify specific path to python if required |
| <code>louvain_gamma</code> | louvain param: gamma or resolution |
| <code>louvain_omega</code> | louvain param: omega |
| <code>walk_steps</code> | randomwalk: number of steps |
| <code>walk_clusters</code> | 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 | <i>clusterSpatialCorGenes</i> |
|------------------------|-------------------------------|

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 | <i>combCCcom</i> |
|-----------|------------------|

Description

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

Usage

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

Arguments

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

Value

combined data.table with spatial and expression communication data

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

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

Value

`cpgObject` that contains the filtered differential gene scores

Examples

```
combineCellProximityGenes(gobject)
```

`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

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

Value

`cpgObject` that contains the filtered differential gene scores

Examples

```
combineCPG(gobject)
```

| | |
|-----------------|------------------------|
| combineMetadata | <i>combineMetadata</i> |
|-----------------|------------------------|

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)
```

| | |
|----------------------------|-----------------------------------|
| convertEnsemblToGeneSymbol | <i>convertEnsemblToGeneSymbol</i> |
|----------------------------|-----------------------------------|

Description

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

Usage

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

Arguments

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

Details

This function requires that the biomaRt library is installed

Value

expression matrix with gene symbols as rownames

| | |
|--------------------|---------------------------|
| createCrossSection | <i>createCrossSection</i> |
|--------------------|---------------------------|

Description

Create a virtual 2D cross section.

Usage

```
createCrossSection(
  gobject,
  name = "cross_section",
  spatial_network_name = "Delaunay_network",
  thickness_unit = c("cell", "natural"),
  slice_thickness = 2,
  cell_distance_estimate_method = "mean",
  extend_ratio = 0.2,
  method = c("equation", "3 points", "point and norm vector",
    "point and two plane vectors"),
  equation = NULL,
  point1 = NULL,
  point2 = NULL,
  point3 = NULL,
  normVector = NULL,
  planeVector1 = NULL,
  planeVector2 = NULL,
  mesh_grid_n = 20,
  return_gobject = TRUE
)
```

Arguments

| | |
|--|--|
| <code>gobject</code> | giotto object |
| <code>name</code> | name of cross section object. (default = cross_sectino) |
| <code>spatial_network_name</code> | name of spatial network object. (default = Delaunay_network) |
| <code>thickness_unit</code> | unit of the virtual section thickness. If "cell", average size of the observed cells is used as length unit. If "natural", the unit of cell location coordinates is used.(default = cell) |
| <code>slice_thickness</code> | thickness of slice. default = 2 |
| <code>cell_distance_estimate_method</code> | method to estimate average distance between neigobring cells. (default = mean) |
| <code>extend_ratio</code> | deciding the span of the cross section meshgrid, as a ratio of extension compared to the borders of the vitural tissue section. (default = 0.2) |
| <code>method</code> | method to define the cross section plane. If equation, the plane is defined by a four element numerical vector (equation) in the form of c(A,B,C,D), corresponding to a plane with equation $Ax+By+Cz=D$. If 3 points, the plane is define by the coordinates of 3 points, as given by point1, point2, and point3. If point |

| | |
|----------------|--|
| | and norm vector, the plane is defined by the coordinates of one point (point1) in the plane and the coordinates of one norm vector (normVector) to the plane. If point and two plane vector, the plane is defined by the coordinates of one point (point1) in the plane and the coordinates of two vectors (planeVector1, planeVector2) in the plane. (default = equation) |
| equation | equation required by method "equation".equations needs to be a numerical vector of length 4, in the form of c(A,B,C,D), which defines plane $Ax+By+Cz=D$. |
| point1 | coordinates of the first point required by method "3 points", "point and norm vector", and "point and two plane vectors". |
| point2 | coordinates of the second point required by method "3 points" |
| point3 | coordinates of the third point required by method "3 points" |
| normVector | coordinates of the norm vector required by method "point and norm vector" |
| planeVector1 | coordinates of the first plane vector required by method "point and two plane vectors" |
| planeVector2 | coordinates of the second plane vector required by method "point and two plane vectors" |
| mesh_grid_n | numer of meshgrid lines to generate along both directions for the cross section plane. |
| return_gobject | boolean: return giotto object (default = TRUE) |

Details

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

Value

giotto object with updated spatial network slot

| | |
|-------------------|--------------------------|
| createGiottoImage | <i>createGiottoImage</i> |
|-------------------|--------------------------|

Description

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

Usage

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

Arguments

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

Value

a giotto image object

Examples

```
createGiottoImage(mg_object)
```

```
createGiottoInstructions
```

```
createGiottoInstructions
```

Description

Function to set global instructions for giotto functions

Usage

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

Arguments

| | |
|--------------------------|--|
| <code>python_path</code> | path to python binary to use |
| <code>show_plot</code> | print plot to console, default = TRUE |
| <code>return_plot</code> | return plot as object, default = TRUE |
| <code>save_plot</code> | automatically save plot, default = FALSE |
| <code>save_dir</code> | path to directory where to save plots |

| | |
|-------------|-----------------------------------|
| plot_format | format of plots (defaults to png) |
| dpi | resolution for raster images |
| units | units of format (defaults to in) |
| height | height of plots |
| width | width of plots |

Value

named vector with giotto instructions

See Also

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

Examples

```
createGiottoInstructions()
```

| | |
|--------------------|-----------------------------|
| createGiottoObject | <i>create Giotto object</i> |
|--------------------|-----------------------------|

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,
  images = NULL,
  offset_file = NULL,
  instructions = NULL,
  cores = NA
)
```

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) |
| images | list of images |
| offset_file | file used to stitch fields together (optional) |
| instructions | list of instructions or output result from createGiottoInstructions |
| cores | how many cores or threads to use to read data if paths are provided |

Details

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

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

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

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

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

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

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

Value

giotto object

Examples

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

```
createGiottoVisiumObject
      createGiottoVisiumObject
```

Description

creates Giotto object directly from a 10X visium folder

Usage

```
createGiottoVisiumObject(
  visium_dir = NULL,
  expr_data = c("raw", "filter"),
  gene_column_index = 1,
  png_name = NULL,
  xmax_adj = 0,
  xmin_adj = 0,
  ymax_adj = 0,
  ymin_adj = 0,
  instructions = NULL,
  cores = NA
)
```

Arguments

| | |
|-------------------|---|
| visium_dir | path to the 10X visium directory [required] |
| expr_data | raw or filtered data (see details) |
| gene_column_index | which column index to select (see details) |
| png_name | select name of png to use (see details) |
| xmax_adj | adjustment of the maximum x-value to align the image |
| xmin_adj | adjustment of the minimum x-value to align the image |
| ymax_adj | adjustment of the maximum y-value to align the image |
| ymin_adj | adjustment of the minimum y-value to align the image |
| instructions | list of instructions or output result from createGiottoInstructions |
| cores | how many cores or threads to use to read data if paths are provided |

Details

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

Value

giotto object

Examples

```
createGiottoVisiumObject(visium_dir)
```

| | |
|-------------------------------|-------------------------|
| <code>createHeatmap_DT</code> | <i>createHeatmap_DT</i> |
|-------------------------------|-------------------------|

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("correlation", "custom"),
  gene_custom_order = NULL,
  gene_cor_method = "pearson",
  gene_hclust_method = "complete"
)
```

Arguments

| | |
|-----------------------------------|------------------------------------|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>genes</code> | genes to use |
| <code>cluster_column</code> | name of column to use for clusters |
| <code>cluster_order</code> | method to determine cluster order |
| <code>cluster_custom_order</code> | 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 | <i>createMetagenes</i> |
|-----------------|------------------------|

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

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>type</code> | sNN or kNN |
| <code>dim_reduction_to_use</code> | dimension reduction method to use |
| <code>dim_reduction_name</code> | name of dimension reduction set to use |
| <code>dimensions_to_use</code> | number of dimensions to use as input |
| <code>genes_to_use</code> | if <code>dim_reduction_to_use = NULL</code> , which genes to use |
| <code>expression_values</code> | 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: $\text{weight} = 1/(1 + \text{distance})$

Output for sNN:

- from: cell_ID for source cell
- to: cell_ID for target cell
- distance: distance between cells
- weight: $1/(1 + \text{distance})$
- 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)
```

```
createSpatialDefaultGrid  
    createSpatialDefaultGrid
```

Description

Create a spatial grid using the default method

Usage

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

Arguments

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

Details

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

Value

giotto object with updated spatial grid slot

```
createSpatialDelaunayNetwork
      createSpatialDelaunayNetwork
```

Description

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

Usage

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

Arguments

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

Details

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

Value

giotto object with updated spatial network slot

Examples

```
createSpatialDelaunayNetwork(gobject)
```

```
createSpatialEnrich     createSpatialEnrich
```

Description

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

Usage

```
createSpatialEnrich(...)
```

Arguments

```
...                    Arguments passed on to runSpatialEnrich
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 = FALSE)
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
```

See Also

[runSpatialEnrich](#)

| | |
|-------------------|--------------------------|
| createSpatialGrid | <i>createSpatialGrid</i> |
|-------------------|--------------------------|

Description

Create a spatial grid using the default method

Usage

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

Arguments

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

Details

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

- default method: [createSpatialDefaultGrid](#)

Value

giotto object with updated spatial grid slot

```
createSpatialKNNnetwork
      createSpatialKNNnetwork
```

Description

Create a spatial knn network.

Usage

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

Arguments

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

Value

giotto object with updated spatial network slot

dimensions: default = 'all' which takes all possible dimensions. Alternatively you can provide a character vector that specifies 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`

Examples

```
createSpatialKNNnetwork(gobject)
```

```
createSpatialNetwork  createSpatialNetwork
```

Description

Create a spatial network based on cell centroid physical distances.

Usage

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

Arguments

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

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

Details

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

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

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 expression values for each factor

| | |
|-------------------|--------------------------|
| create_average_DT | <i>create_average_DT</i> |
|-------------------|--------------------------|

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 expression values for each factor

| | |
|----------------------------------|---|
| create_cell_type_random_cell_IDs | <i>create_cell_type_random_cell_IDs</i> |
|----------------------------------|---|

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_crossSection_object
      create_crossSection_object
```

Description

create a crossSection object

Usage

```

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

Arguments

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

| | |
|-------------------|--------------------------|
| create_screepplot | <i>create_screepplot</i> |
|-------------------|--------------------------|

Description

create screepplot with ggplot

Usage

```
create_screepplot(pca_obj, ncp = 20, ylim = c(0, 20))
```

Arguments

| | |
|---------|---|
| pca_obj | pca dimension reduction object |
| ncp | number of principal components to calculate |
| ylim | y-axis limits on scree plot |

Value

ggplot

crossSectionGenePlot *crossSectionGenePlot*

Description

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

Usage

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

Arguments

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

Details

Description of parameters.

Value

ggplot

See Also

[spatGenePlot3D](#) and [spatGenePlot2D](#)

crossSectionGenePlot3D

crossSectionGenePlot3D

Description

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

Usage

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

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>crossSection_obj</code> | cross section object as alternative input. default = NULL. |
| <code>name</code> | name of virtual cross section to use |
| <code>spatial_network_name</code> | name of spatial network to use |
| <code>other_cell_color</code> | color of cells outside the cross section. default = transparent. |
| <code>default_save_name</code> | default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code> |
| <code>...</code> | parameters for <code>spatGenePlot3D</code> |

Details

Description of parameters.

Value

ggplot

Examples

```
crossSectionGenePlot3D(gobject)
```

| | |
|------------------|-------------------------|
| crossSectionPlot | <i>crossSectionPlot</i> |
|------------------|-------------------------|

Description

Visualize cells in a virtual cross section according to spatial coordinates

Usage

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

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>crossSection_obj</code> | cross section object as alternative input. default = NULL. |
| <code>name</code> | name of virtual cross section to use |
| <code>spatial_network_name</code> | name of spatial network to use |
| <code>default_save_name</code> | default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code> |
| <code>...</code> | parameters for <code>spatPlot2D</code> |

Details

Description of parameters.

Value

ggplot

See Also

[crossSectionPlot](#)

| | |
|--------------------|---------------------------|
| crossSectionPlot3D | <i>crossSectionPlot3D</i> |
|--------------------|---------------------------|

Description

Visualize cells in a virtual cross section according to spatial coordinates

Usage

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

Arguments

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

Details

Description of parameters.

Value

ggplot

Examples

```
crossSectionPlot3D(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 = "Delaunay_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 between 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 |
| cor_method | correlation method |

Details

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

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

The `spatCorObject` can be further explored with `showSpatialCorGenes()`

Value

returns a spatial correlation object: "spatCorObject"

See Also

[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

| | |
|---------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>spatial_grid_name</code> | name of spatial grid to use (default = 'spatial_grid') |
| <code>min_cells_per_grid</code> | minimum number of cells in a grid to be considered |
| <code>scale_unit</code> | scale features |
| <code>ncp</code> | number of principal components to calculate |
| <code>show_plot</code> | show plots |
| <code>PC_zscore</code> | 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 principal components (PCs) to z-scores and select PCs based on a z-score threshold

Value

spatial pattern object 'spatPatObj'

Examples

```
detectSpatialPatterns(gobject)
```

| | |
|-------------|--------------------|
| dimCellPlot | <i>dimCellPlot</i> |
|-------------|--------------------|

Description

Visualize cells according to dimension reduction coordinates

Usage

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

Arguments

| | |
|---------|--|
| gobject | giotto object |
| ... | Arguments passed on to dimCellPlot2D |
| | dim_reduction_to_use dimension reduction to use |
| | dim_reduction_name dimension reduction name |
| | dim1_to_use dimension to use on x-axis |
| | dim2_to_use dimension to use on y-axis |
| | spat_enr_names names of spatial enrichment results to include |
| | cell_annotation_values numeric cell annotation columns |
| | show_NN_network show underlying NN network |
| | nn_network_to_use type of NN network to use (kNN vs sNN) |
| | network_name name of NN network to use, if show_NN_network = TRUE |
| | cell_color_code named vector with colors for cell annotation values |
| | cell_color_gradient vector with 3 colors for numeric data |
| | gradient_midpoint midpoint for color gradient |
| | gradient_limits vector with lower and upper limits |
| | select_cell_groups select subset of cells/clusters based on cell_color parameter |
| | select_cells select subset of cells based on cell IDs |
| | show_other_cells display not selected cells |

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

Details

Description of parameters. For 3D plots see [dimCellPlot2D](#)

Value

ggplot

See Also

Other dimension reduction cell annotation visualizations: [dimCellPlot2D\(\)](#)

Examples

```
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_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  edge_alpha = NULL,
  point_shape = c("border", "no_border"),
  point_size = 1,
  point_alpha = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
```

```

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

```

Arguments

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

| | |
|----------------------------|--|
| center_point_border_col | border color of center points |
| center_point_border_stroke | border stroke size of center points |
| label_size | size of labels |
| label_fontface | font of labels |
| edge_alpha | column to use for alpha of the edges |
| point_shape | point with border or not (border or no_border) |
| point_size | size of point (cell) |
| point_alpha | transparency of dim. reduction points |
| point_border_col | color of border around points |
| point_border_stroke | stroke size of border around points |
| show_legend | show legend |
| legend_text | size of legend text |
| legend_symbol_size | size of legend symbols |
| background_color | color of plot background |
| axis_text | size of axis text |
| axis_title | size of axis title |
| cow_n_col | cowplot param: how many columns |
| cow_rel_h | cowplot param: relative height |
| cow_rel_w | cowplot param: relative width |
| cow_align | cowplot param: how to align |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters. For 3D plots see [dimPlot3D](#)

Value

ggplot

See Also

Other dimension reduction cell annotation visualizations: [dimCellPlot\(\)](#)

Examples

```
dimCellPlot2D(gobject)
```


dimGenePlot

*dimGenePlot***Description**

Visualize gene expression according to dimension reduction coordinates

Usage

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

Arguments

```
...           Arguments passed on to dimGenePlot2D
gobject      giotto object
expression_values  gene expression values to use
genes        genes to show
dim_reduction_to_use  dimension reduction to use
dim_reduction_name  dimension reduction name
dim1_to_use  dimension to use on x-axis
dim2_to_use  dimension to use on y-axis
show_NN_network  show underlying NN network
nn_network_to_use  type of NN network to use (kNN vs sNN)
network_name  name of NN network to use, if show_NN_network = TRUE
network_color  color of NN network
edge_alpha  column to use for alpha of the edges
scale_alpha_with_expression  scale expression with ggplot alpha parameter
point_shape  point with border or not (border or no_border)
point_size  size of point (cell)
point_alpha  transparency of points
cell_color_gradient  vector with 3 colors for numeric data
gradient_midpoint  midpoint for color gradient
gradient_limits  vector with lower and upper limits
point_border_col  color of border around points
point_border_stroke  stroke size of border around points
show_legend  show legend
legend_text  size of legend text
background_color  color of plot background
axis_text  size of axis text
axis_title  size of axis title
cow_n_col  cowplot param: how many columns
cow_rel_h  cowplot param: relative height
cow_rel_w  cowplot param: relative width
cow_align  cowplot param: how to align
show_plot  show plots
return_plot  return ggplot object
```

save_plot directly save the plot [boolean]
save_param list of saving parameters, see [showSaveParameters](#)
default_save_name default save name for saving, don't change, change save_name
in save_param

Details

Description of parameters.

Value

ggplot

See Also

[dimGenePlot3D](#)
Other dimension reduction gene expression visualizations: [dimGenePlot2D\(\)](#), [dimGenePlot3D\(\)](#)

Examples

dimGenePlot(gobject)

| | |
|---------------|----------------------|
| dimGenePlot2D | <i>dimGenePlot2D</i> |
|---------------|----------------------|

Description

Visualize gene expression according to dimension reduction coordinates

Usage

```
dimGenePlot2D(  
  gobject,  
  expression_values = c("normalized", "scaled", "custom"),  
  genes = NULL,  
  dim_reduction_to_use = "umap",  
  dim_reduction_name = "umap",  
  dim1_to_use = 1,  
  dim2_to_use = 2,  
  show_NN_network = F,  
  nn_network_to_use = "sNN",  
  network_name = "sNN.pca",  
  network_color = "lightgray",  
  edge_alpha = NULL,  
  scale_alpha_with_expression = FALSE,  
  point_shape = c("border", "no_border"),  
  point_size = 1,  
  point_alpha = 1,  
  cell_color_gradient = c("blue", "white", "red"),  
  gradient_midpoint = NULL,  
  gradient_limits = NULL,
```

```

    point_border_col = "black",
    point_border_stroke = 0.1,
    show_legend = T,
    legend_text = 8,
    background_color = "white",
    axis_text = 8,
    axis_title = 8,
    cow_n_col = 2,
    cow_rel_h = 1,
    cow_rel_w = 1,
    cow_align = "h",
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "dimGenePlot2D"
)

```

Arguments

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

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

Details

Description of parameters.

Value

ggplot

See Also

[dimGenePlot3D](#)

Other dimension reduction gene expression visualizations: [dimGenePlot3D\(\)](#), [dimGenePlot\(\)](#)

Examples

```
dimGenePlot2D(gobject)
```

| | |
|---------------|----------------------|
| dimGenePlot3D | <i>dimGenePlot3D</i> |
|---------------|----------------------|

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

| | |
|-----------------------------------|-------------------------------|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | gene expression values to use |
| <code>genes</code> | genes to show |
| <code>dim_reduction_to_use</code> | dimension reduction to use |
| <code>dim_reduction_name</code> | dimension reduction name |

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

Details

Description of parameters.

Value

ggplot

See Also

Other dimension reduction gene expression visualizations: [dimGenePlot2D\(\)](#), [dimGenePlot\(\)](#)

Examples

```
dimGenePlot3D(gobject)
```

dimPlot

*dimPlot***Description**

Visualize cells according to dimension reduction coordinates

Usage

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

Arguments

```
...           Arguments passed on to dimPlot2D
gobject      giotto object
group_by     create multiple plots based on cell annotation column
group_by_subset subset the group_by factor column
dim_reduction_to_use dimension reduction to use
dim_reduction_name dimension reduction name
dim1_to_use  dimension to use on x-axis
dim2_to_use  dimension to use on y-axis
spat_enr_names names of spatial enrichment results to include
show_NN_network show underlying NN network
nn_network_to_use type of NN network to use (kNN vs sNN)
network_name name of NN network to use, if show_NN_network = TRUE
cell_color   color for cells (see details)
color_as_factor convert color column to factor
cell_color_code named vector with colors
cell_color_gradient vector with 3 colors for numeric data
gradient_midpoint midpoint for color gradient
gradient_limits vector with lower and upper limits
select_cell_groups select subset of cells/clusters based on cell_color parameter
select_cells select subset of cells based on cell IDs
show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size size of not selected cells
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
center_point_border_col border color of center points
center_point_border_stroke border stroke size of center points
label_size size of labels
label_fontface font of labels
edge_alpha column to use for alpha of the edges
point_shape point with border or not (border or no_border)
```

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

Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [dimPlot3D](#)

Value

ggplot

See Also

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

Examples

```
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_alpha = 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

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

| | |
|----------------------------|--|
| center_point_border_col | border color of center points |
| center_point_border_stroke | border stroke size of center points |
| label_size | size of labels |
| label_fontface | font of labels |
| edge_alpha | column to use for alpha of the edges |
| point_shape | point with border or not (border or no_border) |
| point_size | size of point (cell) |
| point_alpha | transparency of point |
| point_border_col | color of border around points |
| point_border_stroke | stroke size of border around points |
| title | title for plot, defaults to cell_color parameter |
| show_legend | show legend |
| legend_text | size of legend text |
| legend_symbol_size | size of legend symbols |
| background_color | color of plot background |
| axis_text | size of axis text |
| axis_title | size of axis title |
| cow_n_col | cowplot param: how many columns |
| cow_rel_h | cowplot param: relative height |
| cow_rel_w | cowplot param: relative width |
| cow_align | cowplot param: how to align |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters. For 3D plots see [dimPlot3D](#)

Value

ggplot

See Also

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

Examples

```
dimPlot2D(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,
  spat_enr_names = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 2,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  color_as_factor = T,
  cell_color = NULL,
  cell_color_code = NULL,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 4,
  edge_alpha = NULL,
  point_size = 3,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "dim3D"
)
```

Arguments

| | |
|-----------------------------------|----------------------------|
| <code>gobject</code> | giotto object |
| <code>dim_reduction_to_use</code> | dimension reduction to use |
| <code>dim_reduction_name</code> | dimension reduction name |
| <code>dim1_to_use</code> | dimension to use on x-axis |
| <code>dim2_to_use</code> | dimension to use on y-axis |

| | |
|---------------------|--|
| dim3_to_use | dimension to use on z-axis |
| spat_enr_names | names of spatial enrichment results to include |
| select_cell_groups | select subset of cells/clusters based on cell_color parameter |
| select_cells | select subset of cells based on cell IDs |
| show_other_cells | display not selected cells |
| other_cell_color | color of not selected cells |
| other_point_size | size of not selected cells |
| show_NN_network | show underlying NN network |
| nn_network_to_use | type of NN network to use (kNN vs sNN) |
| network_name | name of NN network to use, if show_NN_network = TRUE |
| color_as_factor | convert color column to factor |
| cell_color | color for cells (see details) |
| cell_color_code | named vector with colors |
| show_cluster_center | plot center of selected clusters |
| show_center_label | plot label of selected clusters |
| center_point_size | size of center points |
| label_size | size of labels |
| edge_alpha | column to use for alpha of the edges |
| point_size | size of point (cell) |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

plotly

See Also

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

Examples

```
dimPlot3D(gobject)
```

| | |
|----------|-----------------|
| doHclust | <i>doHclust</i> |
|----------|-----------------|

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 = "Delaunay_network",
  spatial_genes = NULL,
  spatial_dimensions = c("sdimx", "sdimy", "sdimz"),
  dim_reduction_to_use = NULL,
  dim_reduction_name = "pca",
  dimensions_to_use = 1:10,
  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

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>spatial_network_name</code> | name of spatial network to use for HMRF |
| <code>spatial_genes</code> | spatial genes to use for HMRF |
| <code>spatial_dimensions</code> | select spatial dimensions to use, default is all possible dimensions |
| <code>dim_reduction_to_use</code> | use another dimension reduction set as input |
| <code>dim_reduction_name</code> | name of dimension reduction set to use |
| <code>dimensions_to_use</code> | number of dimensions to use as input |
| <code>name</code> | name of HMRF run |
| <code>k</code> | number of HMRF domains |
| <code>betas</code> | betas to test for |
| <code>tolerance</code> | tolerance |
| <code>zscore</code> | zscore |
| <code>numinit</code> | number of initializations |
| <code>python_path</code> | python path to use |
| <code>output_folder</code> | output folder to save results |
| <code>overwrite_output</code> | overwrite output folder |

Details

Description of HMRF parameters ...

Value

Creates a directory with results that can be viewed with `viewHMRResults`

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

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

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 iterations 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/leidenalg> github page or the <https://leidenalg.readthedocs.io/en/stable/index.html> readthedocs page for more information.

Partition types available and information:

- **RBCConfigurationVertexPartition**: 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 | <i>doLeidenSubCluster</i> |
|--------------------|---------------------------|

Description

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

Usage

```
doLeidenSubCluster(
  gobject,
  name = "sub_pleiden_clus",
  cluster_column = NULL,
  selected_clusters = NULL,
  hvg_param = list(reverse_log_scale = T, difference_in_cov = 1, expression_values =
    "normalized"),
```

```

    hvg_min_perc_cells = 5,
    hvg_mean_expr_det = 1,
    use_all_genes_as_hvg = FALSE,
    min_nr_of_hvg = 5,
    pca_param = list(expression_values = "normalized", scale_unit = T),
    nn_param = list(dimensions_to_use = 1:20),
    k_neighbors = 10,
    resolution = 0.5,
    n_iterations = 500,
    python_path = NULL,
    nn_network_to_use = "sNN",
    network_name = "sNN.pca",
    return_gobject = TRUE,
    verbose = T
)

```

Arguments

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

Description

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

Usage

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

Arguments

| | |
|-------------------|--|
| gobject | giotto object |
| version | implemented version of Louvain clustering to use |
| name | name for cluster |
| nn_network_to_use | type of NN network to use (kNN vs sNN) |

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

Details

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

Value

giotto object with new clusters appended to cell metadata

See Also

[doLouvainCluster_community](#) and [doLouvainCluster_multinet](#)

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

| | |
|--------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>name</code> | name for cluster |
| <code>nn_network_to_use</code> | type of NN network to use (kNN vs sNN) |
| <code>network_name</code> | name of NN network to use |
| <code>python_path</code> | specify specific path to python if required |
| <code>resolution</code> | resolution |
| <code>weight_col</code> | weight column to use for edges |
| <code>louv_random</code> | Will randomize the node evaluation order and the community evaluation order to get different partitions at each call |
| <code>return_gobject</code> | boolean: return giotto object (default = TRUE) |
| <code>set_seed</code> | set seed |
| <code>seed_number</code> | 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.html> readthedocs 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

| | |
|--------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>name</code> | name for cluster |
| <code>nn_network_to_use</code> | type of NN network to use (kNN vs sNN) |
| <code>network_name</code> | name of NN network to use |
| <code>gamma</code> | Resolution parameter for modularity in the generalized louvain method. |
| <code>omega</code> | Inter-layer weight parameter in the generalized louvain method. |
| <code>return_gobject</code> | boolean: return giotto object (default = TRUE) |
| <code>set_seed</code> | set seed |
| <code>seed_number</code> | 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 | <i>doLouvainSubCluster</i> |
|---------------------|----------------------------|

Description

subcluster cells using a NN-network and the Louvain algorithm

Usage

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

Arguments

| | |
|-----------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>name</code> | name for new clustering result |
| <code>version</code> | version of Louvain algorithm to use |
| <code>cluster_column</code> | cluster column to subcluster |
| <code>selected_clusters</code> | only do subclustering on these clusters |
| <code>hvg_param</code> | parameters for calculateHVG |
| <code>hvg_min_perc_cells</code> | threshold for detection in min percentage of cells |
| <code>hvg_mean_expr_det</code> | threshold for mean expression level in cells with detection |
| <code>use_all_genes_as_hvg</code> | forces all genes to be HVG and to be used as input for PCA |
| <code>min_nr_of_hvg</code> | minimum number of HVG, or all genes will be used as input for PCA |
| <code>pca_param</code> | parameters for runPCA |
| <code>nn_param</code> | parameters for parameters for createNearestNetwork |
| <code>k_neighbors</code> | number of k for createNearestNetwork |
| <code>resolution</code> | resolution for community algorithm |
| <code>gamma</code> | gamma |
| <code>omega</code> | omega |

| | |
|--------------------------------|--|
| <code>python_path</code> | specify specific path to python if required |
| <code>nn_network_to_use</code> | type of NN network to use (kNN vs sNN) |
| <code>network_name</code> | name of NN network to use |
| <code>return_gobject</code> | boolean: return giotto object (default = TRUE) |
| <code>verbose</code> | 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_cov = 1, expression_values =
    "normalized"),
  hvg_min_perc_cells = 5,
  hvg_mean_expr_det = 1,
  use_all_genes_as_hvg = FALSE,
```

```

min_nr_of_hvg = 5,
pca_param = list(expression_values = "normalized", scale_unit = T),
nn_param = list(dimensions_to_use = 1:20),
k_neighbors = 10,
resolution = 0.5,
python_path = NULL,
nn_network_to_use = "sNN",
network_name = "sNN.pca",
return_gobject = TRUE,
verbose = T
)

```

Arguments

| | |
|-----------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>name</code> | name for new clustering result |
| <code>cluster_column</code> | cluster column to subcluster |
| <code>selected_clusters</code> | only do subclustering on these clusters |
| <code>hvg_param</code> | parameters for calculateHVG |
| <code>hvg_min_perc_cells</code> | threshold for detection in min percentage of cells |
| <code>hvg_mean_expr_det</code> | threshold for mean expression level in cells with detection |
| <code>use_all_genes_as_hvg</code> | forces all genes to be HVG and to be used as input for PCA |
| <code>min_nr_of_hvg</code> | minimum number of HVG, or all genes will be used as input for PCA |
| <code>pca_param</code> | parameters for runPCA |
| <code>nn_param</code> | parameters for parameters for createNearestNetwork |
| <code>k_neighbors</code> | number of k for createNearestNetwork |
| <code>resolution</code> | resolution |
| <code>python_path</code> | specify specific path to python if required |
| <code>nn_network_to_use</code> | type of NN network to use (kNN vs sNN) |
| <code>network_name</code> | name of NN network to use |
| <code>return_gobject</code> | boolean: return giotto object (default = TRUE) |
| <code>verbose</code> | 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_cov = 1, expression_values =
    "normalized"),
  hvg_min_perc_cells = 5,
  hvg_mean_expr_det = 1,
  use_all_genes_as_hvg = FALSE,
  min_nr_of_hvg = 5,
  pca_param = list(expression_values = "normalized", scale_unit = T),
  nn_param = list(dimensions_to_use = 1:20),
  k_neighbors = 10,
  gamma = 1,
  omega = 1,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  return_gobject = TRUE,
  verbose = T
)
```

Arguments

| | |
|--------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>name</code> | name for new clustering result |
| <code>cluster_column</code> | cluster column to subcluster |
| <code>selected_clusters</code> | 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 |

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 | <i>doSNNCluster</i> |
|--------------|---------------------|

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)
```

| | |
|-----------------|------------------------|
| estimateImageBg | <i>estimateImageBg</i> |
|-----------------|------------------------|

Description

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

Usage

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

Arguments

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

Value

vector of pixel color frequencies and an associated barplot

Examples

```
estimateImageBg(mg_object)
```

| | |
|--------------------|---------------------------|
| exportGiottoViewer | <i>exportGiottoViewer</i> |
|--------------------|---------------------------|

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

| | |
|----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>output_directory</code> | directory where to save the files |
| <code>spat_enr_names</code> | spatial enrichment results to include for annotations |
| <code>factor_annotations</code> | giotto cell annotations to view as factor |
| <code>numeric_annotations</code> | giotto cell annotations to view as numeric |
| <code>dim_reductions</code> | high level dimension reductions to view |
| <code>dim_reduction_names</code> | specific dimension reduction names |
| <code>expression_values</code> | expression values to use in Viewer |
| <code>dim_red_rounding</code> | numerical indicating how to round the coordinates |
| <code>dim_red_rescale</code> | numericals to rescale the coordinates |
| <code>expression_rounding</code> | numerical indicating how to round the expression data |
| <code>overwrite_dir</code> | overwrite files in the directory if it already existed |
| <code>verbose</code> | 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 = 1000,
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  detailed = FALSE,
  adjust_method = c("fdr", "bonferroni", "BH", "holm", "hochberg", "hommel", "BY",
    "none"),
  adjust_target = c("genes", "cells"),
  verbose = T
)

```

Arguments

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

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(
  cpqObject,
  min_cells = 4,
  min_cells_expr = 1,
  min_int_cells = 4,
  min_int_cells_expr = 1,
  min_fdr = 0.1,
  min_spat_diff = 0.2,
  min_log2_fc = 0.2,
  min_zscore = 2,
  zscores_column = c("cell_type", "genes"),
  direction = c("both", "up", "down")
)
```

Arguments

| | |
|--------------------|---|
| cpgObject | cell proximity gene score object |
| min_cells | minimum number of source cell type |
| min_cells_expr | minimum expression level for source cell type |
| min_int_cells | minimum number of interacting neighbor cell type |
| min_int_cells_expr | minimum expression level for interacting neighbor cell type |
| min_fdr | minimum adjusted p-value |
| min_spat_diff | minimum absolute spatial expression difference |
| min_log2_fc | minimum log2 fold-change |
| min_zscore | minimum z-score change |
| zscores_column | calculate z-scores over cell types or genes |
| direction | differential expression directions to keep |

Value

cpgObject that contains the filtered differential gene scores

Examples

```
filterCellProximityGenes(gobject)
```

| | |
|--------------------|---------------------------|
| filterCombinations | <i>filterCombinations</i> |
|--------------------|---------------------------|

Description

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

Usage

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

Arguments

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

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 = 4,
  min_cells_expr = 1,
  min_int_cells = 4,
  min_int_cells_expr = 1,
  min_fdr = 0.1,
  min_spat_diff = 0.2,
  min_log2_fc = 0.2,
  min_zscore = 2,
  zscores_column = c("cell_type", "genes"),
  direction = c("both", "up", "down")
)
```

Arguments

| | |
|--------------------|---|
| cpgObject | cell proximity gene score object |
| min_cells | minimum number of source cell type |
| min_cells_expr | minimum expression level for source cell type |
| min_int_cells | minimum number of interacting neighbor cell type |
| min_int_cells_expr | minimum expression level for interacting neighbor cell type |
| min_fdr | minimum adjusted p-value |
| min_spat_diff | minimum absolute spatial expression difference |
| min_log2_fc | minimum log2 fold-change |
| min_zscore | minimum z-score change |
| zscores_column | calculate z-scores over cell types or genes |
| direction | differential expression directions to keep |

Value

cpgObject that contains the filtered differential gene scores

Examples

```
filterCPG(gobject)
```

| | |
|---------------------|----------------------------|
| filterDistributions | <i>filterDistributions</i> |
|---------------------|----------------------------|

Description

show gene or cell distribution after filtering on expression threshold

Usage

```
filterDistributions(
  gobject,
  expression_values = c("raw", "normalized", "scaled", "custom"),
  expression_threshold = 1,
  detection = c("genes", "cells"),
  plot_type = c("histogram", "violin"),
  nr_bins = 30,
  fill_color = "lightblue",
  scale_axis = "identity",
  axis_offset = 0,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "filterDistributions"
)
```

Arguments

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

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

| | |
|-------------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>expression_threshold</code> | threshold to consider a gene expressed |
| <code>gene_det_in_min_cells</code> | minimum # of cells that need to express a gene |
| <code>min_det_genes_per_cell</code> | minimum # of genes that need to be detected in a cell |
| <code>verbose</code> | 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",
  selected_genes = NULL,
  cluster_column,
  spatial_network_name = "Delaunay_network",
  minimum_unique_cells = 1,
  minimum_unique_int_cells = 1,
  diff_test = c("permutation", "limma", "t.test", "wilcox"),
  mean_method = c("arithmetic", "geometric"),
  offset = 0.1,
  adjust_method = c("bonferroni", "BH", "holm", "hochberg", "hommel", "BY", "fdr",
    "none"),
  nr_permutations = 1000,
  exclude_selected_cells_from_test = T,
  do_parallel = TRUE,
  cores = NA
)
```

Arguments

| | |
|---------------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>selected_genes</code> | subset of selected genes (optional) |
| <code>cluster_column</code> | name of column to use for cell types |
| <code>spatial_network_name</code> | name of spatial network to use |
| <code>minimum_unique_cells</code> | minimum number of target cells required |
| <code>minimum_unique_int_cells</code> | minimum number of interacting cells required |
| <code>diff_test</code> | which differential expression test |
| <code>mean_method</code> | method to use to calculate the mean |
| <code>offset</code> | offset value to use when calculating log2 ratio |
| <code>adjust_method</code> | which method to adjust p-values |
| <code>nr_permutations</code> | number of permutations if <code>diff_test = permutation</code> |

| | |
|----------------------------------|--|
| 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)
```

findCPG

findCPG

Description

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

Usage

```
findCPG(
  gobject,
  expression_values = "normalized",
  selected_genes = NULL,
  cluster_column,
  spatial_network_name = "Delaunay_network",
  minimum_unique_cells = 1,
  minimum_unique_int_cells = 1,
  diff_test = c("permutation", "limma", "t.test", "wilcox"),
  mean_method = c("arithmetic", "geometric"),
  offset = 0.1,
  adjust_method = c("bonferroni", "BH", "holm", "hochberg", "hommel", "BY", "fdr",
    "none"),
  nr_permutations = 100,
  exclude_selected_cells_from_test = T,
  do_parallel = TRUE,
  cores = NA
)
```

Arguments

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

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

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

Details

Detection of marker genes using the https://en.wikipedia.org/wiki/Gini_coefficient gini 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 selectively 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 specify 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

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

Value

data.table with marker genes

See Also

[findGiniMarkers](#)

Examples

```
findGiniMarkers_one_vs_all(gobject)
```

| | |
|-------------|--------------------|
| findMarkers | <i>findMarkers</i> |
|-------------|--------------------|

Description

Identify marker genes for selected clusters.

Usage

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

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

Description

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

Usage

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

Arguments

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

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

Value

data.table with marker genes

See Also

[findMastMarkers](#)

Examples

```
findMastMarkers_one_vs_all(gobject)
```

findNetworkNeighbors *findNetworkNeighbors*

Description

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

Usage

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

Arguments

| | |
|-----------------------------------|---|
| <code>gobject</code> | Giotto object |
| <code>spatial_network_name</code> | name of spatial network |
| <code>source_cell_ids</code> | cell ids for which you want to know the spatial neighbors |
| <code>name</code> | name of the results |

Value

data.table

Examples

```
findNetworkNeighbors(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,
  verbose = FALSE,
  ...
)
```

Arguments

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

Details

This is a minimal convenience wrapper around the [findMarkers](#) function from the `scrn` package.

To perform differential expression between cluster groups you need to specify 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 `scrn`'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 scan |

Value

data.table with marker genes

See Also

[findScranMarkers](#)

Examples

```
findScranMarkers_one_vs_all(gobject)
```

| | |
|--------------|---------------------|
| get10Xmatrix | <i>get10Xmatrix</i> |
|--------------|---------------------|

Description

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

Usage

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

Arguments

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

Details

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

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

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

Value

sparse expression matrix from 10X

| | |
|----------------------|-----------------------------|
| getClusterSimilarity | <i>getClusterSimilarity</i> |
|----------------------|-----------------------------|

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 | <i>getDendrogramSplits</i> |
|---------------------|----------------------------|

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

| | |
|--------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>cluster_column</code> | name of column to use for clusters |
| <code>cor</code> | correlation score to calculate distance |
| <code>distance</code> | distance method to use for hierarchical clustering |
| <code>h</code> | height of horizontal lines to plot |
| <code>h_color</code> | color of horizontal lines |
| <code>show_dend</code> | show dendrogram |
| <code>verbose</code> | 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 | <i>getDistinctColors</i> |
|-------------------|--------------------------|

Description

Returns a number of distinct colors based on the RGB scale

Usage

```
getDistinctColors(n)
```

Arguments

| | |
|---|-------------------------|
| n | number of colors wanted |
|---|-------------------------|

Value

number of distinct colors

| | |
|----------------|-----------------------|
| getGiottoImage | <i>getGiottoImage</i> |
|----------------|-----------------------|

Description

get get a giotto image from a giotto object

Usage

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

Arguments

| | |
|------------|---|
| gobject | giotto object |
| image_name | name of giotto image showGiottoImageNames |

Value

a giotto image

Examples

```
getGiottoImage(gobject)
```

| | |
|-------------------|--------------------------|
| getSpatialDataset | <i>getSpatialDataset</i> |
|-------------------|--------------------------|

Description

This package will automatically download the spatial locations and expression matrix for the chosen dataset. These files are already in the right format to create a Giotto object.

Usage

```
getSpatialDataset(
  dataset = c("ST_OB_1", "ST_OB_2", "codex_spleen", "cycif_PDAC", "starmap_3D_cortex",
    "osmfish_SS_cortex", "merfish_preoptic", "seqfish_SS_cortex", "seqfish_OB"),
  directory = getwd()
)
```

Arguments

| | |
|-----------|-------------------------------|
| dataset | dataset to download |
| directory | directory to save the data to |

| | |
|--------------|------------------------|
| giotto-class | <i>S4 giotto Class</i> |
|--------------|------------------------|

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 |
| spatial_enrichment | slot to save spatial enrichment-like results |
| dimension_reduction | slot to save dimension reduction coordinates |
| nn_network | nearest neighbor network in igraph format |
| images | slot to store giotto images |

parameters slot to save parameters that have been used
 instructions slot for global function instructions
 offset_file offset file used to stitch together image fields
 OS_platform Operating System to run Giotto analysis on

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, see [showSaveParameters](#)
 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(...)
```

Arguments

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

See Also

[runHyperGeometricEnrich](#)

```
insertCrossSectionGenePlot3D
      insertCrossSectionGenePlot3D
```

Description

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

Usage

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

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>crossSection_obj</code> | cross section object as alternative input. default = NULL. |
| <code>name</code> | name of virtual cross section to use |
| <code>spatial_network_name</code> | name of spatial network to use |
| <code>mesh_grid_color</code> | color for the meshgrid lines |
| <code>mesh_grid_width</code> | width for the meshgrid lines |
| <code>mesh_grid_style</code> | style for the meshgrid lines |
| <code>sdimx</code> | x-axis dimension name (default = 'sdimx') |
| <code>sdimy</code> | y-axis dimension name (default = 'sdimy') |
| <code>sdimz</code> | z-axis dimension name (default = 'sdimy') |

| | |
|-------------------|--|
| show_other_cells | display not selected cells |
| axis_scale | axis_scale |
| custom_ratio | custom_ratio |
| show_plot | show plots |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters from all_plots_save_function |
| default_save_name | default save name for saving, don't change, change save_name in save_param |
| ... | parameters for spatGenePlot3D |

Details

Description of parameters.

Value

ggplot

Examples

```
insertCrossSectionGenePlot3D(gobject)
```

```
insertCrossSectionSpatPlot3D
      insertCrossSectionSpatPlot3D
```

Description

Visualize the meshgrid lines of cross section together with cells

Usage

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

Arguments

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

Details

Description of parameters.

Value

ggplot

Examples

```
insertCrossSectionSpatPlot3D(gobject)
```

| | |
|---------------|----------------------|
| jackstrawPlot | <i>jackstrawPlot</i> |
|---------------|----------------------|

Description

identify significant principal components (PCs)

Usage

```
jackstrawPlot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "genes"),
  genes_to_use = NULL,
  center = FALSE,
  scale_unit = FALSE,
  ncp = 20,
  ylim = c(0, 1),
  iter = 10,
  threshold = 0.01,
  verbose = T,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "jackstrawPlot"
)
```

Arguments

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

Details

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

Value

ggplot object for jackstraw method

Examples

jackstrawPlot(gobject)

| | |
|----------|-----------------|
| loadHMRF | <i>loadHMRF</i> |
|----------|-----------------|

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 | <i>makeSignMatrixPAGE</i> |
|--------------------|---------------------------|

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 | <i>makeSignMatrixRank</i> |
|--------------------|---------------------------|

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()
```

| | |
|---------------|----------------------|
| mergeClusters | <i>mergeClusters</i> |
|---------------|----------------------|

Description

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

Usage

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

Arguments

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

Details

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

Value

Giotto object

Examples

```
mergeClusters(gobject)
```

| | |
|----------------|---|
| mini_giotto_3D | <i>mini Giotto object for spatial single-cell 3D data</i> |
|----------------|---|

Description

Mini Giotto object created from the STARmap data.

Usage

```
data(mini_giotto_3D)
```

Format

An object of class "giotto"; see [createGiottoObject](#).

References

Wang et al. (2018) Science ([PubMed](#))

Examples

```
data(mini_giotto_3D)

spatPlot3D(mini_giotto_3D, cell_color = 'cell_types', point_size = 5)
```

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

Description

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

Usage

```
data(mini_giotto_multi_cell)
```

Format

An object of class "giotto"; see [createGiottoObject](#).

References

10 Genomics Visium technology ([10xgenomics](#))

Examples

```
data(mini_giotto_multi_cell)

spatPlot(mini_giotto_multi_cell, cell_color = 'cell_types', point_size = 5)
```

`mini_giotto_single_cell`*mini Giotto object for spatial single-cell resolution data*

Description

Mini Giotto object created from the seqFISH+ data.

Usage

```
data(mini_giotto_single_cell)
```

Format

An object of class "giotto"; see [createGiottoObject](#).

References

Eng et al. (2019) Nature ([PubMed](#))

Examples

```
data(mini_giotto_single_cell)

spatPlot2D(mini_giotto_single_cell, cell_color = 'cell_types', point_size = 5)
```

| | |
|-----------------|------------------------|
| normalizeGiotto | <i>normalizeGiotto</i> |
|-----------------|------------------------|

Description

fast normalize and/or scale expression 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)
```

| | |
|------------|----------------------|
| PAGEEnrich | <i>runPAGEEnrich</i> |
|------------|----------------------|

Description

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

Usage

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

Arguments

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

See Also

[runPAGEEnrich](#)

| | |
|---------|----------------|
| pDataDT | <i>pDataDT</i> |
|---------|----------------|

Description

show cell metadata

Usage

pDataDT(gobject)

Arguments

gobject giotto object

Value

data.table with cell metadata

Examples

pDataDT(gobject)

| | |
|------------------|-------------------------|
| plotCCcomDotplot | <i>plotCCcomDotplot</i> |
|------------------|-------------------------|

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

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

Value

ggplot

Examples

```
plotCCcomDotplot(CPGscores)
```

| | |
|-------------------------------|-------------------------|
| <code>plotCCcomHeatmap</code> | <i>plotCCcomHeatmap</i> |
|-------------------------------|-------------------------|

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

```

Arguments

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

Value

plot

Examples

```
plotCellProximityGenes(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 communication 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

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

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

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

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

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

Value

ggplot

Examples

```
plotCombineCPG(CPGscores)
```

| | |
|---------|----------------|
| plotCPG | <i>plotCPG</i> |
|---------|----------------|

Description

Create visualization for cell proximity gene scores

Usage

```
plotCPG(
  gobject,
  cpgObject,
  method = c("volcano", "cell_barplot", "cell-cell", "cell_sankey", "heatmap",
    "dotplot"),
  min_cells = 5,
  min_cells_expr = 1,
  min_int_cells = 3,
  min_int_cells_expr = 1,
  min_fdr = 0.05,
  min_spat_diff = 0.2,
  min_log2_fc = 0.2,
  min_zscore = 2,
  zscores_column = c("cell_type", "genes"),
  direction = c("both", "up", "down"),
  cell_color_code = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotCPG"
)
```

Arguments

| | |
|---------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>cpgObject</code> | cell proximity gene score object |
| <code>method</code> | plotting method to use |
| <code>min_cells</code> | minimum number of source cell type |
| <code>min_cells_expr</code> | minimum expression level for source cell type |
| <code>min_int_cells</code> | minimum number of interacting neighbor cell type |
| <code>min_int_cells_expr</code> | minimum expression level for interacting neighbor cell type |

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

Value

plot

Examples

```
plotCPG(CPGscores)
```

| | |
|-----------------|------------------------|
| plotGiottoImage | <i>plotGiottoImage</i> |
|-----------------|------------------------|

Description

get plot a giotto image from a giotto object

Usage

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

Arguments

| | |
|------------|---|
| gobject | giotto object |
| image_name | name of giotto image showGiottoImageNames |

Value

plot

Examples

```
plotGiottoImage(gobject)
```

plotHeatmap

*plotHeatmap***Description**

Creates heatmap for genes and clusters.

Usage

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

Arguments

| | |
|-----------------------------------|------------------------------------|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | expression values to use |
| <code>genes</code> | genes to use |
| <code>cluster_column</code> | name of column to use for clusters |
| <code>cluster_order</code> | method to determine cluster order |
| <code>cluster_custom_order</code> | custom order for clusters |
| <code>cluster_color_code</code> | color code for clusters |
| <code>cluster_cor_method</code> | method for cluster correlation |

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

Details

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

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

Value

ggplot

Examples

```
## Not run:
plotHeatmap(gobject)

## End(Not run)
```

plotICG

plotICG

Description

Create barplot to visualize interaction changed genes

Usage

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

Arguments

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

Value

plot

Examples

```
plotICG(CPGscores)
```

```
plotInteractionChangedGenes
      plotInteractionChangedGenes
```

Description

Create barplot to visualize interaction changed genes

Usage

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

Arguments

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

Value

plot

Examples

```
plotInteractionChangedGenes(CPGscores)
```

```
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

| | |
|-----------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>metadata_cols</code> | annotation columns found in <code>pDataDT(gobject)</code> |
| <code>spat_enr_names</code> | spatial enrichment results to include |
| <code>value_cols</code> | value columns to use |
| <code>first_meta_col</code> | if more than 1 metadata column, select the x-axis factor |
| <code>second_meta_col</code> | if more than 1 metadata column, select the facetting factor |
| <code>show_values</code> | which values to show on heatmap |
| <code>custom_cluster_order</code> | custom cluster order (default = NULL) |

| | |
|------------------------------------|--|
| <code>clus_cor_method</code> | correlation method for clusters |
| <code>clus_cluster_method</code> | hierarchical cluster method for the clusters |
| <code>custom_values_order</code> | custom values order (default = NULL) |
| <code>values_cor_method</code> | correlation method for values |
| <code>values_cluster_method</code> | hierarchical cluster method for the values |
| <code>midpoint</code> | midpoint of <code>show_values</code> |
| <code>x_text_size</code> | size of x-axis text |
| <code>x_text_angle</code> | angle of x-axis text |
| <code>y_text_size</code> | size of y-axis text |
| <code>strip_text_size</code> | size of strip text |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters, see showSaveParameters |
| <code>default_save_name</code> | default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code> |

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 | <i>plotMetaDataHeatmap</i> |
|---------------------|----------------------------|

Description

Creates heatmap for genes within aggregated clusters.

Usage

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

Arguments

| | |
|----------------------|---|
| gobject | giotto object |
| expression_values | expression values to use |
| metadata_cols | annotation columns found in pDataDT(gobject) |
| selected_genes | subset of genes to use |
| first_meta_col | if more than 1 metadata column, select the x-axis factor |
| second_meta_col | if more than 1 metadata column, select the facetting factor |
| show_values | which values to show on heatmap |
| custom_cluster_order | custom cluster order (default = NULL) |

| | |
|---------------------|---|
| clus_cor_method | correlation method for clusters |
| clus_cluster_method | hierarchical cluster method for the clusters |
| custom_gene_order | custom gene order (default = NULL) |
| gene_cor_method | correlation method for genes |
| gene_cluster_method | hierarchical cluster method for the genes |
| gradient_color | vector with 3 colors for numeric data |
| gradient_midpoint | midpoint for color gradient |
| gradient_limits | vector with lower and upper limits |
| x_text_size | size of x-axis text |
| x_text_angle | angle of x-axis text |
| y_text_size | size of y-axis text |
| strip_text_size | size of strip text |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name |

Details

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

Value

ggplot or data.table

See Also

[plotMetaDataCellsHeatmap](#) for numeric cell annotation instead of gene expression.

Examples

```
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 | name of PCA |
| default_save_name | default save name of PCA plot |
| ... | Arguments passed on to dimPlot2D |
| | group_by create multiple plots based on cell annotation column |
| | group_by_subset subset the group_by factor column |
| | dim1_to_use dimension to use on x-axis |
| | dim2_to_use dimension to use on y-axis |
| | spat_enr_names names of spatial enrichment results to include |
| | show_NN_network show underlying NN network |
| | nn_network_to_use type of NN network to use (kNN vs sNN) |
| | network_name name of NN network to use, if show_NN_network = TRUE |
| | cell_color color for cells (see details) |
| | color_as_factor convert color column to factor |
| | cell_color_code named vector with colors |
| | cell_color_gradient vector with 3 colors for numeric data |
| | gradient_midpoint midpoint for color gradient |
| | gradient_limits vector with lower and upper limits |
| | select_cell_groups select subset of cells/clusters based on cell_color parameter |
| | select_cells select subset of cells based on cell IDs |
| | show_other_cells display not selected cells |
| | other_cell_color color of not selected cells |
| | other_point_size size of not selected cells |
| | show_cluster_center plot center of selected clusters |
| | show_center_label plot label of selected clusters |
| | center_point_size size of center points |
| | center_point_border_col border color of center points |
| | center_point_border_stroke border stroke size of center points |
| | label_size size of labels |
| | label_fontface font of labels |

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

Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotPCA_3D](#)

Value

ggplot

See Also

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

Examples

```
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

| | |
|---------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>dim_reduction_name</code> | name of PCA |
| <code>default_save_name</code> | default save name of PCA plot |
| <code>...</code> | Arguments passed on to dimPlot2D |
| | <code>group_by</code> create multiple plots based on cell annotation column |
| | <code>group_by_subset</code> subset the <code>group_by</code> factor column |
| | <code>dim1_to_use</code> dimension to use on x-axis |
| | <code>dim2_to_use</code> dimension to use on y-axis |
| | <code>spat_enr_names</code> names of spatial enrichment results to include |
| | <code>show_NN_network</code> show underlying NN network |
| | <code>nn_network_to_use</code> type of NN network to use (kNN vs sNN) |
| | <code>network_name</code> name of NN network to use, if <code>show_NN_network = TRUE</code> |
| | <code>cell_color</code> color for cells (see details) |
| | <code>color_as_factor</code> convert color column to factor |
| | <code>cell_color_code</code> named vector with colors |
| | <code>cell_color_gradient</code> vector with 3 colors for numeric data |
| | <code>gradient_midpoint</code> midpoint for color gradient |
| | <code>gradient_limits</code> vector with lower and upper limits |
| | <code>select_cell_groups</code> select subset of cells/clusters based on <code>cell_color</code> parameter |
| | <code>select_cells</code> select subset of cells based on cell IDs |
| | <code>show_other_cells</code> display not selected cells |
| | <code>other_cell_color</code> color of not selected cells |
| | <code>other_point_size</code> size of not selected cells |
| | <code>show_cluster_center</code> plot center of selected clusters |
| | <code>show_center_label</code> plot label of selected clusters |
| | <code>center_point_size</code> size of center points |
| | <code>center_point_border_col</code> border color of center points |
| | <code>center_point_border_stroke</code> border stroke size of center points |
| | <code>label_size</code> size of labels |
| | <code>label_fontface</code> font of labels |
| | <code>edge_alpha</code> column to use for alpha of the edges |
| | <code>point_shape</code> point with border or not (border or no_border) |
| | <code>point_size</code> size of point (cell) |
| | <code>point_alpha</code> transparency of point |

point_border_col color of border around points
 point_border_stroke stroke size of border around points
 title title for plot, defaults to cell_color parameter
 show_legend show legend
 legend_text size of legend text
 legend_symbol_size size of legend symbols
 background_color color of plot background
 axis_text size of axis text
 axis_title size of axis title
 cow_n_col cowplot param: how many columns
 cow_rel_h cowplot param: relative height
 cow_rel_w cowplot param: relative width
 cow_align cowplot param: how to align
 show_plot show plot
 return_plot return ggplot object
 save_plot directly save the plot [boolean]
 save_param list of saving parameters, see [showSaveParameters](#)

Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotPCA_3D](#)

Value

ggplot

See Also

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

Examples

```
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 name of PCA
 default_save_name default save name of PCA plot
 ... Arguments passed on to [dimPlot3D](#)
 dim1_to_use dimension to use on x-axis
 dim2_to_use dimension to use on y-axis
 dim3_to_use dimension to use on z-axis
 spat_enr_names names of spatial enrichment results to include
 show_NN_network show underlying NN network
 nn_network_to_use type of NN network to use (kNN vs sNN)
 network_name name of NN network to use, if show_NN_network = TRUE
 cell_color color for cells (see details)
 color_as_factor convert color column to factor
 cell_color_code named vector with colors
 select_cell_groups select subset of cells/clusters based on cell_color parameter
 select_cells select subset of cells based on cell IDs
 show_other_cells display not selected cells
 other_cell_color color of not selected cells
 other_point_size size of not selected cells
 show_cluster_center plot center of selected clusters
 show_center_label plot label of selected clusters
 center_point_size size of center points
 label_size size of labels
 edge_alpha column to use for alpha of the edges
 point_size size of point (cell)
 show_plot show plot
 return_plot return ggplot object
 save_plot directly save the plot [boolean]
 save_param list of saving parameters, see [showSaveParameters](#)

Details

Description of parameters.

Value

plotly

See Also

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

Examples

```
plotPCA_3D(gobject)
```

| | |
|--------------------|---------------------------|
| plotRankSpatvsExpr | <i>plotRankSpatvsExpr</i> |
|--------------------|---------------------------|

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 communication 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 | <i>plotRecovery</i> |
|--------------|---------------------|

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 communication 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 | <i>plotRecovery_sub</i> |
|------------------|-------------------------|

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 communication scores from combCCcom |
| first_col | first column to use |
| second_col | second column to use |

Examples

```
plotRecovery_sub(CPGscores)
```

| | |
|-------------------------|--------------------------------|
| plotStatDelaunayNetwork | <i>plotStatDelaunayNetwork</i> |
|-------------------------|--------------------------------|

Description

Plots network statistics for a Delaunay network..

Usage

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

Arguments

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

Value

giotto object with updated spatial network slot

Examples

```
plotStatDelaunayNetwork(gobject)
```

plotTSNE

plotTSNE

Description

Short wrapper for tSNE visualization

Usage

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

Arguments

gobject giotto object
dim_reduction_name name of TSNE
default_save_name default save name of TSNE plot
... Arguments passed on to [dimPlot2D](#)
group_by create multiple plots based on cell annotation column
group_by_subset subset the group_by factor column
dim1_to_use dimension to use on x-axis
dim2_to_use dimension to use on y-axis
spat_enr_names names of spatial enrichment results to include
show_NN_network show underlying NN network
nn_network_to_use type of NN network to use (kNN vs sNN)
network_name name of NN network to use, if show_NN_network = TRUE
cell_color color for cells (see details)
color_as_factor convert color column to factor
cell_color_code named vector with colors
cell_color_gradient vector with 3 colors for numeric data
gradient_midpoint midpoint for color gradient
gradient_limits vector with lower and upper limits
select_cell_groups select subset of cells/clusters based on cell_color parameter
select_cells select subset of cells based on cell IDs
show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size size of not selected cells
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
center_point_border_col border color of center points
center_point_border_stroke border stroke size of center points
label_size size of labels
label_fontface font of labels
edge_alpha column to use for alpha of the edges
point_shape point with border or not (border or no_border)
point_size size of point (cell)
point_alpha transparency of point
point_border_col color of border around points
point_border_stroke stroke size of border around points
title title for plot, defaults to cell_color parameter
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
background_color color of plot background

axis_text size of axis text
 axis_title size of axis title
 cow_n_col cowplot param: how many columns
 cow_rel_h cowplot param: relative height
 cow_rel_w cowplot param: relative width
 cow_align cowplot param: how to align
 show_plot show plot
 return_plot return ggplot object
 save_plot directly save the plot [boolean]
 save_param list of saving parameters, see [showSaveParameters](#)

Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotTSNE_3D](#)

Value

ggplot

See Also

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

Examples

```
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 name of TSNE
default_save_name default save name of TSNE plot
... Arguments passed on to [dimPlot2D](#)
group_by create multiple plots based on cell annotation column
group_by_subset subset the group_by factor column
dim1_to_use dimension to use on x-axis
dim2_to_use dimension to use on y-axis
spat_enr_names names of spatial enrichment results to include
show_NN_network show underlying NN network
nn_network_to_use type of NN network to use (kNN vs sNN)
network_name name of NN network to use, if show_NN_network = TRUE
cell_color color for cells (see details)
color_as_factor convert color column to factor
cell_color_code named vector with colors
cell_color_gradient vector with 3 colors for numeric data
gradient_midpoint midpoint for color gradient
gradient_limits vector with lower and upper limits
select_cell_groups select subset of cells/clusters based on cell_color parameter
select_cells select subset of cells based on cell IDs
show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size size of not selected cells
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
center_point_border_col border color of center points
center_point_border_stroke border stroke size of center points
label_size size of labels
label_fontface font of labels
edge_alpha column to use for alpha of the edges
point_shape point with border or not (border or no_border)
point_size size of point (cell)
point_alpha transparency of point
point_border_col color of border around points
point_border_stroke stroke size of border around points
title title for plot, defaults to cell_color parameter
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
background_color color of plot background

axis_text size of axis text
 axis_title size of axis title
 cow_n_col cowplot param: how many columns
 cow_rel_h cowplot param: relative height
 cow_rel_w cowplot param: relative width
 cow_align cowplot param: how to align
 show_plot show plot
 return_plot return ggplot object
 save_plot directly save the plot [boolean]
 save_param list of saving parameters, see [showSaveParameters](#)

Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotTSNE_3D](#)

Value

ggplot

See Also

Other reduced dimension visualizations: [dimPlot2D\(\)](#), [dimPlot3D\(\)](#), [dimPlot\(\)](#), [plotPCA_2D\(\)](#), [plotPCA_3D\(\)](#), [plotPCA\(\)](#), [plotTSNE_3D\(\)](#), [plotTSNE\(\)](#), [plotUMAP_2D\(\)](#), [plotUMAP_3D\(\)](#), [plotUMAP\(\)](#)

Examples

```
plotTSNE_2D(gobject)
```

| | |
|-------------|--------------------|
| plotTSNE_3D | <i>plotTSNE_3D</i> |
|-------------|--------------------|

Description

Visualize cells according to dimension reduction coordinates

Usage

```

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

Arguments

gobject giotto object
dim_reduction_name name of TSNE
default_save_name default save name of TSNE plot
... Arguments passed on to [dimPlot3D](#)
dim1_to_use dimension to use on x-axis
dim2_to_use dimension to use on y-axis
dim3_to_use dimension to use on z-axis
spat_enr_names names of spatial enrichment results to include
show_NN_network show underlying NN network
nn_network_to_use type of NN network to use (kNN vs sNN)
network_name name of NN network to use, if **show_NN_network** = TRUE
cell_color color for cells (see details)
color_as_factor convert color column to factor
cell_color_code named vector with colors
select_cell_groups select subset of cells/clusters based on **cell_color** parameter
select_cells select subset of cells based on cell IDs
show_other_cells display not selected cells
other_cell_color color of not selected cells
other_point_size size of not selected cells
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
label_size size of labels
edge_alpha column to use for alpha of the edges
point_size size of point (cell)
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see [showSaveParameters](#)

Details

Description of parameters.

Value

plotly

See Also

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

Examples

```
plotTSNE_3D(gobject)
```

| | |
|----------|-----------------|
| plotUMAP | <i>plotUMAP</i> |
|----------|-----------------|

Description

Short wrapper for UMAP visualization

Usage

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

Arguments

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

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

Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotUMAP_3D](#)

Value

ggplot

See Also

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

Examples

```
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

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

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

Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotUMAP_3D](#)

Value

ggplot

See Also

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

Examples

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

return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see [showSaveParameters](#)

Details

Description of parameters.

Value

plotly

See Also

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

Examples

plotUMAP_3D(gobject)

| | |
|--------------|------------------------------|
| print.giotto | <i>Prints giotto object.</i> |
|--------------|------------------------------|

Description

Prints giotto object

Usage

```
## S3 method for class 'giotto'  
print(object, nr_genes = 5, nr_cells = 5)
```

Arguments

| | |
|----------|------------------------------------|
| object | giotto object |
| nr_genes | number of genes (rows) to print |
| nr_cells | number of cells (columns) to print |

| | |
|------------|-------------------|
| rankEnrich | <i>rankEnrich</i> |
|------------|-------------------|

Description

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

Usage

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

Arguments

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

See Also

[runRankEnrich](#)

| | |
|----------------------|-----------------------------|
| rankSpatialCorGroups | <i>rankSpatialCorGroups</i> |
|----------------------|-----------------------------|

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

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

Value

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

Examples

```
rankSpatialCorGroups(gobject)
```

`readExprMatrix`

readExprMatrix

Description

Function to read an expression matrix into a sparse matrix.

Usage

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

Arguments

| | |
|------------------------|-------------------------------|
| <code>path</code> | path to the expression matrix |
| <code>cores</code> | number of cores to use |
| <code>transpose</code> | transpose matrix |

Details

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

Value

sparse matrix

Examples

```
readExprMatrix()
```

| |
|-------------------------------|
| readGiottoInstructions |
| <i>readGiottoInstructions</i> |

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

```
readGiottoInstructions()
```

| | |
|----------------------|-----------------------------|
| removeCellAnnotation | <i>removeCellAnnotation</i> |
|----------------------|-----------------------------|

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

giotto object with replaces instructions

Examples

```
replaceGiottoInstructions()
```

| | |
|---------------|----------------------|
| runDWLSDeconv | <i>runDWLSDeconv</i> |
|---------------|----------------------|

Description

Function to perform DWLS deconvolution based on single cell expression data

Usage

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

Arguments

| | |
|-------------------|---|
| gobject | giotto object |
| expression_values | expression values to use |
| logbase | base used for log normalization |
| cluster_column | name of cluster column |
| sign_matrix | sig matrix for deconvolution |
| n_cell | number of cells per spot |
| cutoff | cut off (default = 2) |
| name | name to give to spatial deconvolution results, default = DWLS |
| return_gobject | return giotto object |

Value

giotto object or deconvolution results

```
runHyperGeometricEnrich
      runHyperGeometricEnrich
```

Description

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

Usage

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

Arguments

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

Details

The enrichment score is calculated based on the p-value from the hypergeometric test, $-\log_{10}(p\text{-value})$.

Value

data.table with enrichment results

| | |
|---------------|----------------------|
| runPAGEEnrich | <i>runPAGEEnrich</i> |
|---------------|----------------------|

Description

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

Usage

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

Arguments

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

Details

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

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

Value

data.table with enrichment results

See Also

[makeSignMatrixPAGE](#)

runPatternSimulation *runPatternSimulation*

Description

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

Usage

```
runPatternSimulation(
  gobject,
  pattern_name = "pattern",
  pattern_cell_ids = NULL,
  gene_names = NULL,
  spatial_probs = c(0.5, 1),
  reps = 2,
  save_plot = T,
  save_dir = "~",
  max_col = 4,
  height = 7,
  width = 7,
  ...
)
```

Arguments

| | |
|------------------|--|
| gobject | giotto object |
| pattern_name | name of spatial pattern |
| pattern_cell_ids | cell ids that make up the spatial pattern |
| gene_names | selected genes |
| spatial_probs | probabilities to test for a high expressing gene value to be part of the spatial pattern |
| reps | number of random simulation repetitions |
| save_plot | save intermediate random simulation plots or not |
| save_dir | directory to save results to |
| max_col | maximum number of columns for final plots |
| height | height of final plots |
| width | width of final plots |
| ... | additional parameters for spatial gene detection tests |

Value

data.table with results

Examples

```
runPatternSimulation(gobject)
```

| | |
|--------|---------------|
| runPCA | <i>runPCA</i> |
|--------|---------------|

Description

runs a Principal Component Analysis

Usage

```
runPCA(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  reduction = c("cells", "genes"),
  name = "pca",
  genes_to_use = "hvg",
  return_gobject = TRUE,
  center = F,
  scale_unit = F,
  ncp = 100,
  method = c("irlba", "factominer"),
  rev = FALSE,
  verbose = TRUE,
  ...
)
```

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) |
| center | center data first (default = FALSE) |
| scale_unit | scale features before PCA (default = FALSE) |
| ncp | number of principal components to calculate |
| method | which implementation to use |
| rev | do a reverse PCA |
| verbose | verbosity of the function |
| ... | additional parameters for PCA (see details) |

Details

See [prcomp_irlba](#) and [PCA](#) for more information about other parameters.

- `genes_to_use = NULL`: will use all genes from the selected matrix
- `genes_to_use = <hvg name>`: can be used to select a column name of highly variable genes, created by (see [calculateHVG](#))
- `genes_to_use = c('geneA', 'geneB', ...)`: will use all manually provided genes

Value

giotto object with updated PCA dimension reduction

Examples

```
# 1. create giotto object
expr_path = system.file("extdata", "seqfish_field_expr.txt", package = 'Giotto')
loc_path = system.file("extdata", "seqfish_field_locs.txt", package = 'Giotto')
VC_small <- createGiottoObject(raw_exprs = expr_path, spatial_locs = loc_path)

# 2. normalize giotto
VC_small <- normalizeGiotto(gobject = VC_small, scalefactor = 6000)
VC_small <- addStatistics(gobject = VC_small)

# 3. dimension reduction
VC_small <- calculateHVG(gobject = VC_small)
VC_small <- runPCA(gobject = VC_small)
plotPCA(VC_small)
```

runRankEnrich

runRankEnrich

Description

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

Usage

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


Arguments

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

Details

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

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

Value

data.table with enrichment results

See Also

[makeSignMatrixRank](#)

runSpatialDeconv

runSpatialDeconv

Description

Function to perform deconvolution based on single cell expression data

Usage

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

Arguments

| | |
|-------------------|---|
| gobject | giotto object |
| deconv_method | method to use for deconvolution |
| expression_values | expression values to use |
| logbase | base used for log normalization |
| cluster_column | name of cluster column |
| sign_matrix | signature matrix for deconvolution |
| n_cell | number of cells per spot |
| cutoff | cut off (default = 2) |
| name | name to give to spatial deconvolution results |
| return_gobject | return giotto object |

Value

giotto object or deconvolution results

| | |
|------------------|-------------------------|
| runSpatialEnrich | <i>runSpatialEnrich</i> |
|------------------|-------------------------|

Description

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

Usage

```
runSpatialEnrich(
  gobject,
  enrich_method = c("PAGE", "rank", "hypergeometric"),
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
```

```

    p_value = FALSE,
    n_times = 1000,
    top_percentage = 5,
    output_enrichment = c("original", "zscore"),
    name = NULL,
    return_gobject = TRUE
  )

```

Arguments

| | |
|--------------------------------|--|
| <code>gobject</code> | Giotto object |
| <code>enrich_method</code> | method for gene signature enrichment calculation |
| <code>sign_matrix</code> | Matrix of signature genes for each cell type / process |
| <code>expression_values</code> | expression values to use |
| <code>reverse_log_scale</code> | reverse expression values from log scale |
| <code>logbase</code> | log base to use if <code>reverse_log_scale = TRUE</code> |
| <code>p_value</code> | calculate p-value (default = FALSE) |
| <code>n_times</code> | (page/rank) number of permutation iterations to calculate p-value |
| <code>top_percentage</code> | (hyper) percentage of cells that will be considered to have gene expression with matrix binarization |
| <code>output_enrichment</code> | how to return enrichment output |
| <code>name</code> | to give to spatial enrichment results, default = PAGE |
| <code>return_gobject</code> | return giotto object |

Details

For details see the individual functions:

- PAGE: [runPAGEEnrich](#)
- Rank: [runRankEnrich](#)
- Hypergeometric: [runHyperGeometricEnrich](#)

Value

Giotto object or enrichment results if `return_gobject = FALSE`

runtSNE

runtSNE

Description

run tSNE

Usage

```

runtSNE(
  gobject,
  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,
  verbose = TRUE,
  ...
)

```

Arguments

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

Details

See [Rtsne](#) for more information about these and other parameters.

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

Value

giotto object with updated tSNE dimension reduction

Examples

```
# 1. create giotto object
expr_path = system.file("extdata", "seqfish_field_expr.txt", package = 'Giotto')
loc_path = system.file("extdata", "seqfish_field_locs.txt", package = 'Giotto')
VC_small <- createGiottoObject(raw_exprs = expr_path, spatial_locs = loc_path)

# 2. normalize giotto
VC_small <- normalizeGiotto(gobject = VC_small, scalefactor = 6000)
VC_small <- addStatistics(gobject = VC_small)

# 3. dimension reduction
VC_small <- calculateHVG(gobject = VC_small)
VC_small <- runPCA(gobject = VC_small)
VC_small <- runTSNE(VC_small, dimensions_to_use = 1:5, n_threads = 2)
plotTSNE(gobject = VC_small)
```

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,
    verbose = T,
    ...
)

```

Arguments

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

Details

See [umap](#) for more information about these and other parameters.

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

Value

giotto object with updated UMAP dimension reduction

Examples

```
# 1. create giotto object
expr_path = system.file("extdata", "seqfish_field_expr.txt", package = 'Giotto')
loc_path = system.file("extdata", "seqfish_field_locs.txt", package = 'Giotto')
VC_small <- createGiottoObject(raw_exprs = expr_path, spatial_locs = loc_path)

# 2. normalize giotto
VC_small <- normalizeGiotto(gobject = VC_small, scalefactor = 6000)
VC_small <- addStatistics(gobject = VC_small)

# 3. dimension reduction
VC_small <- calculateHVG(gobject = VC_small)
VC_small <- runPCA(gobject = VC_small)
VC_small <- runUMAP(VC_small, dimensions_to_use = 1:5, n_threads = 2)
plotUMAP(gobject = VC_small)
```

screePlot

screePlot

Description

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

Usage

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

Arguments

| | |
|--------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>name</code> | name of PCA object if available |
| <code>expression_values</code> | expression values to use |
| <code>reduction</code> | cells or genes |
| <code>method</code> | which implementation to use |
| <code>rev</code> | do a reverse PCA |
| <code>genes_to_use</code> | subset of genes to use for PCA |
| <code>center</code> | center data before PCA |
| <code>scale_unit</code> | scale features before PCA |
| <code>ncp</code> | number of principal components to calculate |
| <code>ylim</code> | y-axis limits on scree plot |
| <code>verbose</code> | verbosity |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters from <code>all_plots_save_function()</code> |
| <code>default_save_name</code> | default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code> |
| <code>...</code> | additional arguments to <code>pca</code> function, see runPCA |

Details

Screeplot works by plotting the explained variance of each individual PC in a barplot allowing you to identify which PC provides a significant contribution (a.k.a 'elbow method').

Screeplot will use an available `pca` object, based on the parameter 'name', or it will create it if it's not available (see [runPCA](#))

Value

ggplot object for scree method

Examples

```
screePlot(gobject)
```

| | |
|--------------------|---------------------------|
| selectPatternGenes | <i>selectPatternGenes</i> |
|--------------------|---------------------------|

Description

Select genes correlated with spatial patterns

Usage

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

Arguments

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

Details

Description.

Value

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

Examples

```
selectPatternGenes(gobject)
```

| | |
|--------------------|-------------------------------------|
| show,giotto-method | <i>show method for giotto class</i> |
|--------------------|-------------------------------------|

Description

show method for giotto class

Usage

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

Arguments

| | |
|--------|---------------|
| object | giotto object |
|--------|---------------|

| | |
|-----------------------|------------------------------|
| showClusterDendrogram | <i>showClusterDendrogram</i> |
|-----------------------|------------------------------|

Description

Creates dendrogram for selected clusters.

Usage

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

Arguments

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

| | |
|-------------------|--|
| distance | distance method to use for hierarchical clustering |
| h | height of horizontal lines to plot |
| h_color | color of horizontal lines |
| rotate | rotate dendrogram 90 degrees |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |
| ... | additional parameters for ggdendrogram() |

Details

Expression correlation dendrogram for selected clusters.

Value

ggplot

Examples

```
showClusterDendrogram(gobject)
```

| | |
|--------------------|---------------------------|
| showClusterHeatmap | <i>showClusterHeatmap</i> |
|--------------------|---------------------------|

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 = "showClustHeatmap",
  ...
)
```

Arguments

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

Details

Correlation heatmap of selected clusters.

Value

ggplot

Examples

```
showClusterHeatmap(gobject)
```

```
showGiottoImageNames  showGiottoImageNames
```

Description

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

Usage

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

Arguments

| | |
|----------------------|-----------------------|
| <code>gobject</code> | a giotto object |
| <code>verbose</code> | verbosity of function |

Value

a vector of giotto image names attached to the giotto object

Examples

```
showGiottoImageNames(gobject)
```

| | |
|------------------------|-------------------------------|
| showGiottoInstructions | <i>showGiottoInstructions</i> |
|------------------------|-------------------------------|

Description

Function to display all instructions from giotto object

Usage

```
showGiottoInstructions(gobject)
```

Arguments

| | |
|---------|---------------|
| gobject | giotto object |
|---------|---------------|

Value

named vector with giotto instructions

Examples

```
showGiottoInstructions()
```

| | |
|-----------|------------------|
| showGrids | <i>showGrids</i> |
|-----------|------------------|

Description

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

Usage

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

Arguments

| | |
|---------|-------------------------|
| gobject | a giotto object |
| verbose | verbosity of function#' |

Value

vector

Examples

```
showGrids()
```

| | |
|--------------|---------------------|
| showNetworks | <i>showNetworks</i> |
|--------------|---------------------|

Description

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

Usage

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

Arguments

| | |
|---------|-------------------------|
| gobject | a giotto object |
| verbose | verbosity of function#' |

Value

vector

Examples

```
showNetworks()
```

| | |
|-------------|--------------------|
| showPattern | <i>showPattern</i> |
|-------------|--------------------|

Description

show patterns for 2D spatial data

Usage

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

Arguments

| | |
|-------------------|--|
| gobject | giotto object |
| spatPatObj | Output from detectSpatialPatterns |
| ... | Arguments passed on to showPattern2D |
| dimension | dimension to plot |
| trim | Trim ends of the PC values. |
| background_color | background color for plot |
| grid_border_color | color for grid |
| show_legend | show legend of ggplot |
| point_size | size of points |
| show_plot | show plot |
| return_plot | return ggplot object |

save_plot directly save the plot [boolean]
save_param list of saving parameters, see [showSaveParameters](#)
default_save_name default save name for saving, don't change, change save_name
in save_param

Value

ggplot

See Also

[showPattern2D](#)

Examples

showPattern(gobject)

| | |
|---------------|----------------------|
| showPattern2D | <i>showPattern2D</i> |
|---------------|----------------------|

Description

show patterns for 2D spatial data

Usage

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

Arguments

| | |
|------------------|-----------------------------------|
| gobject | giotto object |
| spatPatObj | Output from detectSpatialPatterns |
| dimension | dimension to plot |
| trim | Trim ends of the PC values. |
| background_color | background color for plot |

| | |
|-------------------|--|
| grid_border_color | color for grid |
| show_legend | show legend of ggplot |
| point_size | size of points |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Value

ggplot

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

Value

plotly

Examples

```
showPattern3D(gobject)
```

| | |
|------------------|-------------------------|
| showPatternGenes | <i>showPatternGenes</i> |
|------------------|-------------------------|

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

| | |
|--------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>spatPatObj</code> | Output from <code>detectSpatialPatterns</code> |
| <code>dimension</code> | dimension to plot genes for. |
| <code>top_pos_genes</code> | Top positively correlated genes. |
| <code>top_neg_genes</code> | Top negatively correlated genes. |
| <code>point_size</code> | size of points |
| <code>return_DT</code> | if TRUE, it will return the data.table used to generate the plots |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters, see showSaveParameters |
| <code>default_save_name</code> | default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code> |

Value

ggplot

Examples

```
showPatternGenes(gobject)
```

| | |
|---------------------|----------------------------|
| showProcessingSteps | <i>showProcessingSteps</i> |
|---------------------|----------------------------|

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)
```

| | |
|--------------------|---------------------------|
| showSaveParameters | <i>showSaveParameters</i> |
|--------------------|---------------------------|

Description

Description of Giotto saving options, links to [all_plots_save_function](#)

Usage

```
showSaveParameters()
```

Value

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

Examples

```
showSaveParameters()
```

| | |
|---------------------|----------------------------|
| showSpatialCorGenes | <i>showSpatialCorGenes</i> |
|---------------------|----------------------------|

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)
```

signPCA

*signPCA***Description**

identify significant principal components (PCs)

Usage

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

Arguments

| | |
|--------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>name</code> | name of PCA object if available |
| <code>method</code> | method to use to identify significant PCs |
| <code>expression_values</code> | expression values to use |
| <code>reduction</code> | cells or genes |
| <code>pca_method</code> | which implementation to use |
| <code>rev</code> | do a reverse PCA |
| <code>genes_to_use</code> | subset of genes to use for PCA |
| <code>center</code> | center data before PCA |
| <code>scale_unit</code> | scale features before PCA |
| <code>ncp</code> | number of principal components to calculate |
| <code>scree_ylim</code> | y-axis limits on scree plot |

| | |
|-------------------|--|
| jack_iter | number of iterations for jackstraw |
| jack_threshold | p-value threshold to call a PC significant |
| jack_ylim | y-axis limits on jackstraw plot |
| verbose | verbosity |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters from all_plots_save_function() |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Two different methods can be used to assess the number of relevant or significant principal components (PC's).

1. Screeplot works by plotting the explained variance of each individual PC in a barplot allowing you to identify which PC provides a significant contribution (a.k.a. 'elbow method').
2. The Jackstraw method uses the [permutationPA](#) function. By systematically permuting genes it identifies robust, and thus significant, PCs.

Value

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

Examples

```
signPCA(gobject)
```

| | |
|----------------|-----------------------|
| silhouetteRank | <i>silhouetteRank</i> |
|----------------|-----------------------|

Description

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

Usage

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

Arguments

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

Value

data.table with spatial scores

Examples

```
silhouetteRank(gobject)
```

```
simulateOneGenePatternGiottoObject
```

```
simulateOneGenePatternGiottoObject
```

Description

Create a simulated spatial pattern for one selected gene

Usage

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

Arguments

| | |
|-------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>pattern_name</code> | name of spatial pattern |
| <code>pattern_cell_ids</code> | cell ids that make up the spatial pattern |
| <code>gene_name</code> | selected gene |
| <code>spatial_prob</code> | probability for a high expressing gene value to be part of the spatial pattern |

gradient_direction direction of gradient
show_pattern show the discrete spatial pattern
pattern_colors 2 color vector for the spatial pattern
... additional parameters for (re-)normalizing

Value

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

Examples

```
simulateOneGenePatternGiottoObject(gobject)
```

| | |
|-------|--------------|
| spark | <i>spark</i> |
|-------|--------------|

Description

Compute spatially expressed genes with SPARK method

Usage

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

Arguments

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

Details

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

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

Value

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

| | |
|-----------------|------------------------|
| spatCellCellcom | <i>spatCellCellcom</i> |
|-----------------|------------------------|

Description

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

Usage

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

Arguments

- | | |
|----------------------|--|
| gobject | giotto object to use |
| spatial_network_name | spatial network to use for identifying interacting cells |
| cluster_column | cluster column with cell type information |
| random_iter | number of iterations |
| gene_set_1 | first specific gene set from gene pairs |
| gene_set_2 | second specific gene set from gene pairs |

| | |
|------------------|---|
| log2FC_addendum | addendum to add when calculating log2FC |
| min_observations | minimum number of interactions needed to be considered |
| detailed | provide more detailed information (random variance and z-score) |
| adjust_method | which method to adjust p-values |
| adjust_target | adjust multiple hypotheses at the cell or gene level |
| do_parallel | run calculations in parallel with mclapply |
| cores | number of cores to use if do_parallel = TRUE |
| 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 each other..

- LR_comb: Pair of ligand and receptor
- lig_cell_type: cell type to assess expression level of ligand
- lig_expr: average expression of ligand in lig_cell_type
- ligand: ligand name
- rec_cell_type: cell type to assess expression level of receptor
- rec_expr: average expression of receptor in rec_cell_type
- receptor: receptor name
- LR_expr: combined average ligand and receptor expression
- lig_nr: total number of cells from lig_cell_type that spatially interact with cells from rec_cell_type
- rec_nr: total number of cells from rec_cell_type that spatially interact with cells from lig_cell_type
- rand_expr: average combined ligand and receptor expression from random spatial permutations
- av_diff: average difference between LR_expr and rand_expr over all random spatial permutations
- sd_diff: (optional) standard deviation of the difference between LR_expr and rand_expr over all random spatial permutations
- z_score: (optional) z-score
- log2fc: log2 fold-change (LR_expr/rand_expr)
- pvalue: p-value
- LR_cell_comb: cell type pair combination
- p.adj: adjusted p-value
- PI: significance score: $\log_2\text{fc} * -\log_{10}(\text{p.adj})$

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(...)
```

Arguments

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

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

Details

Description of parameters.

Value

ggplot

See Also

Other spatial cell annotation visualizations: [spatCellPlot2D\(\)](#)

Examples

```
spatCellPlot(gobject)
```

spatCellPlot2D

spatCellPlot2D

Description

Visualize cells according to spatial coordinates

Usage

```
spatCellPlot2D(
  gobject,
  show_image = F,
  gimage = NULL,
  image_name = "image",
  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", "voronoi"),
  point_size = 3,
  point_alpha = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_cluster_center = F,
  show_center_label = F,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  show_network = F,
  spatial_network_name = "Delaunay_network",
  network_color = NULL,
  network_alpha = 1,
  show_grid = F,
  spatial_grid_name = "spatial_grid",
  grid_color = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1,
  other_cells_alpha = 0.1,
  coord_fix_ratio = NULL,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  background_color = "white",
```

```

    vor_border_color = "white",
    vor_max_radius = 200,
    vor_alpha = 1,
    axis_text = 8,
    axis_title = 8,
    cow_n_col = 2,
    cow_rel_h = 1,
    cow_rel_w = 1,
    cow_align = "h",
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spatCellPlot2D"
)

```

Arguments

| | |
|-------------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>show_image</code> | show a tissue background image |
| <code>gimage</code> | a giotto image |
| <code>image_name</code> | name of a giotto image |
| <code>sdimx</code> | x-axis dimension name (default = 'sdimx') |
| <code>sdimy</code> | y-axis dimension name (default = 'sdimy') |
| <code>spat_enr_names</code> | names of spatial enrichment results to include |
| <code>cell_annotation_values</code> | numeric cell annotation columns |
| <code>cell_color_gradient</code> | vector with 3 colors for numeric data |
| <code>gradient_midpoint</code> | midpoint for color gradient |
| <code>gradient_limits</code> | vector with lower and upper limits |
| <code>select_cell_groups</code> | select subset of cells/clusters based on <code>cell_color</code> parameter |
| <code>select_cells</code> | select subset of cells based on cell IDs |
| <code>point_shape</code> | shape of points (border, no_border or voronoi) |
| <code>point_size</code> | size of point (cell) |
| <code>point_alpha</code> | transparency of spatial points |
| <code>point_border_col</code> | color of border around points |
| <code>point_border_stroke</code> | stroke size of border around points |
| <code>show_cluster_center</code> | plot center of selected clusters |
| <code>show_center_label</code> | plot label of selected clusters |

| | |
|----------------------------|-------------------------------------|
| center_point_size | size of center points |
| center_point_border_col | border color of center points |
| center_point_border_stroke | border stroke size of center points |
| label_size | size of labels |
| label_fontface | font of labels |
| show_network | show underlying spatial network |
| spatial_network_name | name of spatial network to use |
| network_color | color of spatial network |
| network_alpha | alpha of spatial network |
| show_grid | show spatial grid |
| spatial_grid_name | name of spatial grid to use |
| grid_color | color of spatial grid |
| show_other_cells | display not selected cells |
| other_cell_color | color of not selected cells |
| other_point_size | point size of not selected cells |
| other_cells_alpha | alpha of not selected cells |
| coord_fix_ratio | fix ratio between x and y-axis |
| show_legend | show legend |
| legend_text | size of legend text |
| legend_symbol_size | size of legend symbols |
| background_color | color of plot background |
| vor_border_color | border color for voronoi plot |
| vor_max_radius | maximum radius for voronoi 'cells' |
| vor_alpha | transparency of voronoi 'cells' |
| axis_text | size of axis text |
| axis_title | size of axis title |
| cow_n_col | cowplot param: how many columns |
| cow_rel_h | cowplot param: relative height |
| cow_rel_w | cowplot param: relative width |
| cow_align | cowplot param: how to align |
| show_plot | show plot |
| return_plot | return ggplot object |

save_plot directly save the plot [boolean]
save_param list of saving parameters, see [showSaveParameters](#)
default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

Other spatial cell annotation visualizations: [spatCellPlot\(\)](#)

Examples

spatCellPlot2D(gobject)

| | |
|-----------------|------------------------|
| spatDimCellPlot | <i>spatDimCellPlot</i> |
|-----------------|------------------------|

Description

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

Usage

spatDimCellPlot(...)

Arguments

... Arguments passed on to [spatDimCellPlot2D](#)
gobject giotto object
show_image show a tissue background image
gimage a giotto image
image_name name of a giotto image
plot_alignment direction to align plot
spat_enr_names names of spatial enrichment results to include
cell_annotation_values numeric cell annotation columns
dim_reduction_to_use dimension reduction to use
dim_reduction_name dimension reduction name
dim1_to_use dimension to use on x-axis
dim2_to_use dimension to use on y-axis
sdimx = spatial dimension to use on x-axis
sdimy = spatial dimension to use on y-axis

cell_color_gradient vector with 3 colors for numeric data
 gradient_midpoint midpoint for color gradient
 gradient_limits vector with lower and upper limits
 select_cell_groups select subset of cells/clusters based on cell_color parameter
 select_cells select subset of cells based on cell IDs
 dim_point_shape dim reduction points with border or not (border or no_border)
 dim_point_size size of points in dim. reduction space
 dim_point_alpha transparency of dim. reduction points
 dim_point_border_col border color of points in dim. reduction space
 dim_point_border_stroke border stroke of points in dim. reduction space
 spat_point_shape shape of points (border, no_border or voronoi)
 spat_point_size size of spatial points
 spat_point_alpha transparency of spatial points
 spat_point_border_col border color of spatial points
 spat_point_border_stroke border stroke of spatial points
 dim_show_cluster_center show the center of each cluster
 dim_show_center_label provide a label for each cluster
 dim_center_point_size size of the center point
 dim_center_point_border_col border color of center point
 dim_center_point_border_stroke stroke size of center point
 dim_label_size size of the center label
 dim_label_fontface font of the center label
 spat_show_cluster_center show the center of each cluster
 spat_show_center_label provide a label for each cluster
 spat_center_point_size size of the spatial center points
 spat_center_point_border_col border color of the spatial center points
 spat_center_point_border_stroke stroke size of the spatial center points
 spat_label_size size of the center label
 spat_label_fontface font of the center label
 show_NN_network show underlying NN network
 nn_network_to_use type of NN network to use (kNN vs sNN)
 nn_network_name name of NN network to use, if show_NN_network = TRUE
 dim_edge_alpha column to use for alpha of the edges
 spat_show_network show spatial network
 spatial_network_name name of spatial network to use
 spat_network_color color of spatial network
 spat_network_alpha alpha of spatial network
 spat_show_grid show spatial grid
 spatial_grid_name name of spatial grid to use
 spat_grid_color color of spatial grid
 show_other_cells display not selected cells
 other_cell_color color of not selected cells
 dim_other_point_size size of not selected dim cells
 spat_other_point_size size of not selected spat cells
 spat_other_cells_alpha alpha of not selected spat cells

coord_fix_ratio ratio for coordinates
cow_n_col cowplot param: how many columns
cow_rel_h cowplot param: relative height
cow_rel_w cowplot param: relative width
cow_align cowplot param: how to align
show_legend show legend
legend_text size of legend text
legend_symbol_size size of legend symbols
dim_background_color background color of points in dim. reduction space
spat_background_color background color of spatial points
vor_border_color border color for voronoi plot
vor_max_radius maximum radius for voronoi 'cells'
vor_alpha transparency of voronoi 'cells'
axis_text size of axis text
axis_title size of axis title
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see [showSaveParameters](#)
default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

Other spatial and dimension reduction cell annotation visualizations: [spatDimCellPlot2D\(\)](#)

Examples

spatDimCellPlot(gobject)

| | |
|-------------------|--------------------------|
| spatDimCellPlot2D | <i>spatDimCellPlot2D</i> |
|-------------------|--------------------------|

Description

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

Usage

```
spatDimCellPlot2D(  
  gobject,  
  show_image = F,  
  gimage = NULL,  
  image_name = "image",  
  plot_alignment = c("vertical", "horizontal"),  
  spat_enr_names = NULL,  
  cell_annotation_values = NULL,  
  dim_reduction_to_use = "umap",  
  dim_reduction_name = "umap",  
  dim1_to_use = 1,  
  dim2_to_use = 2,  
  sdimx = "sdimx",  
  sdimy = "sdimy",  
  cell_color_gradient = c("blue", "white", "red"),  
  gradient_midpoint = NULL,  
  gradient_limits = NULL,  
  select_cell_groups = NULL,  
  select_cells = NULL,  
  dim_point_shape = c("border", "no_border"),  
  dim_point_size = 1,  
  dim_point_alpha = 1,  
  dim_point_border_col = "black",  
  dim_point_border_stroke = 0.1,  
  spat_point_shape = c("border", "no_border", "voronoi"),  
  spat_point_size = 1,  
  spat_point_alpha = 1,  
  spat_point_border_col = "black",  
  spat_point_border_stroke = 0.1,  
  dim_show_cluster_center = F,  
  dim_show_center_label = T,  
  dim_center_point_size = 4,  
  dim_center_point_border_col = "black",  
  dim_center_point_border_stroke = 0.1,  
  dim_label_size = 4,  
  dim_label_fontface = "bold",  
  spat_show_cluster_center = F,  
  spat_show_center_label = F,  
  spat_center_point_size = 4,  
  spat_center_point_border_col = "black",  
  spat_center_point_border_stroke = 0.1,  
  spat_label_size = 4,  
  spat_label_fontface = "bold",  
  show_NN_network = F,  
  nn_network_to_use = "sNN",  
  nn_network_name = "sNN.pca",  
  dim_edge_alpha = 0.5,  
  spat_show_network = F,  
  spatial_network_name = "Delaunay_network",  
  spat_network_color = "red",  
  spat_network_alpha = 0.5,
```

```

    spat_show_grid = F,
    spatial_grid_name = "spatial_grid",
    spat_grid_color = "green",
    show_other_cells = TRUE,
    other_cell_color = "grey",
    dim_other_point_size = 0.5,
    spat_other_point_size = 0.5,
    spat_other_cells_alpha = 0.5,
    show_legend = T,
    legend_text = 8,
    legend_symbol_size = 1,
    dim_background_color = "white",
    spat_background_color = "white",
    vor_border_color = "white",
    vor_max_radius = 200,
    vor_alpha = 1,
    axis_text = 8,
    axis_title = 8,
    coord_fix_ratio = NULL,
    cow_n_col = 2,
    cow_rel_h = 1,
    cow_rel_w = 1,
    cow_align = "h",
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spatDimCellPlot2D"
  )

```

Arguments

| | |
|-------------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>show_image</code> | show a tissue background image |
| <code>gimage</code> | a giotto image |
| <code>image_name</code> | name of a giotto image |
| <code>plot_alignment</code> | direction to align plot |
| <code>spat_enr_names</code> | names of spatial enrichment results to include |
| <code>cell_annotation_values</code> | numeric cell annotation columns |
| <code>dim_reduction_to_use</code> | dimension reduction to use |
| <code>dim_reduction_name</code> | dimension reduction name |
| <code>dim1_to_use</code> | dimension to use on x-axis |
| <code>dim2_to_use</code> | dimension to use on y-axis |
| <code>sdimx</code> | = spatial dimension to use on x-axis |
| <code>sdimy</code> | = spatial dimension to use on y-axis |
| <code>cell_color_gradient</code> | vector with 3 colors for numeric data |

| | |
|--------------------------------|---|
| gradient_midpoint | midpoint for color gradient |
| gradient_limits | vector with lower and upper limits |
| select_cell_groups | select subset of cells/clusters based on cell_color parameter |
| select_cells | select subset of cells based on cell IDs |
| dim_point_shape | dim reduction points with border or not (border or no_border) |
| dim_point_size | size of points in dim. reduction space |
| dim_point_alpha | transparency of dim. reduction points |
| dim_point_border_col | border color of points in dim. reduction space |
| dim_point_border_stroke | border stroke of points in dim. reduction space |
| spat_point_shape | shape of points (border, no_border or voronoi) |
| spat_point_size | size of spatial points |
| spat_point_alpha | transparency of spatial points |
| spat_point_border_col | border color of spatial points |
| spat_point_border_stroke | border stroke of spatial points |
| dim_show_cluster_center | show the center of each cluster |
| dim_show_center_label | provide a label for each cluster |
| dim_center_point_size | size of the center point |
| dim_center_point_border_col | border color of center point |
| dim_center_point_border_stroke | stroke size of center point |
| dim_label_size | size of the center label |
| dim_label_fontface | font of the center label |
| spat_show_cluster_center | show the center of each cluster |
| spat_show_center_label | provide a label for each cluster |
| spat_center_point_size | size of the spatial center points |
| spat_center_point_border_col | border color of the spatial center points |

```

spat_center_point_border_stroke
    stroke size of the spatial center points
spat_label_size
    size of the center label
spat_label_fontface
    font of the center label
show_NN_network
    show underlying NN network
nn_network_to_use
    type of NN network to use (kNN vs sNN)
nn_network_name
    name of NN network to use, if show_NN_network = TRUE
dim_edge_alpha
    column to use for alpha of the edges
spat_show_network
    show spatial network
spatial_network_name
    name of spatial network to use
spat_network_color
    color of spatial network
spat_network_alpha
    alpha of spatial network
spat_show_grid
    show spatial grid
spatial_grid_name
    name of spatial grid to use
spat_grid_color
    color of spatial grid
show_other_cells
    display not selected cells
other_cell_color
    color of not selected cells
dim_other_point_size
    size of not selected dim cells
spat_other_point_size
    size of not selected spat cells
spat_other_cells_alpha
    alpha of not selected spat cells
show_legend
    show legend
legend_text
    size of legend text
legend_symbol_size
    size of legend symbols
dim_background_color
    background color of points in dim. reduction space
spat_background_color
    background color of spatial points
vor_border_color
    border color for voronoi plot
vor_max_radius
    maximum radius for voronoi 'cells'

```

| | |
|-------------------|--|
| vor_alpha | transparancy of voronoi 'cells' |
| axis_text | size of axis text |
| axis_title | size of axis title |
| coord_fix_ratio | ratio for coordinates |
| cow_n_col | cowplot param: how many columns |
| cow_rel_h | cowplot param: relative height |
| cow_rel_w | cowplot param: relative width |
| cow_align | cowplot param: how to align |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

ggplot

See Also

Other spatial and dimension reduction cell annotation visualizations: [spatDimCellPlot\(\)](#)

Examples

```
spatDimCellPlot2D(gobject)
```

| | |
|-----------------|------------------------|
| spatDimGenePlot | <i>spatDimGenePlot</i> |
|-----------------|------------------------|

Description

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

Usage

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

Arguments

... Arguments passed on to [spatDimGenePlot2D](#)

`gobject` giotto object

`show_image` show a tissue background image

`gimage` a giotto image

`image_name` name of a giotto image

`expression_values` gene expression values to use

`plot_alignment` direction to align plot

`genes` genes to show

`dim_reduction_to_use` dimension reduction to use

`dim_reduction_name` dimension reduction name

`dim1_to_use` dimension to use on x-axis

`dim2_to_use` dimension to use on y-axis

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

`dim_point_size` dim reduction plot: point size

`dim_point_alpha` transparency of dim. reduction points

`dim_point_border_col` color of border around points

`dim_point_border_stroke` stroke size of border around points

`show_NN_network` show underlying NN network

`show_spatial_network` show underlying spatial 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_network_color` color of NN network

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

`scale_alpha_with_expression` scale expression with ggplot alpha parameter

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

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

`spatial_network_name` name of spatial network to use

`spatial_network_color` color of spatial network

`show_spatial_grid` show spatial grid

`grid_color` color of spatial grid

`spatial_grid_name` name of spatial grid to use

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

`spat_point_size` spatial plot: point size

`spat_point_alpha` transparency of spatial points

`spat_point_border_col` color of border around points

`spat_point_border_stroke` stroke size of border around points

`spat_edge_alpha` edge alpha

`cell_color_gradient` vector with 3 colors for numeric data

`gradient_midpoint` midpoint for color gradient

`gradient_limits` vector with lower and upper limits

`show_legend` show legend

`legend_text` size of legend text

`dim_background_color` color of plot background for dimension plot

`spat_background_color` color of plot background for spatial plot

vor_border_color border color for voronoi plot
 vor_max_radius maximum radius for voronoi 'cells'
 vor_alpha transparency of voronoi 'cells'
 axis_text size of axis text
 axis_title size of axis title
 cow_n_col cowplot param: how many columns
 cow_rel_h cowplot param: relative height
 cow_rel_w cowplot param: relative width
 cow_align cowplot param: how to align
 show_plot show plots
 return_plot return ggplot object
 save_plot directly save the plot [boolean]
 save_param list of saving parameters, see [showSaveParameters](#)
 default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

[spatDimGenePlot3D](#)

Other spatial and dimension reduction gene expression visualizations: [spatDimGenePlot2D\(\)](#), [spatDimGenePlot3D\(\)](#)

Examples

```
spatDimGenePlot(gobject)
```

| | |
|-------------------|--------------------------|
| spatDimGenePlot2D | <i>spatDimGenePlot2D</i> |
|-------------------|--------------------------|

Description

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

Usage

```

spatDimGenePlot2D(
  gobject,
  show_image = F,
  gimage = NULL,
  image_name = "image",
  expression_values = c("normalized", "scaled", "custom"),
  plot_alignment = c("vertical", "horizontal"),

```

```

genes,
dim_reduction_to_use = "umap",
dim_reduction_name = "umap",
dim1_to_use = 1,
dim2_to_use = 2,
dim_point_shape = c("border", "no_border"),
dim_point_size = 1,
dim_point_alpha = 1,
dim_point_border_col = "black",
dim_point_border_stroke = 0.1,
show_NN_network = F,
show_spatial_network = F,
dim_network_color = "gray",
nn_network_to_use = "sNN",
network_name = "sNN.pca",
dim_edge_alpha = NULL,
scale_alpha_with_expression = FALSE,
sdmx = "sdmx",
sdmy = "sdmy",
spatial_network_name = "Delaunay_network",
spatial_network_color = NULL,
show_spatial_grid = F,
grid_color = NULL,
spatial_grid_name = "spatial_grid",
spat_point_shape = c("border", "no_border", "voronoi"),
spat_point_size = 1,
spat_point_alpha = 1,
spat_point_border_col = "black",
spat_point_border_stroke = 0.1,
spat_edge_alpha = NULL,
cell_color_gradient = c("blue", "white", "red"),
gradient_midpoint = NULL,
gradient_limits = NULL,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_legend = T,
legend_text = 8,
dim_background_color = "white",
spat_background_color = "white",
vor_border_color = "white",
vor_max_radius = 200,
vor_alpha = 1,
axis_text = 8,
axis_title = 8,
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatDimGenePlot2D"
)

```

Arguments

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

| | |
|--------------------------|--|
| spatial_grid_name | name of spatial grid to use |
| spat_point_shape | spatial points with border or not (border or no_border) |
| spat_point_size | spatial plot: point size |
| spat_point_alpha | transparency of spatial points |
| spat_point_border_col | color of border around points |
| spat_point_border_stroke | stroke size of border around points |
| spat_edge_alpha | edge alpha |
| cell_color_gradient | vector with 3 colors for numeric data |
| gradient_midpoint | midpoint for color gradient |
| gradient_limits | vector with lower and upper limits |
| cow_n_col | cowplot param: how many columns |
| cow_rel_h | cowplot param: relative height |
| cow_rel_w | cowplot param: relative width |
| cow_align | cowplot param: how to align |
| show_legend | show legend |
| legend_text | size of legend text |
| dim_background_color | color of plot background for dimension plot |
| spat_background_color | color of plot background for spatial plot |
| vor_border_color | border color for voronoi plot |
| vor_max_radius | maximum radius for voronoi 'cells' |
| vor_alpha | transparency of voronoi 'cells' |
| axis_text | size of axis text |
| axis_title | size of axis title |
| show_plot | show plots |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

ggplot

See Also

[spatDimGenePlot3D](#)

Other spatial and dimension reduction gene expression visualizations: [spatDimGenePlot3D\(\)](#), [spatDimGenePlot\(\)](#)

Examples

```
spatDimGenePlot2D(gobject)
```

| | |
|-------------------|--------------------------|
| spatDimGenePlot3D | <i>spatDimGenePlot3D</i> |
|-------------------|--------------------------|

Description

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

Usage

```
spatDimGenePlot3D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  plot_alignment = c("horizontal", "vertical"),
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  sdimx = "sdimx",
  sdimy = "sdimy",
  sdimz = "sdimz",
  genes,
  cluster_column = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1.5,
  show_NN_network = FALSE,
  nn_network_to_use = "sNN",
  nn_network_color = "lightgrey",
  nn_network_alpha = 0.5,
  network_name = "sNN.pca",
  label_size = 16,
  genes_low_color = "blue",
  genes_mid_color = "white",
  genes_high_color = "red",
  dim_point_size = 3,
```

```

show_spatial_network = FALSE,
spatial_network_name = "Delaunay_network",
spatial_network_color = "lightgray",
spatial_network_alpha = 0.5,
show_spatial_grid = FALSE,
spatial_grid_name = "spatial_grid",
spatial_grid_color = NULL,
spatial_grid_alpha = 0.5,
spatial_point_size = 3,
legend_text_size = 12,
axis_scale = c("cube", "real", "custom"),
custom_ratio = NULL,
x_ticks = NULL,
y_ticks = NULL,
z_ticks = NULL,
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatDimGenePlot3D"
)

```

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | gene expression values to use |
| <code>plot_alignment</code> | direction to align plot |
| <code>dim_reduction_to_use</code> | dimension reduction to use |
| <code>dim_reduction_name</code> | dimension reduction name |
| <code>dim1_to_use</code> | dimension to use on x-axis |
| <code>dim2_to_use</code> | dimension to use on y-axis |
| <code>dim3_to_use</code> | dimension to use on z-axis |
| <code>sdimx</code> | spatial dimension to use on x-axis |
| <code>sdimy</code> | spatial dimension to use on y-axis |
| <code>sdimz</code> | spatial dimension to use on z-axis |
| <code>genes</code> | genes to show |
| <code>cluster_column</code> | cluster column to select groups |
| <code>select_cell_groups</code> | select subset of cells/clusters based on <code>cell_color</code> parameter |
| <code>select_cells</code> | select subset of cells based on cell IDs |
| <code>show_other_cells</code> | display not selected cells |
| <code>other_cell_color</code> | color of not selected cells |
| <code>other_point_size</code> | size of not selected cells |

| | |
|-----------------------|--|
| show_NN_network | show underlying NN network |
| nn_network_to_use | type of NN network to use (kNN vs sNN) |
| nn_network_color | color of NN network |
| nn_network_alpha | alpha of NN network |
| network_name | name of NN network to use, if show_NN_network = TRUE |
| label_size | size of labels |
| genes_low_color | color for low expression levels |
| genes_mid_color | color for medium expression levels |
| genes_high_color | color for high expression levels |
| dim_point_size | dim reduction plot: point size |
| show_spatial_network | show spatial network (boolean) |
| spatial_network_name | name of spatial network to use |
| spatial_network_color | color of spatial network |
| spatial_network_alpha | alpha of spatial network |
| show_spatial_grid | show spatial grid (boolean) |
| spatial_grid_name | name of spatial grid to use |
| spatial_grid_color | color of spatial grid |
| spatial_grid_alpha | alpha of spatial grid |
| spatial_point_size | spatial plot: point size |
| legend_text_size | size of legend |
| axis_scale | the way to scale the axis |
| custom_ratio | customize the scale of the plot |
| x_ticks | set the number of ticks on the x-axis |
| y_ticks | set the number of ticks on the y-axis |
| z_ticks | set the number of ticks on the z-axis |
| show_plot | show plots |
| return_plot | return plotly object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

plotly

See Also

Other spatial and dimension reduction gene expression visualizations: [spatDimGenePlot2D\(\)](#), [spatDimGenePlot\(\)](#)

spatDimPlot

spatDimPlot

Description

Visualize cells according to spatial AND dimension reduction coordinates 2D

Usage

```
spatDimPlot(...)
```

Arguments

```
...           Arguments passed on to spatDimPlot2D
gobject      giotto object
show_image   show a tissue background image
gimage       a giotto image
image_name   name of a giotto image
plot_alignment direction to align plot
dim_reduction_to_use dimension reduction to use
dim_reduction_name dimension reduction name
dim1_to_use  dimension to use on x-axis
dim2_to_use  dimension to use on y-axis
sdmx         spatial dimension to use on x-axis
sdimy        spatial dimension to use on y-axis
spat_enr_names names of spatial enrichment results to include
cell_color   color for cells (see details)
color_as_factor convert color column to factor
cell_color_code named vector with colors
cell_color_gradient vector with 3 colors for numeric data
gradient_midpoint midpoint for color gradient
gradient_limits vector with lower and upper limits
select_cell_groups select subset of cells/clusters based on cell_color parameter
select_cells  select subset of cells based on cell IDs
dim_point_shape point with border or not (border or no_border)
```


dim_point_size size of points in dim. reduction space
 dim_point_alpha transparency of point in dim. reduction space
 dim_point_border_col border color of points in dim. reduction space
 dim_point_border_stroke border stroke of points in dim. reduction space
 spat_point_shape shape of points (border, no_border or voronoi)
 spat_point_size size of spatial points
 spat_point_alpha transparency of spatial points
 spat_point_border_col border color of spatial points
 spat_point_border_stroke border stroke of spatial points
 dim_show_cluster_center show the center of each cluster
 dim_show_center_label provide a label for each cluster
 dim_center_point_size size of the center point
 dim_center_point_border_col border color of center point
 dim_center_point_border_stroke stroke size of center point
 dim_label_size size of the center label
 dim_label_fontface font of the center label
 spat_show_cluster_center show the center of each cluster
 spat_show_center_label provide a label for each cluster
 spat_center_point_size size of the center point
 spat_center_point_border_col border color of spatial center points
 spat_center_point_border_stroke border strike size of spatial center points
 spat_label_size size of the center label
 spat_label_fontface font of the center label
 show_NN_network show underlying NN network
 nn_network_to_use type of NN network to use (kNN vs sNN)
 network_name name of NN network to use, if show_NN_network = TRUE
 nn_network_alpha column to use for alpha of the edges
 show_spatial_network show spatial network
 spat_network_name name of spatial network to use
 spat_network_color color of spatial network
 spat_network_alpha alpha of spatial network
 show_spatial_grid show spatial grid
 spat_grid_name name of spatial grid to use
 spat_grid_color color of spatial grid
 show_other_cells display not selected cells
 other_cell_color color of not selected cells
 dim_other_point_size size of not selected dim cells
 spat_other_point_size size of not selected spat cells
 spat_other_cells_alpha alpha of not selected spat cells
 dim_show_legend show legend of dimension reduction plot
 spat_show_legend show legend of spatial plot
 legend_text size of legend text
 legend_symbol_size size of legend symbols
 dim_background_color background color of points in dim. reduction space
 spat_background_color background color of spatial points

vor_border_color border color for voronoi plot
vor_max_radius maximum radius for voronoi 'cells'
vor_alpha transparency of voronoi 'cells'
axis_text size of axis text
axis_title size of axis title
show_plot show plot
return_plot return ggplot object
save_plot directly save the plot [boolean]
save_param list of saving parameters, see [showSaveParameters](#)
default_save_name default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

[spatDimPlot2D](#) and [spatDimPlot3D](#) for 3D visualization.
Other spatial and dimension reduction visualizations: [spatDimPlot2D\(\)](#), [spatDimPlot3D\(\)](#)

Examples

spatDimPlot(gobject)

| | |
|---------------|----------------------|
| spatDimPlot2D | <i>spatDimPlot2D</i> |
|---------------|----------------------|

Description

Visualize cells according to spatial AND dimension reduction coordinates 2D

Usage

```
spatDimPlot2D(  
  gobject,  
  show_image = F,  
  gimage = NULL,  
  image_name = "image",  
  plot_alignment = c("vertical", "horizontal"),  
  dim_reduction_to_use = "umap",  
  dim_reduction_name = "umap",  
  dim1_to_use = 1,  
  dim2_to_use = 2,  
  sdinx = "sdinx",  
  sdimy = "sdimy",
```

```
spat_enr_names = NULL,
cell_color = NULL,
color_as_factor = T,
cell_color_code = NULL,
cell_color_gradient = c("blue", "white", "red"),
gradient_midpoint = NULL,
gradient_limits = NULL,
select_cell_groups = NULL,
select_cells = NULL,
dim_point_shape = c("border", "no_border"),
dim_point_size = 1,
dim_point_alpha = 1,
dim_point_border_col = "black",
dim_point_border_stroke = 0.1,
spat_point_shape = c("border", "no_border", "voronoi"),
spat_point_size = 1,
spat_point_alpha = 1,
spat_point_border_col = "black",
spat_point_border_stroke = 0.1,
dim_show_cluster_center = F,
dim_show_center_label = T,
dim_center_point_size = 4,
dim_center_point_border_col = "black",
dim_center_point_border_stroke = 0.1,
dim_label_size = 4,
dim_label_fontface = "bold",
spat_show_cluster_center = F,
spat_show_center_label = F,
spat_center_point_size = 4,
spat_center_point_border_col = "blue",
spat_center_point_border_stroke = 0.1,
spat_label_size = 4,
spat_label_fontface = "bold",
show_NN_network = F,
nn_network_to_use = "sNN",
network_name = "sNN.pca",
nn_network_alpha = 0.05,
show_spatial_network = F,
spat_network_name = "Delaunay_network",
spat_network_color = "blue",
spat_network_alpha = 0.5,
show_spatial_grid = F,
spat_grid_name = "spatial_grid",
spat_grid_color = "blue",
show_other_cells = T,
other_cell_color = "lightgrey",
dim_other_point_size = 1,
spat_other_point_size = 1,
spat_other_cells_alpha = 0.5,
dim_show_legend = F,
spat_show_legend = F,
legend_text = 8,
```

```

    legend_symbol_size = 1,
    dim_background_color = "white",
    spat_background_color = "white",
    vor_border_color = "white",
    vor_max_radius = 200,
    vor_alpha = 1,
    axis_text = 8,
    axis_title = 8,
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spatDimPlot2D"
)

```

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>show_image</code> | show a tissue background image |
| <code>gimage</code> | a giotto image |
| <code>image_name</code> | name of a giotto image |
| <code>plot_alignment</code> | direction to align plot |
| <code>dim_reduction_to_use</code> | dimension reduction to use |
| <code>dim_reduction_name</code> | dimension reduction name |
| <code>dim1_to_use</code> | dimension to use on x-axis |
| <code>dim2_to_use</code> | dimension to use on y-axis |
| <code>sdimx</code> | = spatial dimension to use on x-axis |
| <code>sdimy</code> | = spatial dimension to use on y-axis |
| <code>spat_enr_names</code> | names of spatial enrichment results to include |
| <code>cell_color</code> | color for cells (see details) |
| <code>color_as_factor</code> | convert color column to factor |
| <code>cell_color_code</code> | named vector with colors |
| <code>cell_color_gradient</code> | vector with 3 colors for numeric data |
| <code>gradient_midpoint</code> | midpoint for color gradient |
| <code>gradient_limits</code> | vector with lower and upper limits |
| <code>select_cell_groups</code> | select subset of cells/clusters based on <code>cell_color</code> parameter |
| <code>select_cells</code> | select subset of cells based on cell IDs |
| <code>dim_point_shape</code> | point with border or not (<code>border</code> or <code>no_border</code>) |
| <code>dim_point_size</code> | size of points in dim. reduction space |

```

dim_point_alpha
    transparency of point in dim. reduction space
dim_point_border_col
    border color of points in dim. reduction space
dim_point_border_stroke
    border stroke of points in dim. reduction space
spat_point_shape
    shape of points (border, no_border or voronoi)
spat_point_size
    size of spatial points
spat_point_alpha
    transparency of spatial points
spat_point_border_col
    border color of spatial points
spat_point_border_stroke
    border stroke of spatial points
dim_show_cluster_center
    show the center of each cluster
dim_show_center_label
    provide a label for each cluster
dim_center_point_size
    size of the center point
dim_center_point_border_col
    border color of center point
dim_center_point_border_stroke
    stroke size of center point
dim_label_size
    size of the center label
dim_label_fontface
    font of the center label
spat_show_cluster_center
    show the center of each cluster
spat_show_center_label
    provide a label for each cluster
spat_center_point_size
    size of the center point
spat_center_point_border_col
    border color of spatial center points
spat_center_point_border_stroke
    border strike size of spatial center points
spat_label_size
    size of the center label
spat_label_fontface
    font of the center label
show_NN_network
    show underlying NN network
nn_network_to_use
    type of NN network to use (kNN vs sNN)
network_name
    name of NN network to use, if show_NN_network = TRUE

```

| | |
|------------------------|--|
| nn_network_alpha | column to use for alpha of the edges |
| show_spatial_network | show spatial network |
| spat_network_name | name of spatial network to use |
| spat_network_color | color of spatial network |
| spat_network_alpha | alpha of spatial network |
| show_spatial_grid | show spatial grid |
| spat_grid_name | name of spatial grid to use |
| spat_grid_color | color of spatial grid |
| show_other_cells | display not selected cells |
| other_cell_color | color of not selected cells |
| dim_other_point_size | size of not selected dim cells |
| spat_other_point_size | size of not selected spat cells |
| spat_other_cells_alpha | alpha of not selected spat cells |
| dim_show_legend | show legend of dimension reduction plot |
| spat_show_legend | show legend of spatial plot |
| legend_text | size of legend text |
| legend_symbol_size | size of legend symbols |
| dim_background_color | background color of points in dim. reduction space |
| spat_background_color | background color of spatial points |
| vor_border_color | border color for voronoi plot |
| vor_max_radius | maximum radius for voronoi 'cells' |
| vor_alpha | transparency of voronoi 'cells' |
| axis_text | size of axis text |
| axis_title | size of axis title |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

ggplot

See Also

[spatDimPlot3D](#)

Other spatial and dimension reduction visualizations: [spatDimPlot3D\(\)](#), [spatDimPlot\(\)](#)

Examples

`spatDimPlot2D(gobject)`

| | |
|----------------------------|-----------------------------------|
| <code>spatDimPlot3D</code> | <i><code>spatDimPlot3D</code></i> |
|----------------------------|-----------------------------------|

Description

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

Usage

```
spatDimPlot3D(  
  gobject,  
  plot_alignment = c("horizontal", "vertical"),  
  dim_reduction_to_use = "umap",  
  dim_reduction_name = "umap",  
  dim1_to_use = 1,  
  dim2_to_use = 2,  
  dim3_to_use = 3,  
  sdimx = "sdimx",  
  sdimy = "sdimy",  
  sdimz = "sdimz",  
  spat_enr_names = NULL,  
  show_NN_network = FALSE,  
  nn_network_to_use = "sNN",  
  network_name = "sNN.pca",  
  nn_network_color = "lightgray",  
  nn_network_alpha = 0.5,  
  show_cluster_center = F,  
  show_center_label = T,  
  center_point_size = 4,  
  label_size = 16,  
  select_cell_groups = NULL,  
  select_cells = NULL,  
  show_other_cells = T,  
  other_cell_color = "lightgrey",  
  other_point_size = 1.5,
```

```

cell_color = NULL,
color_as_factor = T,
cell_color_code = NULL,
dim_point_size = 3,
show_spatial_network = F,
spatial_network_name = "Delaunay_network",
spatial_network_color = "lightgray",
spatial_network_alpha = 0.5,
show_spatial_grid = F,
spatial_grid_name = "spatial_grid",
spatial_grid_color = NULL,
spatial_grid_alpha = 0.5,
spatial_point_size = 3,
axis_scale = c("cube", "real", "custom"),
custom_ratio = NULL,
x_ticks = NULL,
y_ticks = NULL,
z_ticks = NULL,
legend_text_size = 12,
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatDimPlot3D"
)

```

Arguments

| | |
|-----------------------------------|---|
| <code>gobject</code> | giotto object |
| <code>plot_alignment</code> | direction to align plot |
| <code>dim_reduction_to_use</code> | dimension reduction to use |
| <code>dim_reduction_name</code> | dimension reduction name |
| <code>dim1_to_use</code> | dimension to use on x-axis |
| <code>dim2_to_use</code> | dimension to use on y-axis |
| <code>dim3_to_use</code> | dimension to use on z-axis |
| <code>sdimx</code> | = spatial dimension to use on x-axis |
| <code>sdimy</code> | = spatial dimension to use on y-axis |
| <code>sdimz</code> | = spatial dimension to use on z-axis |
| <code>spat_enr_names</code> | names of spatial enrichment results to include |
| <code>show_NN_network</code> | show underlying NN network |
| <code>nn_network_to_use</code> | type of NN network to use (kNN vs sNN) |
| <code>network_name</code> | name of NN network to use, if <code>show_NN_network = TRUE</code> |
| <code>nn_network_color</code> | color of nn network |
| <code>nn_network_alpha</code> | column to use for alpha of the edges |


```

show_cluster_center      show the center of each cluster
show_center_label        provide a label for each cluster
center_point_size        size of the center point
label_size               size of the center label
select_cell_groups        select subset of cells/clusters based on cell_color parameter
select_cells             select subset of cells based on cell IDs
show_other_cells          display not selected cells
other_cell_color          color of not selected cells
other_point_size         size of not selected cells
cell_color               color for cells (see details)
color_as_factor           convert color column to factor
cell_color_code           named vector with colors
dim_point_size           size of points in dim. reduction space
show_spatial_network     show spatial network
spatial_network_name      name of spatial network to use
spatial_network_color     color of spatial network
spatial_network_alpha     alpha of spatial network
show_spatial_grid        show spatial grid
spatial_grid_name         name of spatial grid to use
spatial_grid_color        color of spatial grid
spatial_grid_alpha        alpha of spatial grid
spatial_point_size        size of spatial points
axis_scale               the way to scale the axis
custom_ratio             customize the scale of the plot
x_ticks                  set the number of ticks on the x-axis
y_ticks                  set the number of ticks on the y-axis
z_ticks                  set the number of ticks on the z-axis
legend_text_size          size of legend

```

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

Details

Description of parameters.

Value

plotly

See Also

Other spatial and dimension reduction visualizations: [spatDimPlot2D\(\)](#), [spatDimPlot\(\)](#)

Examples

spatDimPlot3D(gobject)

| | |
|--------------|---------------------|
| spatGenePlot | <i>spatGenePlot</i> |
|--------------|---------------------|

Description

Visualize cells and gene expression according to spatial coordinates

Usage

spatGenePlot(...)

Arguments

| | |
|---------------------|---|
| ... | Arguments passed on to spatGenePlot2D |
| gobject | giotto object |
| show_image | show a tissue background image |
| gimage | a giotto image |
| image_name | name of a giotto image |
| sdimx | x-axis dimension name (default = 'sdimx') |
| sdimy | y-axis dimension name (default = 'sdimy') |
| expression_values | gene expression values to use |
| genes | genes to show |
| cell_color_gradient | vector with 3 colors for numeric data |
| gradient_midpoint | midpoint for color gradient |
| gradient_limits | vector with lower and upper limits |
| show_network | show underlying spatial network |

network_color color of spatial network
 spatial_network_name name of spatial network to use
 edge_alpha alpha of edge
 show_grid show spatial grid
 grid_color color of spatial grid
 spatial_grid_name name of spatial grid to use
 midpoint expression midpoint
 scale_alpha_with_expression scale expression with ggplot alpha parameter
 point_shape shape of points (border, no_border or voronoi)
 point_size size of point (cell)
 point_alpha transparency of points
 point_border_col color of border around points
 point_border_stroke stroke size of border around points
 cow_n_col cowplot param: how many columns
 cow_rel_h cowplot param: relative height
 cow_rel_w cowplot param: relative width
 cow_align cowplot param: how to align
 show_legend show legend
 legend_text size of legend text
 background_color color of plot background
 vor_border_color border color for voronoi plot
 vor_max_radius maximum radius for voronoi 'cells'
 vor_alpha transparency of voronoi 'cells'
 axis_text size of axis text
 axis_title size of axis title
 show_plot show plots
 return_plot return ggplot object
 save_plot directly save the plot [boolean]
 save_param list of saving parameters, see [showSaveParameters](#)
 default_save_name default save name for saving, don't change, change save_name
 in save_param

Details

Description of parameters.

Value

ggplot

See Also

[spatGenePlot3D](#) and [spatGenePlot2D](#)

Other spatial gene expression visualizations: [spatGenePlot2D\(\)](#), [spatGenePlot3D\(\)](#)

Examples

```
spatGenePlot(gobject)
```

spatGenePlot2D

spatGenePlot2D

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```
spatGenePlot2D(
  gobject,
  show_image = F,
  gimage = NULL,
  image_name = "image",
  sdimx = "sdimx",
  sdimy = "sdimy",
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  show_network = F,
  network_color = NULL,
  spatial_network_name = "Delaunay_network",
  edge_alpha = NULL,
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  midpoint = 0,
  scale_alpha_with_expression = FALSE,
  point_shape = c("border", "no_border", "voronoi"),
  point_size = 1,
  point_alpha = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  legend_text = 8,
  background_color = "white",
  vor_border_color = "white",
  vor_alpha = 1,
  vor_max_radius = 200,
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
```

```

    default_save_name = "spatGenePlot2D"
)

```

Arguments

| | |
|--|--|
| <code>gobject</code> | giotto object |
| <code>show_image</code> | show a tissue background image |
| <code>gimage</code> | a giotto image |
| <code>image_name</code> | name of a giotto image |
| <code>sdimx</code> | x-axis dimension name (default = 'sdimx') |
| <code>sdimy</code> | y-axis dimension name (default = 'sdimy') |
| <code>expression_values</code> | gene expression values to use |
| <code>genes</code> | genes to show |
| <code>cell_color_gradient</code> | vector with 3 colors for numeric data |
| <code>gradient_midpoint</code> | midpoint for color gradient |
| <code>gradient_limits</code> | vector with lower and upper limits |
| <code>show_network</code> | show underlying spatial network |
| <code>network_color</code> | color of spatial network |
| <code>spatial_network_name</code> | name of spatial network to use |
| <code>edge_alpha</code> | alpha of edge |
| <code>show_grid</code> | show spatial grid |
| <code>grid_color</code> | color of spatial grid |
| <code>spatial_grid_name</code> | name of spatial grid to use |
| <code>midpoint</code> | expression midpoint |
| <code>scale_alpha_with_expression</code> | scale expression with ggplot alpha parameter |
| <code>point_shape</code> | shape of points (border, no_border or voronoi) |
| <code>point_size</code> | size of point (cell) |
| <code>point_alpha</code> | transparency of points |
| <code>point_border_col</code> | color of border around points |
| <code>point_border_stroke</code> | stroke size of border around points |
| <code>show_legend</code> | show legend |
| <code>legend_text</code> | size of legend text |
| <code>background_color</code> | color of plot background |
| <code>vor_border_color</code> | border color for voronoi plot |

| | |
|-------------------|--|
| vor_alpha | transparency of voronoi 'cells' |
| vor_max_radius | maximum radius for voronoi 'cells' |
| axis_text | size of axis text |
| axis_title | size of axis title |
| cow_n_col | cowplot param: how many columns |
| cow_rel_h | cowplot param: relative height |
| cow_rel_w | cowplot param: relative width |
| cow_align | cowplot param: how to align |
| show_plot | show plots |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

ggplot

See Also

[spatGenePlot3D](#)
Other spatial gene expression visualizations: [spatGenePlot3D\(\)](#), [spatGenePlot\(\)](#)

Examples

spatGenePlot2D(gobject)

| | |
|----------------|-----------------------|
| spatGenePlot3D | <i>spatGenePlot3D</i> |
|----------------|-----------------------|

Description

Visualize cells and gene expression according to spatial coordinates

Usage

```

spatGenePlot3D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  show_network = FALSE,
  network_color = NULL,
  spatial_network_name = "Delaunay_network",
  edge_alpha = NULL,
  cluster_column = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  show_grid = FALSE,
  spatial_grid_name = "spatial_grid",
  point_size = 2,
  show_legend = TRUE,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatGenePlot3D"
)

```

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>expression_values</code> | gene expression values to use |
| <code>genes</code> | genes to show |
| <code>show_network</code> | show underlying spatial network |
| <code>network_color</code> | color of spatial network |
| <code>spatial_network_name</code> | name of spatial network to use |
| <code>edge_alpha</code> | alpha of edges |
| <code>cluster_column</code> | cluster column to select groups |
| <code>select_cell_groups</code> | select subset of cells/clusters based on <code>cell_color</code> parameter |
| <code>select_cells</code> | select subset of cells based on cell IDs |

| | |
|-------------------|--|
| show_other_cells | display not selected cells |
| other_cell_color | color of not selected cells |
| other_point_size | size of not selected cells |
| genes_high_color | color represents high gene expression |
| genes_mid_color | color represents middle gene expression |
| genes_low_color | color represents low gene expression |
| show_grid | show spatial grid |
| spatial_grid_name | name of spatial grid to use |
| point_size | size of point (cell) |
| show_legend | show legend |
| axis_scale | the way to scale the axis |
| custom_ratio | customize the scale of the plot |
| x_ticks | set the number of ticks on the x-axis |
| y_ticks | set the number of ticks on the y-axis |
| z_ticks | set the number of ticks on the z-axis |
| show_plot | show plots |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

ggplot

See Also

Other spatial gene expression visualizations: [spatGenePlot2D\(\)](#), [spatGenePlot\(\)](#)

Examples

```
spatGenePlot3D(gobject)
```

| | |
|------------|-------------------|
| spatialAEH | <i>spatialAEH</i> |
|------------|-------------------|

Description

Compute spatial variable genes with spatialDE method

Usage

```
spatialAEH(  
  gobject = NULL,  
  SpatialDE_results = NULL,  
  name_pattern = "AEH_patterns",  
  expression_values = c("raw", "normalized", "scaled", "custom"),  
  pattern_num = 6,  
  l = 1.05,  
  python_path = NULL,  
  return_gobject = TRUE  
)
```

Arguments

- gobject Giotto object
- SpatialDE_results results of [SpatialDE](#) function
- name_pattern name for the computed spatial patterns
- expression_values gene expression values to use
- pattern_num number of spatial patterns to look for
- l lengthscale
- python_path specify specific path to python if required
- return_gobject show plot

Details

This function is a wrapper for the SpatialAEH method implemented in the ...

Value

An updated giotto object

spatialDE

*spatialDE***Description**

Compute spatial variable genes with spatialDE method

Usage

```
spatialDE(
  gobject = NULL,
  expression_values = c("raw", "normalized", "scaled", "custom"),
  size = c(4, 2, 1),
  color = c("blue", "green", "red"),
  sig_alpha = 0.5,
  unsig_alpha = 0.5,
  python_path = NULL,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "SpatialDE"
)
```

Arguments

| | |
|--------------------------------|--|
| <code>gobject</code> | Giotto object |
| <code>expression_values</code> | gene expression values to use |
| <code>size</code> | size of plot |
| <code>color</code> | low/medium/high color scheme for plot |
| <code>sig_alpha</code> | alpha value for significance |
| <code>unsig_alpha</code> | alpha value for unsignificance |
| <code>python_path</code> | specify specific path to python if required |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters, see showSaveParameters |
| <code>default_save_name</code> | default save name for saving, don't change, change save_name in save_param |

Details

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

Value

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

spatNetwDistributions *spatNetwDistributionsDistance*

Description

This function return histograms displaying the distance distribution for each spatial k-neighbor

Usage

```
spatNetwDistributions(
  gobject,
  spatial_network_name = "spatial_network",
  distribution = c("distance", "k_neighbors"),
  hist_bins = 30,
  test_distance_limit = NULL,
  ncol = 1,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatNetwDistributions"
)
```

Arguments

| | |
|-----------------------------------|--|
| <code>gobject</code> | Giotto object |
| <code>spatial_network_name</code> | name of spatial network |
| <code>distribution</code> | show the distribution of cell-to-cell distance or number of k neighbors |
| <code>hist_bins</code> | number of binds to use for the histogram |
| <code>test_distance_limit</code> | effect of different distance threshold on k-neighbors |
| <code>ncol</code> | number of columns to visualize the histograms in |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters from all_plots_save_function |
| <code>default_save_name</code> | default save name for saving, alternatively change <code>save_name</code> in <code>save_param</code> |

Details

The **distance** option shows the spatial distance distribution for each nearest neighbor rank (1st, 2nd, 3th, ... neighbor). 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 neighbor 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

| | |
|-----------------------------------|--|
| <code>gobject</code> | Giotto object |
| <code>spatial_network_name</code> | name of spatial network |
| <code>hist_bins</code> | number of binds to use for the histogram |
| <code>test_distance_limit</code> | effect of different distance threshold on k-neighbors |
| <code>ncol</code> | number of columns to visualize the histograms in |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters from all_plots_save_function |
| <code>default_save_name</code> | default save name for saving, alternatively change <code>save_name</code> in <code>save_param</code> |

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

| | |
|-----------------------------------|--|
| <code>gobject</code> | Giotto object |
| <code>spatial_network_name</code> | name of spatial network |
| <code>hist_bins</code> | number of binds to use for the histogram |
| <code>show_plot</code> | show plot |
| <code>return_plot</code> | return ggplot object |
| <code>save_plot</code> | directly save the plot [boolean] |
| <code>save_param</code> | list of saving parameters from all_plots_save_function |
| <code>default_save_name</code> | default save name for saving, alternatively change <code>save_name</code> in <code>save_param</code> |

Value

ggplot plot

Examples

```
spatNetwDistributionsKneighbors(gobject)
```

spatPlot

spatPlot

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot(...)
```

Arguments

```
...           Arguments passed on to spatPlot2D
gobject      giotto object
show_image   show a tissue background image
gimage       a giotto image
image_name   name of a giotto image
group_by     create multiple plots based on cell annotation column
group_by_subset subset the group_by factor column
sdimx        x-axis dimension name (default = 'sdimx')
sdimy        y-axis dimension name (default = 'sdimy')
spat_enr_names names of spatial enrichment results to include
cell_color   color for cells (see details)
color_as_factor convert color column to factor
cell_color_code named vector with colors
cell_color_gradient vector with 3 colors for numeric data
gradient_midpoint midpoint for color gradient
gradient_limits vector with lower and upper limits
select_cell_groups select subset of cells/clusters based on cell_color parameter
select_cells select subset of cells based on cell IDs
point_shape  shape of points (border, no_border or voronoi)
point_size   size of point (cell)
point_alpha  transparency of point
point_border_col color of border around points
point_border_stroke stroke size of border around points
show_cluster_center plot center of selected clusters
show_center_label plot label of selected clusters
center_point_size size of center points
center_point_border_col border color of center points
center_point_border_stroke border stroke size of center points
label_size   size of labels
label_fontface font of labels
show_network  show underlying spatial network
spatial_network_name name of spatial network to use
```

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

Details

Description of parameters.

Value

ggplot

See Also

[spatPlot3D](#)

Other spatial visualizations: [spatPlot2D\(\)](#), [spatPlot3D\(\)](#)

Examples

```
spatPlot(gobject)
```

spatPlot2D

spatPlot2D

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot2D(
  gobject,
  show_image = F,
  gimage = NULL,
  image_name = "image",
  group_by = NULL,
  group_by_subset = NULL,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spat_enr_names = NULL,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_shape = c("border", "no_border", "voronoi"),
  point_size = 3,
  point_alpha = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_cluster_center = F,
  show_center_label = F,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  show_network = F,
  spatial_network_name = "Delaunay_network",
  network_color = NULL,
  network_alpha = 1,
  show_grid = F,
  spatial_grid_name = "spatial_grid",
  grid_color = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1,
  other_cells_alpha = 0.1,
  coord_fix_ratio = NULL,
```



```

    title = NULL,
    show_legend = T,
    legend_text = 8,
    legend_symbol_size = 1,
    background_color = "white",
    vor_border_color = "white",
    vor_max_radius = 200,
    vor_alpha = 1,
    axis_text = 8,
    axis_title = 8,
    cow_n_col = 2,
    cow_rel_h = 1,
    cow_rel_w = 1,
    cow_align = "h",
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spatPlot2D"
)

```

Arguments

| | |
|----------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>show_image</code> | show a tissue background image |
| <code>gimage</code> | a giotto image |
| <code>image_name</code> | name of a giotto image |
| <code>group_by</code> | create multiple plots based on cell annotation column |
| <code>group_by_subset</code> | subset the <code>group_by</code> factor column |
| <code>sdimx</code> | x-axis dimension name (default = 'sdimx') |
| <code>sdimy</code> | y-axis dimension name (default = 'sdimy') |
| <code>spat_enr_names</code> | names of spatial enrichment results to include |
| <code>cell_color</code> | color for cells (see details) |
| <code>color_as_factor</code> | convert color column to factor |
| <code>cell_color_code</code> | named vector with colors |
| <code>cell_color_gradient</code> | vector with 3 colors for numeric data |
| <code>gradient_midpoint</code> | midpoint for color gradient |
| <code>gradient_limits</code> | vector with lower and upper limits |
| <code>select_cell_groups</code> | select subset of cells/clusters based on <code>cell_color</code> parameter |
| <code>select_cells</code> | select subset of cells based on cell IDs |
| <code>point_shape</code> | shape of points (border, no_border or voronoi) |
| <code>point_size</code> | size of point (cell) |

| | |
|----------------------------|-------------------------------------|
| point_alpha | transparancy of point |
| point_border_col | color of border around points |
| point_border_stroke | stroke size of border around points |
| show_cluster_center | plot center of selected clusters |
| show_center_label | plot label of selected clusters |
| center_point_size | size of center points |
| center_point_border_col | border color of center points |
| center_point_border_stroke | border stroke size of center points |
| label_size | size of labels |
| label_fontface | font of labels |
| show_network | show underlying spatial network |
| spatial_network_name | name of spatial network to use |
| network_color | color of spatial network |
| network_alpha | alpha of spatial network |
| show_grid | show spatial grid |
| spatial_grid_name | name of spatial grid to use |
| grid_color | color of spatial grid |
| show_other_cells | display not selected cells |
| other_cell_color | color of not selected cells |
| other_point_size | point size of not selected cells |
| other_cells_alpha | alpha of not selected cells |
| coord_fix_ratio | fix ratio between x and y-axis |
| title | title of plot |
| show_legend | show legend |
| legend_text | size of legend text |
| legend_symbol_size | size of legend symbols |
| background_color | color of plot background |
| vor_border_color | border color for voronoi plot |
| vor_max_radius | maximum radius for voronoi 'cells' |

| | |
|-------------------|--|
| vor_alpha | transparancy of voronoi 'cells' |
| axis_text | size of axis text |
| axis_title | size of axis title |
| cow_n_col | cowplot param: how many columns |
| cow_rel_h | cowplot param: relative height |
| cow_rel_w | cowplot param: relative width |
| cow_align | cowplot param: how to align |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Details

Description of parameters.

Value

ggplot

See Also

[spatPlot3D](#)
Other spatial visualizations: [spatPlot3D\(\)](#), [spatPlot\(\)](#)

Examples

spatPlot2D(gobject)

| | |
|------------|-------------------|
| spatPlot3D | <i>spatPlot3D</i> |
|------------|-------------------|

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot3D(  
  gobject,  
  sdimx = "sdimx",  
  sdimy = "sdimy",  
  sdimz = "sdimz",  
  spat_enr_names = NULL,  
  point_size = 3,  
  cell_color = NULL,
```

```

cell_color_code = NULL,
select_cell_groups = NULL,
select_cells = NULL,
show_other_cells = T,
other_cell_color = "lightgrey",
other_point_size = 0.5,
other_cell_alpha = 0.5,
show_network = F,
spatial_network_name = "Delaunay_network",
network_color = NULL,
network_alpha = 1,
show_grid = F,
spatial_grid_name = "spatial_grid",
grid_color = NULL,
grid_alpha = 1,
title = "",
show_legend = T,
axis_scale = c("cube", "real", "custom"),
custom_ratio = NULL,
x_ticks = NULL,
y_ticks = NULL,
z_ticks = NULL,
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spat3D"
)

```

Arguments

| | |
|---------------------------------|--|
| <code>gobject</code> | giotto object |
| <code>sdimx</code> | x-axis dimension name (default = 'sdimx') |
| <code>sdimy</code> | y-axis dimension name (default = 'sdimy') |
| <code>sdimz</code> | z-axis dimension name (default = 'sdimy') |
| <code>spat_enr_names</code> | names of spatial enrichment results to include |
| <code>point_size</code> | size of point (cell) |
| <code>cell_color</code> | color for cells (see details) |
| <code>cell_color_code</code> | named vector with colors |
| <code>select_cell_groups</code> | select subset of cells/clusters based on <code>cell_color</code> parameter |
| <code>select_cells</code> | select subset of cells based on cell IDs |
| <code>show_other_cells</code> | display not selected cells |
| <code>other_cell_color</code> | color of not selected cells |
| <code>other_point_size</code> | size of not selected cells |

| | |
|----------------------|--|
| other_cell_alpha | alpha of not selected cells |
| show_network | show underlying spatial network |
| spatial_network_name | name of spatial network to use |
| network_color | color of spatial network |
| network_alpha | opacity of spatial network |
| show_grid | show spatial grid |
| spatial_grid_name | name of spatial grid to use |
| grid_color | color of spatial grid |
| grid_alpha | opacity of spatial grid |
| title | title of plot |
| show_legend | show legend |
| axis_scale | the way to scale the axis |
| custom_ratio | customize the scale of the plot |
| x_ticks | set the number of ticks on the x-axis |
| y_ticks | set the number of ticks on the y-axis |
| z_ticks | set the number of ticks on the z-axis |
| show_plot | show plot |
| return_plot | return ggplot object |
| save_plot | directly save the plot [boolean] |
| save_param | list of saving parameters, see showSaveParameters |
| default_save_name | default save name for saving, don't change, change save_name in save_param |

Value

ggplot

See Also

Other spatial visualizations: [spatPlot2D\(\)](#), [spatPlot\(\)](#)

Examples

```
spatPlot3D(gobject)
```

```
specificCellCellcommunicationScores
      specificCellCellcommunicationScores
```

Description

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

Usage

```
specificCellCellcommunicationScores(
  gobject,
  spatial_network_name = "Delaunay_network",
  cluster_column = "cell_types",
  random_iter = 100,
  cell_type_1 = "astrocyte",
  cell_type_2 = "endothelial",
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  min_observations = 2,
  detailed = FALSE,
  adjust_method = c("fdr", "bonferroni", "BH", "holm", "hochberg", "hommel", "BY",
    "none"),
  adjust_target = c("genes", "cells"),
  verbose = T
)
```

Arguments

| | |
|-----------------------------------|---|
| <code>gobject</code> | giotto object to use |
| <code>spatial_network_name</code> | spatial network to use for identifying interacting cells |
| <code>cluster_column</code> | cluster column with cell type information |
| <code>random_iter</code> | number of iterations |
| <code>cell_type_1</code> | first cell type |
| <code>cell_type_2</code> | second cell type |
| <code>gene_set_1</code> | first specific gene set from gene pairs |
| <code>gene_set_2</code> | second specific gene set from gene pairs |
| <code>log2FC_addendum</code> | addendum to add when calculating log2FC |
| <code>min_observations</code> | minimum number of interactions needed to be considered |
| <code>detailed</code> | provide more detailed information (random variance and z-score) |
| <code>adjust_method</code> | which method to adjust p-values |
| <code>adjust_target</code> | adjust multiple hypotheses at the cell or gene level |
| <code>verbose</code> | verbose |

Details

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

- LR_comb: Pair of ligand and receptor
- lig_cell_type: cell type to assess expression level of ligand
- lig_expr: average expression of ligand in lig_cell_type
- ligand: ligand name
- rec_cell_type: cell type to assess expression level of receptor
- rec_expr: average expression of receptor in rec_cell_type
- receptor: receptor name
- LR_expr: combined average ligand and receptor expression
- lig_nr: total number of cells from lig_cell_type that spatially interact with cells from rec_cell_type
- rec_nr: total number of cells from rec_cell_type that spatially interact with cells from lig_cell_type
- rand_expr: average combined ligand and receptor expression from random spatial permutations
- av_diff: average difference between LR_expr and rand_expr over all random spatial permutations
- sd_diff: (optional) standard deviation of the difference between LR_expr and rand_expr over all random spatial permutations
- z_score: (optional) z-score
- log2fc: log2 fold-change (LR_expr/rand_expr)
- pvalue: p-value
- LR_cell_comb: cell type pair combination
- p.adj: adjusted p-value
- PI: significanc score: $\log_2fc * -\log_{10}(p.adj)$

Value

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

Examples

```
specificCellCellcommunicationScores(gobject)
```

stitchFieldCoordinates

stitchFieldCoordinates

Description

Helper function to stitch field coordinates together to form one complete picture

Usage

```
stitchFieldCoordinates(
  location_file,
  offset_file,
  cumulate_offset_x = F,
  cumulate_offset_y = F,
  field_col = "Field of View",
  X_coord_col = "X",
  Y_coord_col = "Y",
  reverse_final_x = F,
  reverse_final_y = T
)
```

Arguments

| | |
|-------------------|--|
| location_file | location dataframe with X and Y coordinates |
| offset_file | dataframe that describes the offset for each field (see details) |
| cumulate_offset_x | (boolean) Do the x-axis offset values need to be cumulated? |
| cumulate_offset_y | (boolean) Do the y-axis offset values need to be cumulated? |
| field_col | column that indicates the field within the location_file |
| X_coord_col | column that indicates the x coordinates |
| Y_coord_col | column that indicates the x coordinates |
| reverse_final_x | (boolean) Do the final x coordinates need to be reversed? |
| reverse_final_y | (boolean) Do the final y coordinates need to be reversed? |

Details

Stitching of fields:

- 1. have cell locations: at least 3 columns: field, X, Y
- 2. create offset file: offset file has 3 columns: field, x_offset, y_offset
- 3. create new cell location file by stitching original cell locations with stitchFieldCoordinates
- 4. provide new cell location file to [createGiottoObject](#)

Value

Updated location dataframe with new X ['X_final'] and Y ['Y_final'] coordinates

stitchTileCoordinates *stitchTileCoordinates*

Description

Helper function to stitch tile coordinates together to form one complete picture

Usage

```
stitchTileCoordinates(location_file, Xtilespan, Ytilespan)
```

Arguments

| | |
|---------------|--|
| location_file | location dataframe with X and Y coordinates |
| Xtilespan | numerical value specifying the width of each tile |
| Ytilespan | numerical value specifying the height of each tile |

subClusterCells *subClusterCells*

Description

subcluster cells

Usage

```
subClusterCells(
  gobject,
  name = "sub_clus",
  cluster_method = c("leiden", "louvain_community", "louvain_multinet"),
  cluster_column = NULL,
  selected_clusters = NULL,
  hvg_param = list(reverse_log_scale = T, difference_in_cov = 1, expression_values =
    "normalized"),
  hvg_min_perc_cells = 5,
  hvg_mean_expr_det = 1,
  use_all_genes_as_hvg = FALSE,
  min_nr_of_hvg = 5,
  pca_param = list(expression_values = "normalized", scale_unit = T),
  nn_param = list(dimensions_to_use = 1:20),
  k_neighbors = 10,
  resolution = 1,
  n_iterations = 1000,
  gamma = 1,
  omega = 1,
  python_path = NULL,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  return_gobject = TRUE,
  verbose = T
)
```

Arguments

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

| | |
|-----------------------------|----------------------|
| <code>gobject</code> | giotto object |
| <code>x_max</code> | maximum x-coordinate |
| <code>x_min</code> | minimum x-coordinate |
| <code>y_max</code> | maximum y-coordinate |
| <code>y_min</code> | minimum y-coordinate |
| <code>z_max</code> | maximum z-coordinate |
| <code>z_min</code> | minimum z-coordinate |
| <code>return_gobject</code> | return Giotto object |
| <code>verbose</code> | be verbose |

Details

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

Value

giotto object

Examples

```
subsetGiottoLocs(gobject)
```

| | |
|-------------------------|-------------------|
| <code>trendSceek</code> | <i>trendSceek</i> |
|-------------------------|-------------------|

Description

Compute spatial variable genes with trendsceek method

Usage

```
trendSceek(  
  gobject,  
  expression_values = c("normalized", "raw"),  
  subset_genes = NULL,  
  nrand = 100,  
  ncores = 8,  
  ...  
)
```

Arguments

| | |
|--------------------------------|---|
| <code>gobject</code> | Giotto object |
| <code>expression_values</code> | gene expression values to use |
| <code>subset_genes</code> | subset of genes to run trendsceek on |
| <code>nrand</code> | An integer specifying the number of random resamplings of the mark distribution as to create the null-distribution. |
| <code>ncores</code> | An integer specifying the number of cores to be used by BiocParallel |
| <code>...</code> | 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

| | |
|-------------------|--------------------------|
| updateGiottoImage | <i>updateGiottoImage</i> |
|-------------------|--------------------------|

Description

Updates the boundaries of a giotto image attached to a giotto object

Usage

```
updateGiottoImage(
  gobject,
  image_name,
  xmax_adj = 0,
  xmin_adj = 0,
  ymax_adj = 0,
  ymin_adj = 0,
  return_gobject = TRUE
)
```

Arguments

| | |
|----------------|--|
| gobject | giotto object |
| image_name | spatial locations |
| xmax_adj | adjustment of the maximum x-value to align the image |
| xmin_adj | adjustment of the minimum x-value to align the image |
| ymax_adj | adjustment of the maximum y-value to align the image |
| ymin_adj | adjustment of the minimum y-value to align the image |
| return_gobject | return a giotto object |

Value

a giotto object or an updated giotto image if return_gobject = F

Examples

```
updateGiottoImage(gobject)
```

| | |
|----------------|-----------------------|
| viewHMRResults | <i>viewHMRResults</i> |
|----------------|-----------------------|

Description

View results from doHMRF.

Usage

```
viewHMRResults(  
  gobject,  
  HMRFoutput,  
  k = NULL,  
  betas_to_view = NULL,  
  third_dim = FALSE,  
  ...  
)
```

Arguments

| | |
|---------------|--|
| gobject | giotto object |
| HMRFoutput | HMRF output from doHMRF |
| k | number of HMRF domains |
| betas_to_view | results from different betas that you want to view |
| third_dim | 3D data (boolean) |
| ... | additional paramters (see details) |

Value

spatial plots with HMRF domains

See Also

[spatPlot2D](#) and [spatPlot3D](#)

| | |
|------------------|-------------------------|
| viewHMRResults2D | <i>viewHMRResults2D</i> |
|------------------|-------------------------|

Description

View results from doHMRF.

Usage

```
viewHMRResults2D(gobject, HMRFoutput, k = NULL, betas_to_view = NULL, ...)
```

Arguments

| | |
|----------------------------|--|
| <code>gobject</code> | giotto object |
| <code>HMRFoutput</code> | HMRF output from doHMRF |
| <code>k</code> | number of HMRF domains |
| <code>betas_to_view</code> | results from different betas that you want to view |
| <code>...</code> | additional parameters to <code>spatPlot2D()</code> |

Value

spatial plots with HMRF domains

See Also

[spatPlot2D](#)

| | |
|--------------------------------|---------------------------------------|
| <code>viewHMRFresults3D</code> | <i><code>viewHMRFresults3D</code></i> |
|--------------------------------|---------------------------------------|

Description

View results from doHMRF.

Usage

```
viewHMRFresults3D(gobject, HMRFoutput, k = NULL, betas_to_view = NULL, ...)
```

Arguments

| | |
|----------------------------|--|
| <code>gobject</code> | giotto object |
| <code>HMRFoutput</code> | HMRF output from doHMRF |
| <code>k</code> | number of HMRF domains |
| <code>betas_to_view</code> | results from different betas that you want to view |
| <code>...</code> | additional parameters to <code>spatPlot3D()</code> |

Value

spatial plots with HMRF domains

See Also

[spatPlot3D](#)

violinPlot

violinPlot

Description

Creates violinplot for selected clusters

Usage

```
violinPlot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  cluster_column,
  cluster_custom_order = NULL,
  color_violin = c("genes", "cluster"),
  cluster_color_code = NULL,
  strip_position = c("top", "right", "left", "bottom"),
  strip_text = 7,
  axis_text_x_size = 10,
  axis_text_y_size = 6,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "violinPlot"
)
```

Arguments

| | |
|----------------------|---|
| gobject | giotto object |
| expression_values | expression values to use |
| genes | genes to plot |
| cluster_column | name of column to use for clusters |
| cluster_custom_order | custom order of clusters |
| color_violin | color violin according to genes or clusters |
| cluster_color_code | color code for clusters |
| strip_position | position of gene labels |
| strip_text | size of strip text |
| axis_text_x_size | size of x-axis text |
| axis_text_y_size | size of y-axis text |
| show_plot | show plot |
| return_plot | return ggplot object |

save_plot directly save the plot [boolean]
 save_param list of saving parameters, see [showSaveParameters](#)
 default_save_name default save name for saving, don't change, change save_name in save_param

Value

ggplot

Examples

```
violinPlot(gobject)
```

| | |
|-----------------|------------------------|
| writeHMRResults | <i>writeHMRResults</i> |
|-----------------|------------------------|

Description

write results from doHMRF to a data.table.

Usage

```
writeHMRResults(
  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

```
writeHMRResults(gobject)
```

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