

# Package ‘Giotto’

February 7, 2020

**Title** Spatial single-cell transcriptomics pipeline.

**Version** 0.1.5

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

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**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.1

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

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

Rcpp,  
rlang ( $\geq 0.4.3$ )

**Suggests** knitr,  
rmarkdown,  
MAST,  
scrn ( $\geq 1.10.1$ ),  
png,  
tiff,  
biomaRt,  
trendsceek,  
multinet ( $\geq 3.0.2$ )

**biocViews**

**VignetteBuilder** knitr

**LinkingTo** Rcpp,  
RcppArmadillo

**Remotes** lambdamoses/smfishhmr-f-r

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---

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

---

## Description

adds cell metadata to the giotto object

## Usage

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

## Arguments

gobject	giotto object
new_metadata	new cell metadata to use (data.table, data.frame, ...)
by_column	merge metadata based on cell_ID column in pDataDT (default = FALSE)
column_cell_ID	column name of new metadata to use if by_column = TRUE

## Details

You can add additional cell metadata in two manners: 1. Provide a data.table or data.frame with cell annotations in the same order as the cell\_ID column in pDataDT(gobject) 2. Provide a data.table or data.frame with cell annotations and 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**

**gobject**            giotto object

**expression\_values**  
                    expression values to use

**detection\_threshold**  
                    detection threshold to consider a gene detected

**return\_gobject**   boolean: return giotto object (default = TRUE)

**Details**

This function will add the following statistics to cell metadata:

- **nr\_genes**: Denotes in how many genes are detected per cell
- **perc\_genes**: Denotes what percentage of genes is detected per cell
- **total\_expr**: Shows the total sum of gene expression per cell

**Value**

giotto object if return\_gobject = TRUE

**Examples**

```
addCellStatistics(gobject)
```



---

addGeneMetadata	<i>addGeneMetadata</i>
-----------------	------------------------

---

### Description

adds gene metadata to the giotto object

### Usage

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

### Arguments

<code>gobject</code>	giotto object
<code>new_metadata</code>	new metadata to use
<code>by_column</code>	merge metadata based on gene_ID column in fDataDT
<code>column_cell_ID</code>	column name of new metadata to use if <code>by_column = TRUE</code>

### 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)
```

---

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)
```

---

 addHMRF

*addHMRF*


---

**Description**

Add selected results from doHMRF to the giotto object

**Usage**

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

**Arguments**

gobject            giotto object  
 HMRFOutput        HMRF output from doHMRF()  
 k                   number of domains  
 betas\_to\_add       results from different betas that you want to add  
 name                specify a custom name

**Details**

Description ...

**Value**

giotto object

**Examples**

```
addHMRF(gobject)
```

---

addNetworkLayout	<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**

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

**Details**

This function creates layout coordinates based on the provided kNN or sNN. Currently only the force-directed graph layout "drl", see [layout\\_with\\_drl](#), is implemented. This provides an alternative to tSNE or UMAP based visualizations.

**Value**

giotto object with updated layout for selected NN network

**Examples**

```
addNetworkLayout(gobject)
```

---

addStatistics	<i>addStatistics</i>
---------------	----------------------

---

### Description

adds genes and cells statistics to the giotto object

### Usage

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

### Arguments

gobject            giotto object

expression\_values  
                  expression values to use

detection\_threshold  
                  detection threshold to consider a gene detected

return\_gobject    boolean: return giotto object (default = TRUE)

### Details

See [addGeneStatistics](#) and [addCellStatistics](#)

### Value

giotto object if return\_gobject = TRUE, else a list with results

### Examples

```
addStatistics(gobject)
```

---

adjustGiottoMatrix	<i>adjustGiottoMatrix</i>
--------------------	---------------------------

---

### Description

normalize and/or scale expresion values of Giotto object

**Usage**

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

**Arguments**

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

**Details**

This function implements the [limma::removeBatchEffect](#) function to remove known batch effects and to adjust expression values according to provided covariates.

**Value**

giotto object

**Examples**

```
adjustGiottoMatrix(gobject)
```

---

aes\_string2

*aes\_string2*

---

**Description**

makes sure aes\_string can also be used with names that start with numeric values

**Usage**

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

---

```
allCellCellcommunicationsScores
      allCellCellcommunicationsScores
```

---

## Description

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

## Usage

```
allCellCellcommunicationsScores(
  gobject,
  spatial_network_name = "spatial_network",
  cluster_column = "cell_types",
  random_iter = 100,
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  min_observations = 2,
  verbose = c("a little", "a lot", "none")
)
```

## 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>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>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.. More details will follow soon.

## Value

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

## Examples

```
allCellCellcommunicationsScores(gobject)
```

---

```
all_plots_save_function
    all_plots_save_function
```

---

## Description

Function to automatically save plots to directory of interest

## Usage

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

## Arguments

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

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

**See Also**

[general\\_save\\_function](#)

**Examples**

```
all_plots_save_function(gobject)
```

---

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

---

**Description**

Converts cluster results into provided annotation.

**Usage**

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

**Arguments**

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

**Details**

You need to 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)
```

---

```
annotateSpatialNetwork
```

```
annotateSpatialNetwork
```

---

## Description

Annotate spatial network with cell metadata information.

## Usage

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

## Arguments

gobject            giotto object  
spatial\_network\_name            name of spatial network to use  
cluster\_column    name of column to use for clusters

## Value

annotated network in data.table format

## Examples

```
annotateSpatialNetwork(gobject)
```

---

```
annotate_spatlocs_with_spatgrid_2D
```

```
annotate_spatlocs_with_spatgrid_2D
```

---

## Description

annotate spatial locations with 2D spatial grid information

## Usage

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

## Arguments

spatloc            spatial\_locs slot from giotto object  
spatgrid           selected spatial\_grid slot from giotto object

**Value**

annotated spatial location data.table

**Examples**

```
annotate_spatlocs_with_spatgrid_2D()
```

---

```
annotate_spatlocs_with_spatgrid_3D
```

```
annotate_spatlocs_with_spatgrid_3D
```

---

**Description**

annotate spatial locations with 3D spatial grid information

**Usage**

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

**Arguments**

spatloc            spatial\_locs slot from giotto object

spatgrid          selected spatial\_grid slot from giotto object

**Value**

annotated spatial location data.table

**Examples**

```
annotate_spatlocs_with_spatgrid_3D()
```

---

```
average_gene_gene_expression_in_groups
```

```
average_gene_gene_expression_in_groups
```

---

**Description**

calculate average expression per cluster

**Usage**

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

**Arguments**

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

**Details**

Details will follow soon.

**Value**

data.table with average expression scores for each cluster

**Examples**

```
average_gene_gene_expression_in_groups(gobject)
```

---

<code>binGetSpatialGenes</code>	<i>binGetSpatialGenes</i>
---------------------------------	---------------------------

---

**Description**

Rapid computation of genes that are spatially clustered

**Usage**

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

**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>nstart</code>	kmeans: nstart parameter
<code>iter_max</code>	kmeans: iter.max parameter
<code>percentage_rank</code>	percentage of top cells for binarization
<code>do_fisher_test</code>	perform fisher test
<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>do_parallel</code>	run calculations in parallel with mclapply
<code>cores</code>	number of cores to use if <code>do_parallel = TRUE</code>
<code>verbose</code>	be verbose

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

Additionally 2 other statistics are provided (optional):

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

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

**Value**

data.table with results (see details)

**Examples**

```
binGetSpatialGenes(gobject)
```

---

binGetSpatialGenesOld *binGetSpatialGenesOld*


---

## Description

Rapid computation of genes that are spatially clustered

## Usage

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

## Arguments

<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>nstart</code>	kmeans: nstart parameter
<code>iter_max</code>	kmeans: iter.max parameter
<code>do_fisher_test</code>	perform fisher test
<code>community_expectation</code>	cell degree expectation in spatial communities
<code>verbose</code>	be verbose
<code>rank_percentage</code>	percentage of top cells for binarization

## 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 k-nearest neighbor network

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

Additionally 2 other statistics are provided:

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

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

### Value

data.table with results (see details)

### Examples

```
binGetSpatialGenesOld(gobject)
```

---

calculateHVG

*calculateHVG*

---

### Description

compute highly variable genes

### Usage

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

**Arguments**

<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 <a href="#">all_plots_save_function</a>
<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~log(mean expression)) Genes that show a higher than predicted COV (*difference\_in\_cov*) are considered highly variable.

**Value**

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

**Examples**

```
calculateHVG(gobject)
```

---

calculateMetaTable	<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**

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

**Value**

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

**Examples**

```
calculateMetaTable(gobject)
```

---

calculateMetaTableCells	<i>calculateMetaTableCells</i>
-------------------------	--------------------------------

---

**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**

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

**Value**

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

**Examples**

```
calculateMetaTableCells(gobject)
```

---

```
calculate_spatial_genes_python
      calculate_spatial_genes_python
```

---

**Description**

Calculate spatial genes using distance matrix.

**Usage**

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

**Arguments**

<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

**Details**

Description of how we compute spatial pattern genes.

**Value**

data.table with spatial scores

**Examples**

```
calculate_spatial_genes_python(gobject)
```

---

cellProximityBarplot	<i>cellProximityBarplot</i>
----------------------	-----------------------------

---

**Description**

Create barplot from cell-cell proximity scores

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

ggplot barplot

**Examples**

```
cellProximityBarplot(CPscore)
```

---

```
cellProximityEnrichment
```

```
cellProximityEnrichment
```

---

**Description**

Compute cell-cell interaction enrichment (observed vs expected)

**Usage**

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

**Arguments**

```
gobject          giotto object
spatial_network_name
                  name of spatial network to use
cluster_column  name of column to use for clusters
number_of_simulations
                  number of simulations to create expected observations
```

**Details**

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

**Value**

List of cell Proximity scores (CPscores) in data.table format. The first data.table (raw\_sim\_table) shows the raw observations of both the original and simulated networks. The second data.table (enrichm\_res) shows the enrichment results.

**Examples**

```
cellProximityEnrichment(gobject)
```

---

cellProximityHeatmap    *cellProximityHeatmap*


---

## Description

Create heatmap from cell-cell proximity scores

## Usage

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

## Arguments

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

## Details

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

## Value

ggplot heatmap

**Examples**

```
cellProximityHeatmap(CPscore)
```

---

```
cellProximityNetwork    cellProximityNetwork
```

---

**Description**

Create network from cell-cell proximity scores

**Usage**

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

**Arguments**

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

edge_weight_range_enrichment	numerical vector of length 2 to rescale enriched edge weights
layout	layout algorithm to use to draw nodes and edges
only_show_enrichment_edges	show only the enriched pairwise scores
edge_width_range	range of edge width
node_size	size of nodes
node_text_size	size of node labels
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

### Details

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

### Value

igraph plot

### Examples

```
cellProximityNetwork(CPscore)
```

---

cellProximitySpatPlot *cellProximitySpatPlot*

---

### Description

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

### Usage

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

### Arguments

gobject	giotto object
interaction_name	cell-cell interaction name
cluster_column	cluster column with cell clusters
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')

cell_color	color for cells (see details)
cell_color_code	named vector with colors
color_as_factor	convert color column to factor
show_other_cells	decide if show cells not in network
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
coord_fix_ratio	fix ratio between x and y-axis
show_legend	show legend
point_size_select	size of selected points
point_select_border_col	border color of selected points
point_select_border_stroke	stroke size of selected points
point_size_other	size of other points
point_other_border_col	border color of other points
point_other_border_stroke	stroke size of other points
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

## Details

Description of parameters.

## Value

ggplot

## See Also

[cellProximitySpatPlot2D](#) and [cellProximitySpatPlot3D](#) for 3D

**Examples**

```
cellProximitySpatPlot(gobject)
```

---

```
cellProximitySpatPlot2D
```

```
cellProximitySpatPlot2D
```

---

**Description**

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

**Usage**

```
cellProximitySpatPlot2D(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = "sdimx",
  sdimy = "sdimy",
  cell_color = NULL,
  cell_color_code = NULL,
  color_as_factor = T,
  show_other_cells = F,
  show_network = F,
  show_other_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  coord_fix_ratio = 1,
  show_legend = T,
  point_size_select = 2,
  point_select_border_col = "black",
  point_select_border_stroke = 0.05,
  point_size_other = 1,
  point_alpha_other = 0.3,
  point_other_border_col = "lightgrey",
  point_other_border_stroke = 0.01,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "cellProximitySpatPlot2D"
)
```

**Arguments**

gobject	giotto object
interaction_name	cell-cell interaction name



cluster_column	cluster column with cell clusters
sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
cell_color	color for cells (see details)
cell_color_code	named vector with colors
color_as_factor	convert color column to factor
show_other_cells	decide if show cells not in network
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
coord_fix_ratio	fix ratio between x and y-axis
show_legend	show legend
point_size_select	size of selected points
point_select_border_col	border color of selected points
point_select_border_stroke	stroke size of selected points
point_size_other	size of other points
point_other_border_col	border color of other points
point_other_border_stroke	stroke size of other points
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

## Details

Description of parameters.

## Value

ggplot

**Examples**

```
cellProximitySpatPlot2D(gobject)
```

---

```
cellProximitySpatPlot3D
```

```
cellProximitySpatPlot2D
```

---

**Description**

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

**Usage**

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

**Arguments**

<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 underlying spatial network
<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
<code>point_size_select</code>	size of selected points
<code>point_size_other</code>	size of other points
<code>show_plot</code>	show plots
<code>return_plot</code>	return plotly object
<code>save_plot</code>	directly save the plot [boolean]
<code>save_param</code>	list of saving parameters from <a href="#">all_plots_save_function</a>
<code>default_save_name</code>	default save name for saving, don't change, change save_name in save_param

**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 = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  coord_fix_ratio = 1,
  show_legend = T,
  point_size_select = 2,
  point_select_border_col = "black",
  point_select_border_stroke = 0.05,
  point_size_other = 1,
  point_alpha_other = 0.3,
  point_other_border_col = "lightgrey",
  point_other_border_stroke = 0.01,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  plot_method = c("ggplot", "plotly"),
  ...
)
```

## Arguments

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

sdimx	x-axis dimension name (default = 'sdimx')
sdimy	y-axis dimension name (default = 'sdimy')
sdimz	z-axis dimension name (default = 'sdimz')
cell_color	color for cells (see details)
cell_color_code	named vector with colors
color_as_factor	convert color column to factor
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
coord_fix_ratio	fix ratio between x and y-axis
show_legend	show legend
point_size_select	size of selected points
point_select_border_col	border color of selected points
point_select_border_stroke	stroke size of selected points
point_size_other	size of other points
point_other_border_col	border color of other points
point_other_border_stroke	stroke size of other points

## Details

Description of parameters.

## Value

ggplot or plotly

## Examples

```
cellProximityVisPlot(gobject)
```

---

```
cellProximityVisPlot_2D_ggplot
      cellProximityVisPlot_2D_ggplot
```

---

## Description

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

## Usage

```
cellProximityVisPlot_2D_ggplot(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = NULL,
  sdimy = NULL,
  cell_color = NULL,
  cell_color_code = NULL,
  color_as_factor = T,
  show_other_cells = F,
  show_network = F,
  show_other_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  coord_fix_ratio = 1,
  show_legend = T,
  point_size_select = 2,
  point_select_border_col = "black",
  point_select_border_stroke = 0.05,
  point_size_other = 1,
  point_alpha_other = 0.3,
  point_other_border_col = "lightgrey",
  point_other_border_stroke = 0.01,
  ...
)
```

## Arguments

<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

color_as_factor	convert color column to factor
show_other_cells	decide if show cells not in network
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
coord_fix_ratio	fix ratio between x and y-axis
show_legend	show legend
point_size_select	size of selected points
point_select_border_col	border color of selected points
point_select_border_stroke	stroke size of selected points
point_size_other	size of other points
point_other_border_col	border color of other points
point_other_border_stroke	stroke size of other points

## Details

Description of parameters.

## Value

ggplot

## Examples

```
cellProximityVisPlot_2D_ggplot(gobject)
```

---

```
cellProximityVisPlot_2D_plotly
      cellProximityVisPlot_2D_plotly
```

---

## Description

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

## Usage

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

## Arguments

<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



color_as_factor	convert color column to factor
show_other_cells	decide if show cells not in network
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
show_legend	show legend
point_size_select	size of selected points
coord_fix_ratio	fix ratio between x and y-axis

**Details**

Description of parameters.

**Value**

plotly

**Examples**

```
cellProximityVisPlot_2D_plotly(gobject)
```

---

```
cellProximityVisPlot_3D_plotly
  cellProximityVisPlot_3D_plotly
```

---

**Description**

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

**Usage**

```
cellProximityVisPlot_3D_plotly(
  gobject,
  interaction_name = NULL,
  cluster_column = NULL,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  cell_color = NULL,
  cell_color_code = NULL,
```

```

    color_as_factor = T,
    show_other_cells = F,
    show_network = F,
    show_other_network = F,
    network_color = NULL,
    spatial_network_name = "spatial_network",
    show_grid = F,
    grid_color = NULL,
    spatial_grid_name = "spatial_grid",
    show_legend = T,
    point_size_select = 2,
    point_size_other = 1,
    point_alpha_other = 0.5,
    axis_scale = c("cube", "real", "custom"),
    custom_ratio = NULL,
    x_ticks = NULL,
    y_ticks = NULL,
    z_ticks = NULL,
    ...
)

```

### Arguments

<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 underlying spatial network
<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
<code>point_size_select</code>	size of selected points
<code>coord_fix_ratio</code>	fix ratio between x and y-axis

**Details**

Description of parameters.

**Value**

plotly

**Examples**

```
cellProximityVisPlot_3D_plotly(gobject)
```

---

changeGiottoInstructions  
*changeGiottoInstructions*

---

**Description**

Function to change one or more instructions from giotto object

**Usage**

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

**Arguments**

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

**Value**

named vector with giotto instructions

**Examples**

```
changeGiottoInstructions()
```

clusterCells

*clusterCells***Description**

cluster cells using a variety of different methods

**Usage**

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

```

    seed_number = 1234
)

```

### Arguments

gobject	giotto object
cluster_method	community cluster method to use
name	name for new clustering result
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
pyth_leid_resolution	resolution for leiden
pyth_leid_weight_col	column to use for weights
pyth_leid_part_type	partition type to use
pyth_leid_init_memb	initial membership
pyth_leid_iterations	number of iterations
pyth_louv_resolution	resolution for louvain
pyth_louv_weight_col	python louvain param: weight column
python_louv_random	python louvain param: random
python_path	specify specific path to python if required
louvain_gamma	louvain param: gamma or resolution
louvain_omega	louvain param: omega
walk_steps	randomwalk: number of steps
walk_clusters	randomwalk: number of clusters
walk_weights	randomwalk: weight column
sNNclust_k	SNNclust: k neighbors to use
sNNclust_eps	SNNclust: epsilon
sNNclust_minPts	SNNclust: min points
borderPoints	SNNclust: border points
expression_values	expression values to use
genes_to_use	= NULL,
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	name of reduction 'pca',
dimensions_to_use	dimensions to use

distance_method	distance method
km_centers	kmeans centers
km_iter_max	kmeans iterations
km_nstart	kmeans random starting points
km_algorithm	kmeans algorithm
hc_agglomeration_method	hierarchical clustering method
hc_k	hierachical number of clusters
hc_h	hierarchical tree cutoff
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

**Details**

Wrapper for the different clustering methods.

**Value**

giotto object with new clusters appended to cell metadata

**See Also**

[doLeidenCluster](#), [doLouvainCluster\\_community](#), [doLouvainCluster\\_multinet](#), [doLouvainCluster](#), [doRandomWalkCluster](#), [doSNNCluster](#), [doKmeans](#), [doHclust](#)

**Examples**

```
clusterCells(gobject)
```

---

clusterSpatialCorGenes

*clusterSpatialCorGenes*

---

**Description**

Cluster based on spatially correlated genes

**Usage**

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

**Arguments**

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

**Value**

spatCorObject or cluster results

**Examples**

```
clusterSpatialCorGenes(gobject)
```

---

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)
```

---

combine_ints_f	<i>combine_ints_f</i>
----------------	-----------------------

---

## Description

function to combine gene enrichment interactions

## Usage

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

## Arguments

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

## Value

Gene to gene scores in data.table format



---

```
convertEnsemblToGeneSymbol  
    convertEnsemblToGeneSymbol
```

---

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

This function requires that the biomaRt library is installed

**Value**

expression matrix with gene symbols as rownames

**Examples**

```
convertEnsemblToGeneSymbol(matrix)
```

---

```
createGiottoInstructions  
    createGiottoInstructions
```

---

**Description**

Function to set global instructions for giotto functions

**Usage**

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

**Arguments**

python_path	path to python binary to use
show_plot	print plot to console, default = TRUE
return_plot	return plot as object, default = TRUE
save_plot	automatically save plot, default = FALSE
save_dir	path to directory where to save plots
dpi	resolution for raster images
height	height of plots
width	width of plots

**Value**

named vector with giotto instructions

**Examples**

```
createGiottoInstructions()
```

---

createGiottoObject	<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,
  offset_file = NULL,
  instructions = NULL
)
```

**Arguments**

raw_exprs	matrix with raw expression counts [required]
spatial_locs	data.table or data.frame with coordinates for cell centroids
norm_expr	normalized expression values
norm_scaled_expr	scaled expression values
custom_expr	custom expression values
cell_metadata	cell annotation metadata
gene_metadata	gene annotation metadata
spatial_network	list of spatial network(s)
spatial_network_name	list of spatial network name(s)
spatial_grid	list of spatial grid(s)
spatial_grid_name	list of spatial grid name(s)
spatial_enrichment	list of spatial enrichment score(s) for each spatial region
spatial_enrichment_name	list of spatial enrichment name(s)
dimension_reduction	list of dimension reduction(s)
nn_network	list of nearest neighbor network(s)
offset_file	file used to stitch fields together (optional)
instructions	list of instructions or output result from createGiottoInstructions

**Details**

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

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

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

**[Processed data]** Processed count data, such as normalized data, can be provided using one of the different expression slots (norm\_expr, norm\_scaled\_expr, custom\_expr).

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

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

- spatial networks
- spatial grids
- spatial enrichments
- dimensions reductions
- nearest neighbours networks

**Value**

giotto object

**Examples**

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

---

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

**Arguments**

gobject	giotto object
expression_values	expression values to use
genes	genes to use
cluster_column	name of column to use for clusters
cluster_order	method to determine cluster order
cluster_custom_order	custom order for clusters
cluster_cor_method	method for cluster correlation
cluster_hclust_method	method for hierarchical clustering of clusters
gene_order	method to determine gene order
gene_custom_order	custom order for genes
gene_cor_method	method for gene correlation
gene_hclust_method	method for hierarchical clustering of genes

**Details**

Creates input data.tables for plotHeatmap function.

**Value**

list

**Examples**

```
createHeatmap_DT(gobject)
```

---

createMetagenes	<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
<code>name</code>	arbitrary name for NN network
<code>return_gobject</code>	boolean: return giotto object (default = TRUE)
<code>k</code>	number of k neighbors to use
<code>minimum_shared</code>	minimum shared neighbors
<code>top_shared</code>	keep at ...
<code>verbose</code>	be verbose
<code>...</code>	additional parameters for kNN and sNN functions from dbscan

## Details

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

See also [kNN](#) and [sNN](#) for more information about how the networks are created.

Output for kNN:

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

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)
```

---

createSpatialEnrich	<i>createSpatialEnrich</i>
---------------------	----------------------------

---

## Description

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

**Usage**

```
createSpatialEnrich(
  gobject,
  enrich_method = c("PAGE", "rank", "hypergeometric"),
  sign_matrix,
  expression_values = c("normalized", "scaled", "custom"),
  reverse_log_scale = TRUE,
  logbase = 2,
  p_value = TRUE,
  n_genes = 100,
  n_times = 1000,
  top_percentage = 5,
  output_enrichment = c("original", "zscore"),
  name = "PAGE",
  return_gobject = TRUE
)
```

**Arguments**

<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 = TRUE)
<code>n_genes</code>	(page/rank) number of randomly selected genes for each permutation
<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: [PAGEEnrich](#)
- PAGE: [rankEnrich](#)
- PAGE: [hyperGeometricEnrich](#)

**Value**

Giotto object or enrichment results if `return_gobject = FALSE`



**Examples**

```
createSpatialEnrich(gobject)
```

---

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

---

**Description**

Create a spatial grid.

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

giotto object with updated spatial grid slot

**Examples**

```
createSpatialGrid(gobject)
```

---

createSpatialGrid_2D	<i>createSpatialGrid_2D</i>
----------------------	-----------------------------

---

### Description

create a spatial grid for 2D spatial data.

### Usage

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

### Arguments

<code>gobject</code>	giotto object
<code>sdimx_stepsize</code>	stepsize along the x-axis
<code>sdimy_stepsize</code>	stepsize along the y-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

### Examples

```
createSpatialGrid_2D(gobject)
```

---

`createSpatialGrid_3D`    *createSpatialGrid\_3D*

---

## Description

Create a spatial grid for 3D spatial data.

## Usage

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

## Arguments

<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

## Examples

```
createSpatialGrid_3D(gobject)
```

---

```
createSpatialNetwork    createSpatialNetwork
```

---

## Description

Create a spatial network based on cell centroid physical distances.

## Usage

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

## Arguments

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

## Details

Creates a spatial network connecting single-cells based on their physical distance to each other. Number of neighbors can be determined by `k`, maximum distance from each cell with or without setting a minimum `k` for each cell.

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

## 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      create_average_DT
```

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

data.table with average gene expression values for each factor

---

```
create_cell_type_random_cell_IDs  
      create_cell_type_random_cell_IDs
```

---

**Description**

creates randomized cell ids within a selection of cell types

**Usage**

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

**Arguments**

`gobject`                giotto object to use

`cluster_column`   cluster column with cell type information

`needed_cell_types`  
                      vector of cell type names for which a random id will be found

**Details**

Details will follow.

**Value**

list of randomly sampled cell ids with same cell type composition

**Examples**

```
create_cell_type_random_cell_IDs(gobject)
```

---

```
create_cluster_matrix  create_cluster_matrix
```

---

**Description**

creates aggregated matrix for a given clustering

**Usage**

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

**Examples**

```
create_cluster_matrix(gobject)
```

---

```
create_dimObject      create_dimObject
```

---

**Description**

Creates an object that stores a dimension reduction output

**Usage**

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

**Arguments**

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

**Value**

number of distinct colors

---

decide_cluster_order	<i>decide_cluster_order</i>
----------------------	-----------------------------

---

## Description

creates order for clusters

## Usage

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

## Arguments

gobject	giotto object
expression_values	expression values to use
genes	genes to use
cluster_column	name of column to use for clusters
cluster_order	method to determine cluster order
cluster_custom_order	custom order for clusters
cor_method	method for correlation
hclust_method	method for hierarchical clustering

## Details

Calculates order for clusters.

## Value

custom

## Examples

```
decide_cluster_order(gobject)
```



---

detectSpatialCorGenes *detectSpatialCorGenes*


---

## Description

Detect genes that are spatially correlated

## Usage

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

## Arguments

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

## Details

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

- 1. grid-averaging: average gene expression values within a predefined spatial grid
- 2. network-averaging: smoothens the gene expression matrix by averaging the expression within one cell by using the neighbours within the predefined spatial network. `b` is a smoothing 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,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  spat_enr_names = NULL,
  cell_annotation_values = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
```

```

edge_alpha = NULL,
point_shape = c("border", "no_border"),
point_size = 1,
point_border_col = "black",
point_border_stroke = 0.1,
show_legend = T,
legend_text = 8,
legend_symbol_size = 1,
background_color = "white",
axis_text = 8,
axis_title = 8,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "dimCellPlot"
)

```

### Arguments

<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_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

other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
title	title for plot, defaults to cell_color parameter

## Details

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

## Value

ggplot

**Examples**

```
dimCellPlot(gobject)
```

---

```
dimCellPlot2D
```

```
dimCellPlot2D
```

---

**Description**

Visualize cells according to dimension reduction coordinates

**Usage**

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

```

cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "dimCellPlot2D"
)

```

### Arguments

<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_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>label_size</code>	size of labels

label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
title	title for plot, defaults to cell_color parameter

## Details

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

## Value

ggplot

## Examples

```
dimCellPlot2D(gobject)
```



---

dimGenePlot

dimGenePlot

---

## Description

Visualize cells and gene expression according to dimension reduction coordinates

## Usage

```
dimGenePlot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  network_color = "lightgray",
  edge_alpha = NULL,
  scale_alpha_with_expression = FALSE,
  point_shape = c("border", "no_border"),
  point_size = 1,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  point_border_col = "black",
  point_border_stroke = 0.1,
  midpoint = 0,
  show_legend = T,
  legend_text = 8,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "dimGenePlot"
)
```

## Arguments

gobject                  giotto object

expression_values	gene expression values to use
genes	genes to show
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
edge_alpha	column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
midpoint	size of point (cell)
show_legend	show legend
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for cowplot::save_plot()

## Details

Description of parameters.

## Value

ggplot

## See Also

[dimGenePlot3D](#)

**Examples**

```
dimGenePlot(gobject)
```

---

dimGenePlot2D

*dimGenePlot2D*


---

**Description**

Visualize cells and gene expression according to dimension reduction coordinates

**Usage**

```
dimGenePlot2D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  network_color = "lightgray",
  edge_alpha = NULL,
  scale_alpha_with_expression = FALSE,
  point_shape = c("border", "no_border"),
  point_size = 1,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  point_border_col = "black",
  point_border_stroke = 0.1,
  midpoint = 0,
  show_legend = T,
  legend_text = 8,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "dimGenePlot2D"
)
```

**Arguments**

<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>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_border_col</code>	color of border around points
<code>point_border_stroke</code>	stroke size of border around points
<code>midpoint</code>	size of point (cell)
<code>show_legend</code>	show legend
<code>legend_text</code>	size of legend text
<code>background_color</code>	color of plot background
<code>axis_text</code>	size of axis text
<code>axis_title</code>	size of axis title
<code>cow_n_col</code>	cowplot param: how many columns
<code>cow_rel_h</code>	cowplot param: relative height
<code>cow_rel_w</code>	cowplot param: relative width
<code>cow_align</code>	cowplot param: how to align
<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 from <a href="#">all_plots_save_function</a>
<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>cowplot::save_plot()</code>

**Details**

Description of parameters.

**Value**

ggplot

**See Also**

[dimGenePlot3D](#)

**Examples**

```
dimGenePlot2D(gobject)
```

---

dimGenePlot3D

*dimGenePlot3D*


---

**Description**

Visualize cells and gene expression according to dimension reduction coordinates

**Usage**

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

```

    save_plot = NA,
    save_param = list(),
    default_save_name = "dimGenePlot3D"
  )

```

## Arguments

<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>dim3_to_use</code>	dimension to use on z-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>edge_alpha</code>	column to use for alpha of the edges
<code>point_size</code>	size of point (cell)
<code>show_legend</code>	show legend
<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 from <a href="#">all_plots_save_function</a>
<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>cowplot::save_plot()</code>

## Details

Description of parameters.

## Value

ggplot

## Examples

```
dimGenePlot3D(gobject)
```

dimPlot

*dimPlot***Description**

Visualize cells according to dimension reduction coordinates

**Usage**

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

```

cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "dimPlot"
)

```

### Arguments

<code>gobject</code>	giotto object
<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



show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
title	title for plot, defaults to cell_color parameter
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_by	create multiple plots based on cell annotation column

## Details

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

## Value

ggplot

## Examples

```
dimPlot(gobject)
```

---

dimPlot2D

*dimPlot2D*


---

## Description

Visualize cells according to dimension reduction coordinates

## Usage

```
dimPlot2D(
  gobject,
  group_by = NULL,
  group_by_subset = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  spat_enr_names = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  edge_alpha = NULL,
  point_shape = c("border", "no_border"),
  point_size = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  title = NULL,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
```

```

cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "dimPlot2D"
)

```

## Arguments

<code>gobject</code>	giotto object
<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

show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
title	title for plot, defaults to cell_color parameter
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_by	create multiple plots based on cell annotation column

### Details

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

### Value

ggplot

### Examples

```
dimPlot2D(gobject)
```

---

dimPlot2D_single	<i>dimPlot2D_single</i>
------------------	-------------------------

---

## Description

Visualize cells according to dimension reduction coordinates

## Usage

```
dimPlot2D_single(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  spat_enr_names = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  edge_alpha = NULL,
  point_shape = c("border", "no_border"),
  point_size = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  title = NULL,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  show_plot = NA,
  return_plot = NA,
```

```

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

```

### Arguments

<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>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>label_size</code>	size of labels
<code>label_fontface</code>	font of labels

edge_alpha	column to use for alpha of the edges
point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
title	title for plot, defaults to cell_color parameter
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

## Details

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

## Value

ggplot

## Examples

```
dimPlot2D_single(gobject)
```

---

dimPlot3D	<i>dimPlot3D</i>
-----------	------------------

---

## Description

Visualize cells according to dimension reduction coordinates

**Usage**

```

dimPlot3D(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = 3,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 2,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  color_as_factor = T,
  cell_color = NULL,
  cell_color_code = NULL,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 4,
  edge_alpha = NULL,
  point_size = 3,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "dim3D"
)

```

**Arguments**

<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>dim3_to_use</code>	dimension to use on z-axis
<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)
network_name	name of NN network to use, if show_NN_network = TRUE
color_as_factor	convert color column to factor
cell_color	color for cells (see details)
cell_color_code	named vector with colors
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
show_legend	show legend

## Details

Description of parameters.

## Value

plotly

## Examples

```
dimPlot3D(gobject)
```

---

direction_test_CPG	<i>direction_test_CPG</i>
--------------------	---------------------------

---

### Description

shows direction of change

### Usage

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

### Examples

```
direction_test_CPG()
```

---

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	<i>doHMRF</i>
--------	---------------

---

Description

Run HMRF

Usage

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

```

dimensions_to_use = 1:10,
name = "test",
k = 10,
betas = c(0, 2, 50),
tolerance = 1e-10,
zscore = c("none", "rowcol", "colrow"),
numinit = 100,
python_path = NULL,
output_folder = NULL,
overwrite_output = TRUE
)

```

### Arguments

<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

*doLeidenCluster*


---

**Description**

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

**Usage**

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

**Arguments**

gobject	giotto object
name	name for cluster
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
python_path	specify specific path to python if required
resolution	resolution

weight_col	weight column to use for edges
partition_type	The type of partition to use for optimisation.
init_membership	initial membership of cells for the partition
n_iterations	number of 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:

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

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

## Value

giotto object with new clusters appended to cell metadata

## Examples

```
doLeidenCluster(gobject)
```

---

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

**Arguments**

<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

*doLouvainCluster*


---

**Description**

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

**Usage**

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

**Arguments**

gobject	giotto object
version	implemented version of Louvain clustering to use
name	name for cluster
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
python_path	[community] specify specific path to python if required
resolution	[community] resolution
gamma	[multinet] Resolution parameter for modularity in the generalized louvain method.
omega	[multinet] Inter-layer weight parameter in the generalized louvain method.
return_gobject	boolean: return giotto object (default = TRUE)
set_seed	set seed
seed_number	number for seed

**Details**

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

**Value**

giotto object with new clusters appended to cell metadata

**See Also**

[doLouvainCluster\\_community](#) and [doLouvainCluster\\_multinet](#)

**Examples**

```
doLouvainCluster(gobject)
```

---

```
doLouvainCluster_community
```

```
doLouvainCluster_community
```

---

**Description**

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

**Usage**

```
doLouvainCluster_community(
  gobject,
  name = "louvain_clus",
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  python_path = NULL,
  resolution = 1,
  weight_col = NULL,
  louv_random = F,
  return_gobject = TRUE,
  set_seed = F,
  seed_number = 1234,
  ...
)
```

**Arguments**

<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      *doLouvainSubCluster*


---

## Description

subcluster cells using a NN-network and the Louvain algorithm

## Usage

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

## Arguments

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

## Arguments

<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

nn_param	parameters for parameters for createNearestNetwork
k_neighbors	number of k for createNearestNetwork
resolution	resolution
python_path	specify specific path to python if required
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use
return_gobject	boolean: return giotto object (default = TRUE)
verbose	verbose

### Details

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

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

### Value

giotto object with new subclusters appended to cell metadata

### See Also

[doLouvainCluster\\_community](#)

### Examples

```
doLouvainSubCluster_community(gobject)
```

---

doLouvainSubCluster\_multinet

*doLouvainSubCluster\_multinet*

---

### Description

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



**Usage**

```
doLouvainSubCluster_multinet(
  gobject,
  name = "sub_louvain_mult_clus",
  cluster_column = NULL,
  selected_clusters = NULL,
  hvg_param = list(reverse_log_scale = T, difference_in_variance = 1, expression_values
    = "normalized"),
  hvg_min_perc_cells = 5,
  hvg_mean_expr_det = 1,
  use_all_genes_as_hvg = FALSE,
  min_nr_of_hvg = 5,
  pca_param = list(expression_values = "normalized", scale_unit = T),
  nn_param = list(dimensions_to_use = 1:20),
  k_neighbors = 10,
  gamma = 1,
  omega = 1,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  return_gobject = TRUE,
  verbose = T
)
```

**Arguments**

<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>gamma</code>	gamma
<code>omega</code>	omega
<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
<code>python_path</code>	specify specific path to python if required

**Details**

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

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

**Value**

giotto object with new subclusters appended to cell metadata

**See Also**

[doLouvainCluster\\_multinet](#)

**Examples**

```
doLouvainSubCluster_multinet(gobject)
```

---

doRandomWalkCluster	<i>doRandomWalkCluster</i>
---------------------	----------------------------

---

**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**

<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>walk_steps</code>	number of walking steps
<code>walk_clusters</code>	number of final clusters
<code>walk_weights</code>	cluster column defining the walk weights
<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 [cluster\\_walktrap](#) function from the igraph package in R for more information.

**Value**

giotto object with new clusters appended to cell metadata

**Examples**

```
doRandomWalkCluster(gobject)
```

---

doSNNCluster

doSNNCluster

---

**Description**

Cluster cells using a SNN cluster approach.

**Usage**

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

**Arguments**

<code>gobject</code>	giotto object
<code>name</code>	name for cluster
<code>nn_network_to_use</code>	type of NN network to use (only works on kNN)
<code>network_name</code>	name of kNN network to use
<code>k</code>	Neighborhood size for nearest neighbor sparsification to create the shared NN graph.
<code>eps</code>	Two objects are only reachable from each other if they share at least <code>eps</code> nearest neighbors.
<code>minPts</code>	minimum number of points that share at least <code>eps</code> nearest neighbors for a point to be considered a core points.
<code>borderPoints</code>	should borderPoints be assigned to clusters like in DBSCAN?
<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 [sNNclust](#) from dbscan package

**Value**

giotto object with new clusters appended to cell metadata

**Examples**

```
doSNNcluster(gobject)
```

---

```
do_spatial_grid_averaging
  do_spatial_grid_averaging
```

---

**Description**

smooth gene expression over a defined spatial grid

**Usage**

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

**Arguments**

gobject            giotto object  
 expression\_values            gene expression values to use  
 subset\_genes      subset of genes to use  
 spatial\_grid\_name            name of spatial grid to use  
 min\_cells\_per\_grid            minimum number of cells to consider a grid

**Value**

matrix with smoothened gene expression values based on spatial grid

**Examples**

```
do_spatial_grid_averaging(gobject)
```

---

```
do_spatial_knn_smoothing
do_spatial_knn_smoothing
```

---

**Description**

smooth gene expression over a kNN spatial network

**Usage**

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

**Arguments**

gobject            giotto object  
 expression\_values            gene expression values to use  
 subset\_genes      subset of genes to use  
 spatial\_network\_name            name of spatial network to use  
 b                    smoothing factor between 0 and 1 (default: automatic)

**Details**

This function will smoothen the gene expression values per cell according to its neighbors in the selected spatial network.  
b is a smoothening factor that defaults to  $1 - 1/k$ , where k is the median number of k-neighbors in the selected spatial network. Setting  $b = 0$  means no smoothing and  $b = 1$  means no contribution from its own expression.

**Value**

matrix with smoothened gene expression values based on kNN spatial network

**Examples**

```
do_spatial_knn_smoothing(gobject)
```

---

DT_removeNA	<i>DT_removeNA</i>
-------------	--------------------

---

**Description**

set NA values to 0

**Usage**

```
DT_removeNA(DT)
```

---

dt_to_matrix	<i>dt_to_matrix</i>
--------------	---------------------

---

**Description**

converts data.table to matrix

**Usage**

```
dt_to_matrix(x)
```

**Examples**

```
dt_to_matrix(x)
```

---

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

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

**Details**

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

**Value**

writes the necessary output to use in Giotto Viewer

**Examples**

```
exportGiottoViewer(gobject)
```

---

```
exprOnlyCellCellcommunicationScores
      exprOnlyCellCellcommunicationScores
```

---

**Description**

Cell-Cell communication scores based on expression only

**Usage**

```
exprOnlyCellCellcommunicationScores(
  gobject,
  cluster_column = "cell_types",
  random_iter = 100,
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  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>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**

```
exprOnlyCellCellcommunicationScores(gobject)
```

---

extended_gini_fun	<i>extended_gini_fun</i>
-------------------	--------------------------

---

**Description**

calculate gini coefficient on a minimum length vector

**Usage**

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

**Value**

gini coefficient

---

extractNearestNetwork	<i>extractNearestNetwork</i>
-----------------------	------------------------------

---

**Description**

Extracts a NN-network from a Giotto object

**Usage**

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

**Arguments**

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

**Value**

igraph or data.table object

Examples

```
extractNearestNetwork(gobject)
```

---

fDataDT	<i>fDataDT</i>
---------	----------------

---

Description

show gene metadata

Usage

```
fDataDT(gobject)
```

Arguments

gobject                  giotto object

Value

data.table with gene metadata

Examples

```
pDataDT(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  
)
```

**Arguments**

gobject           giotto object  
 expression\_values           expression values to use  
 expression\_thresholds           all thresholds to consider a gene expressed  
 gene\_det\_in\_min\_cells           minimum number of cells that should express a gene to consider that gene further  
 min\_det\_genes\_per\_cell           minimum number of expressed genes per cell to consider that cell further  
 scale\_x\_axis       ggplot transformation for x-axis (e.g. log2)  
 x\_axis\_offset      x-axis offset to be used together with the scaling transformation  
 scale\_y\_axis       ggplot transformation for y-axis (e.g. log2)  
 y\_axis\_offset      y-axis offset to be used together with the scaling transformation  
 show\_plot          show plot

**Details**

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

**Value**

list of data.table and ggplot object

**Examples**

```
filterCombinations(gobject)
```

---

filterCPGscores	<i>filterCPGscores</i>
-----------------	------------------------

---

**Description**

visualize Cell Proximity Gene enrichment scores

**Usage**

```

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

**Arguments**

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

**Details**

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

**Value**

Gene to gene scores in data.table format

**Examples**

```
filterCPGscores(CPGscore)
```

---

filterDistributions	<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 = TRUE
)
```

**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

**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

gene\_det\_in\_min\_cells      minimum # of cells that need to express a gene  
 min\_det\_genes\_per\_cell      minimum # of genes that need to be detected in a cell  
 verbose      verbose

### Details

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

### Value

giotto object

### Examples

```
filterGiotto(gobject)
```

---

findGiniMarkers	<i>findGiniMarkers</i>
-----------------	------------------------

---

### Description

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

### Usage

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

### Arguments

gobject      giotto object  
 expression\_values      gene expression values to use  
 cluster\_column      clusters to use  
 subset\_clusters      selection of clusters to compare  
 group\_1      group 1 cluster IDs from cluster\_column for pairwise comparison

group_2	group 2 cluster IDs from cluster_column for pairwise comparison
min_expr_gini_score	filter on minimum gini coefficient for expression
min_det_gini_score	filter on minimum gini coefficient for detection
detection_threshold	detection threshold for gene expression
rank_score	rank scores for both detection and expression to include
min_genes	minimum number of top genes to return

### Details

Detection of marker genes using the [https://en.wikipedia.org/wiki/Gini\\_coefficient](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,
  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("scrn", "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,
  ...
)
```

## Arguments

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

## Details

This is a minimal convenience wrapper around the [zlm](#) from the MAST package to detect differentially expressed genes.

## Value

data.table with marker genes

## Examples

```
findMastMarkers(gobject)
```

---

```
findMastMarkers_one_vs_all  
  findMastMarkers_one_vs_all
```

---

## Description

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

## Usage

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

## Arguments

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

## Value

data.table with marker genes

## See Also

[findMastMarkers](#)

## Examples

```
findMastMarkers_one_vs_all(gobject)
```

---

findScranMarkers	<i>findScranMarkers</i>
------------------	-------------------------

---

## Description

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

## Usage

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

## Arguments

<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>...</code>	additional parameters for the <code>findMarkers</code> function in <code>scran</code>

## Details

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

To perform differential expression between cluster groups you need to 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 scran's implementation of findMarkers.

## Usage

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

## Arguments

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

## Value

data.table with marker genes

## See Also

[findScranMarkers](#)

## Examples

```
findScranMarkers_one_vs_all(gobject)
```

---

<code>find_grid_2D</code>	<i>find_grid_2D</i>
---------------------------	---------------------

---

**Description**

find grid location in 2D

**Usage**

`find_grid_2D(grid_DT, x_loc, y_loc)`

---

<code>find_grid_3D</code>	<i>find_grid_3D</i>
---------------------------	---------------------

---

**Description**

find grid location in 3D

**Usage**

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

---

<code>find_grid_x</code>	<i>find_grid_x</i>
--------------------------	--------------------

---

**Description**

find grid location on x-axis

**Usage**

`find_grid_x(grid_DT, x_loc)`

---

<code>find_grid_y</code>	<i>find_grid_y</i>
--------------------------	--------------------

---

**Description**

find grid location on y-axis

**Usage**

`find_grid_y(grid_DT, y_loc)`



---

find_grid_z	<i>find_grid_z</i>
-------------	--------------------

---

**Description**

find grid location on z-axis

**Usage**

find\_grid\_z(grid\_DT, z\_loc)

---

fish_function	<i>fish_function</i>
---------------	----------------------

---

**Description**

perform fisher exact test

**Usage**

fish\_function(x\_to, x\_from)

---

fish_function2	<i>fish_function2</i>
----------------	-----------------------

---

**Description**

perform fisher exact test

**Usage**

fish\_function2(A, B, C, D)

---

FSV_show	<i>FSV_show</i>
----------	-----------------

---

**Description**

Visualize spatial variable genes caculated by spatial\_DE

**Usage**

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

**Arguments**

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

**Details**

Description of parameters.

**Value**

nothing

**Examples**

```
FSV_show(results)
```

---

GenePattern_show	<i>GenePattern_show</i>
------------------	-------------------------

---

**Description**

Visualize genes distribution patterns calculated by spatial\_AEH

**Usage**

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

**Arguments**

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

**Details**

Description of parameters.

**Value**

nothing

**Examples**

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

---

general\_save\_function    *general\_save\_function*

---

## Description

Function to automatically save plots to directory of interest

## Usage

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

## Arguments

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

## Examples

```
general_save_function(gobject)
```

---

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

---

### Description

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

### Usage

```
get10Xmatrix(path_to_data, row_ids = c("gene_symbols", "ensembl_ids"))
```

### Arguments

path_to_data	path to the 10X folder
row_ids	row ids to use (gene symbols or ensembl ids)

### Details

A typical 10X folder is named raw\_feature\_bc\_matrix or raw\_feature\_bc\_matrix. It has 3 files:

- barcodes
- features.tsv.gz
- matrix.mtx.gz

### Value

expression matrix from 10X

### Examples

```
get10Xmatrix(10Xmatrix)
```

---

getCellProximityGeneScores	<i>getCellProximityGeneScores</i>
----------------------------	-----------------------------------

---

### Description

Compute cell-cell interaction enrichment (observed vs expected)

**Usage**

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

**Arguments**

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

## Details

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

- genes: All or selected list of tested genes
- cell\_expr\_1: average gene expression in cell type 1 from unified\_int cell-cell interaction
- cell\_expr\_2: average gene expression in cell type 2 from unified\_int cell-cell interaction
- comb\_expr: combined average gene expression in cell type 1 and 2 from unified\_int cell-cell interaction
- all\_cell\_expr\_1: average gene expression for all cells from cell type 1
- all\_cell\_expr\_2: average gene expression for all cells from cell type 2
- all\_comb\_expr: combined average gene expression for all cells from cell type 1 and 2
- pval\_1: p-value from test between interacting cells and all cells from cell type 1
- pval\_2: p-value from test between interacting cells and all cells from cell type 2
- cell\_type\_1: first cell type of cell-cell interaction
- cell\_type\_2: second cell type of cell-cell interaction
- interaction: the cell-cell interaction, based on physical proximity
- nr\_1: number of cell type 1 in the unified cell-cell interaction
- nr\_2: number of cell type 2 in the unified cell-cell interaction
- all\_nr\_1: number of all cell type 1 in the whole dataset
- all\_nr\_2: number of all cell type 2 in the whole dataset
- diff\_spat: difference between comb\_expr and all\_comb\_expr
- diff\_spat\_1: difference between cell\_expr\_1 and all\_cell\_expr\_1
- diff\_spat\_2: difference between cell\_expr\_2 and all\_cell\_expr\_2
- log2fc\_spat\_1: fold-change of diff\_spat\_1
- log2fc\_spat\_2: fold-change of diff\_spat\_2
- log2fc\_spat: fold-change of diff\_spat
- type\_int: type of interaction
- unified\_int: interaction with alphabetically sorted cell type 1 and cell type 2
- unif\_int\_rank: 1 or 2
- fdr\_1: fdr from test between interacting cells and all cells from cell type 1
- fdr\_2: fdr from test between interacting cells and all cells from cell type 2

## Value

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

## Examples

```
getCellProximityGeneScores(gobject)
```

---

getClusterSimilarity	<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**

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

**Details**

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

**Value**

data.table object

**Examples**

```
getDendrogramSplits(gobject)
```

---

getDistinctColors	<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

---

getGeneToGeneScores	<i>getGeneToGeneScores</i>
---------------------	----------------------------

---

Description

Compute gene-gene enrichment scores.

Usage

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

Arguments

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

**Details**

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

**Value**

Gene to gene scores in data.table format

**Examples**

```
getGeneToGeneScores(CPGscore)
```

---

```
get_cell_to_cell_sorted_name_conversion
      get_cell_to_cell_sorted_name_conversion
```

---

**Description**

creates unified cell-cell interaction names

**Usage**

```
get_cell_to_cell_sorted_name_conversion(all_cell_types)
```

**Examples**

```
get_cell_to_cell_sorted_name_conversion()
```

---

```
get_interaction_gene_enrichment
      get_interaction_gene_enrichment
```

---

**Description**

Computes gene enrichment between all interactions

**Usage**

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

```

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

```

### Examples

```
get_interaction_gene_enrichment()
```

---

```

get_specific_interaction_gene_enrichment
  get_specific_interaction_gene_enrichment

```

---

### Description

Computes gene enrichment between specified interaction

### Usage

```

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

```

### Examples

```
get_specific_interaction_gene_enrichment()
```

---

ggplot\_save\_function    *ggplot\_save\_function*


---

## Description

Function to automatically save plots to directory of interest

## Usage

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

## Arguments

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

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

**See Also**

[cowplot::save\\_plot](#)

**Examples**

```
ggplot_save_function(gobject)
```

---

giotto-class	<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  
dimension\_reduction slot to save dimension reduction coordinates  
nn\_network nearest neighbor network in igraph format  
parameters slot to save parameters that have been used  
instructions slot for global function instructions  
offset\_file offset file used to stitch together image fields  
OS\_platform Operating System to run Giotto analysis on

---

heatmSpatialCorGenes    *heatmSpatialCorGenes*


---

## Description

Create heatmap of spatially correlated genes

## Usage

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

## Arguments

<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_cluster_annot</code>	show cluster annotation on top of heatmap
<code>show_row_dend</code>	show row dendrogram
<code>show_column_dend</code>	show column dendrogram
<code>show_row_names</code>	show row names
<code>show_column_names</code>	show column names
<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 <a href="#">all_plots_save_function</a>
<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 parameters to the <a href="#">Heatmap</a> function from <code>ComplexHeatmap</code>

Value

Heatmap generated by ComplexHeatmap

Examples

```
heatmSpatialCorGenes(gobject)
```

---

hyperGeometricEnrich	<i>hyperGeometricEnrich</i>
----------------------	-----------------------------

---

Description

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

Usage

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

Arguments

gobject	Giotto object
sign_matrix	Matrix of signature genes for each cell type / process
expression_values	expression values to use
reverse_log_scale	reverse expression values from log scale
logbase	log base to use if reverse_log_scale = TRUE
top_percentage	percentage of cells that will be considered to have gene expression with matrix binarization
output_enrichment	how to return enrichment output

Details

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

Value

data.table with enrichment results



Examples

```
hyperGeometricEnrich(gobject)
```

---

kmeans_binarize	<i>kmeans_binarize</i>
-----------------	------------------------

---

Description

create binarized scores using kmeans

Usage

```
kmeans_binarize(x, nstart = 3, iter.max = 10)
```

---

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()
```

---

make\_simulated\_network

*make\_simulated\_network*

---

**Description**

Simulate random network.

**Usage**

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

**Examples**

```
make_simulated_network(gobject)
```

---

mergeClusters

*mergeClusters*

---

**Description**

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

**Usage**

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

```

    return_gobject = TRUE,
    verbose = TRUE
  )

```

### Arguments

<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>new_cluster_name</code>	new name for merged clusters
<code>min_cor_score</code>	min correlation score to merge pairwise clusters
<code>max_group_size</code>	max cluster size that can be merged
<code>force_min_group_size</code>	size of clusters that will be merged with their most similar neighbor(s)
<code>return_gobject</code>	return giotto object
<code>verbose</code>	be verbose

### Details

Merge selected clusters based on pairwise correlation scores and size of cluster. To avoid large clusters to merge the `max_group_size` can be lowered. Small clusters can be forcibly merged with their most similar pairwise cluster by adjusting the `force_min_group_size` parameter. Clusters smaller than this value will be merged independent on the provided `min_cor_score` value. A giotto object is returned by default, if FALSE then the merging vector will be returned.

### Value

Giotto object

### Examples

```
mergeClusters(gobject)
```

---

mygini\_fun

*mygini\_fun*

---

### Description

calculate gini coefficient

### Usage

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

### Value

gini coefficient

---

nnDT\_to\_kNN

*nnDT\_to\_kNN*


---

**Description**

Convert a nearest network data.table to a kNN object

**Usage**

```
nnDT_to_kNN(nnDT)
```

**Arguments**

nnDT                      nearest neighbor network in data.table format

**Value**

kNN object

---

node\_clusters

*node\_clusters*


---

**Description**

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

**Usage**

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

**Arguments**

hclus\_obj                hclus object  
 verbose                be verbose

**Value**

list of splitted dendrogram nodes from high to low node height

**Examples**

```
node_clusters(hclus_obj)
```

---

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

---

## Description

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,
  logbase = 2,
  scale_genes = T,
  scale_cells = T,
  scale_order = c("first_genes", "first_cells"),
  verbose = F
)
```

## Arguments

gobject	giotto object
norm_methods	normalization method to use
library_size_norm	normalize cells by library size
scalefactor	scale factor to use after library size normalization
log_norm	transform values to log-scale
logbase	log base to use to log normalize expression values
scale_genes	z-score genes over all cells
scale_cells	z-score cells over all genes
scale_order	order to scale genes and cells
verbose	be verbose

## Details

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

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

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

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

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

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

### Value

giotto object

### Examples

```
normalizeGiotto(gobject)
```

---

normalizeGiottoFast	<i>normalizeGiottoFast</i>
---------------------	----------------------------

---

### Description

fast normalize and/or scale expresion values of Giotto object

### Usage

```
normalizeGiottoFast(
  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

```
normalizeGiottoFast(gobject)
```

---

OR\_function2

*OR\_function2*

---

## Description

calculate odds-ratio

## Usage

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



PAGEEnrich

*PAGEEnrich***Description**

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

**Usage**

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

**Arguments**

<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

**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,  $\mu$  is the fold change values versus the mean expression and  $\delta$  is the standard deviation.  $Sm$  is the mean fold change value of a specific marker gene set and  $m$  is the size of a given marker gene set.

**Value**

data.table with enrichment results

**See Also**

[makeSignMatrixPAGE](#)

**Examples**

```
PAGEEnrich(gobject)
```

---

pagePermutation	<i>pagePermutation</i>
-----------------	------------------------

---

**Description**

creates permutation for the PAGEEnrich test

**Usage**

pagePermutation(sc\_gene, gene\_number, n)

**Examples**

pagePermutation()

---

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

---

**Description**

show cell metadata

**Usage**

pDataDT(gobject)

**Arguments**

gobject                  giotto object

**Value**

data.table with cell metadata

**Examples**

pDataDT(gobject)

---

plotCPGscores	<i>plotCPGscores</i>
---------------	----------------------

---

## Description

Create heatmap from cell-cell proximity scores

## Usage

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

## Arguments

CPGscores	CPGscores, output from <code>getCellProximityGeneScores()</code>
selected_interactions	interactions to show
selected_genes	genes to show
detail_plot	show detailed info in both interacting cell types
simple_plot	show a simplified plot
simple_plot_facet	facet on interactions or genes with simple plot
facet_scales	ggplot facet scales paramter
facet_ncol	ggplot facet ncol parameter
facet_nrow	ggplot facet nrow parameter
show_plot	show plot

## Details

Give more details ...

## Value

ggplot barplot

## Examples

```
plotCPGscores(CPGscores)
```

---

plotGTGscores	<i>plotGTGscores</i>
---------------	----------------------

---

## Description

Create heatmap from cell-cell proximity scores

## Usage

```
plotGTGscores(
  gobject,
  GTGscore,
  selected_interactions = NULL,
  selected_gene_to_gene = NULL,
  detail_plot = T,
  simple_plot = F,
  simple_plot_facet = c("interaction", "genes"),
  facet_scales = "fixed",
  facet_ncol = length(selected_gene_to_gene),
  facet_nrow = length(selected_interactions),
  colors = c("blue", "red"),
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotGTGscores"
)
```

## Arguments

<code>gobject</code>	giotto object
<code>GTGscore</code>	GTGscore, output from <code>getGeneToGeneScores()</code>
<code>selected_interactions</code>	interactions 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 2 colors to represent respectively all and selected cells
<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 from <a href="#">all_plots_save_function</a>
<code>default_save_name</code>	default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code>
<code>selected_genes</code>	genes to show

**Details**

Give more details ...

**Value**

ggplot barplot

**Examples**

```
plotGTGscores(GTGscore)
```

---

plotHeatmap

*plotHeatmap*


---

**Description**

Creates heatmap for genes and clusters.

**Usage**

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

**Arguments**

<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
<code>cluster_hclust_method</code>	method for hierarchical clustering of clusters
<code>gene_order</code>	method to determine gene order
<code>gene_custom_order</code>	custom order for genes
<code>gene_cor_method</code>	method for gene correlation
<code>gene_hclust_method</code>	method for hierarchical clustering of genes
<code>show_values</code>	which values to show on heatmap
<code>size_vertical_lines</code>	sizes for vertical lines
<code>gradient_colors</code>	colors for heatmap gradient
<code>gene_label_selection</code>	subset of genes to show on y-axis
<code>axis_text_y_size</code>	size for y-axis text
<code>legend_nrows</code>	number of rows for the cluster legend
<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 <a href="#">all_plots_save_function</a>
<code>default_save_name</code>	default save name

**Details**

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

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

## Value

ggplot

## Examples

```
plotHeatmap(gobject)
```

---

plotly_axis_scale_2D	<i>plotly_axis_scale_2D</i>	
----------------------	-----------------------------	--

---

## Description

adjust the axis scale in 3D plotly plot

## Usage

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

## Arguments

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

## Value

edges in spatial grid as data.table()

## Examples

```
plotly_axis_scale_2D(gobject)
```

---

plotly_axis_scale_3D	<i>plotly_axis_scale_3D</i>
----------------------	-----------------------------

---

**Description**

adjust the axis scale in 3D plotly plot

**Usage**

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

**Arguments**

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

**Value**

edges in spatial grid as data.table()

**Examples**

```
plotly_axis_scale_3D(gobject)
```

---

plotly_grid	<i>plotly_grid</i>
-------------	--------------------

---

**Description**

provide grid segment to draw in plot\_ly()

**Usage**

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



**Arguments**

spatial\_grid      spatial\_grid in giotto object

**Value**

edges in spatial grid as data.table()

**Examples**

```
plotly_grid(gobject)
```

---

plotly_network	<i>plotly_network</i>
----------------	-----------------------

---

**Description**

provide network segment to draw in 3D plot\_ly()

**Usage**

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

**Arguments**

gobject              network in giotto object

**Value**

edges in network as data.table()

**Examples**

```
plotly_network(gobject)
```

---

plotMetaDataCellsHeatmap

*plotMetaDataCellsHeatmap*


---

## Description

Creates heatmap for numeric cell metadata within aggregated clusters.

## Usage

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

## Arguments

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

clus_cor_method	correlation method for clusters
clus_cluster_method	hierarchical cluster method for the clusters
midpoint	midpoint of show_values
x_text_size	size of x-axis text
x_text_angle	angle of x-axis text
y_text_size	size of y-axis text
strip_text_size	size of strip text
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
custom_gene_order	custom gene order (default = NULL)
gene_cor_method	correlation method for genes
gene_cluster_method	hierarchical cluster method for the genes

## Details

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

## Value

ggplot or data.table

## See Also

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

## Examples

```
plotMetaDataCellsHeatmap(gobject)
```

---

plotMetaDataHeatmap	<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",
  midpoint = 0,
  x_text_size = 10,
  x_text_angle = 45,
  y_text_size = 10,
  strip_text_size = 8,
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "plotMetaDataHeatmap"
)
```

## Arguments

<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
<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)

clus_cor_method	correlation method for clusters
clus_cluster_method	hierarchical cluster method for the clusters
custom_gene_order	custom gene order (default = NULL)
gene_cor_method	correlation method for genes
gene_cluster_method	hierarchical cluster method for the genes
midpoint	midpoint of show_values
x_text_size	size of x-axis text
x_text_angle	angle of x-axis text
y_text_size	size of y-axis text
strip_text_size	size of strip text
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name

## Details

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

## Value

ggplot or data.table

## See Also

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

## Examples

```
plotMetaDataHeatmap(gobject)
```

plotPCA

*plotPCA***Description**

Short wrapper for PCA visualization

**Usage**

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

**Arguments**

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

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

**Details**

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotPCA\\_3D](#)

**Value**

ggplot

**Examples**

```
plotPCA(gobject)
```

---

plotPCA\_2D

*plotPCA\_2D*


---

## Description

Short wrapper for PCA visualization

## Usage

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

## Arguments

<code>gobject</code>	giotto object
<code>dim_reduction_name</code>	dimension reduction name
<code>default_save_name</code>	default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code>
<code>groub_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



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

## Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotPCA\\_3D](#)

## Value

ggplot

**Examples**

```
plotPCA_2D(gobject)
```

---

plotPCA\_3D

*plotPCA\_3D*


---

**Description**

Visualize cells according to 3D PCA dimension reduction

**Usage**

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

**Arguments**

gobject	giotto object
dim_reduction_name	pca dimension reduction name
default_save_name	default save name for saving, ideally change save_name in save_param
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim3_to_use	dimension to use on z-axis
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells

show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>

### Details

Description of parameters.

### Value

plotly

### Examples

```
plotPCA_3D(gobject)
```

---

plotTSNE	<i>plotTSNE</i>
----------	-----------------

---

### Description

Short wrapper for tSNE visualization

### Usage

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

### Arguments

gobject	giotto object
dim_reduction_name	dimension reduction name
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_by	create multiple plots based on cell annotation column
group_by_subset	subset the group_by factor column

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

legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>

**Details**

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotTSNE\\_3D](#)

**Value**

ggplot

**Examples**

```
plotTSNE(gobject)
```

---

plotTSNE\_2D

*plotTSNE\_2D*


---

**Description**

Short wrapper for tSNE visualization

**Usage**

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

**Arguments**

<code>gobject</code>	giotto object
<code>dim_reduction_name</code>	dimension reduction name
<code>default_save_name</code>	default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code>
<code>groub_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</code> = TRUE
<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>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

point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
title	title for plot, defaults to cell_color parameter
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>

### Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotTSNE\\_3D](#)

### Value

ggplot

### 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	tsne dimension reduction name
default_save_name	default save name for saving, don't change, change save_name in save_param
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim3_to_use	dimension to use on z-axis
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
show_legend	show legend



show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>

**Details**

Description of parameters.

**Value**

plotly

**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	dimension reduction name
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_by	create multiple plots based on cell annotation column
group_by_subset	subset the group_by factor column
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
spat_enr_names	names of spatial enrichment results to include
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
cell_color	color for cells (see details)

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

cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>

### Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotUMAP\\_3D](#)

### Value

ggplot

### Examples

```
plotUMAP(gobject)
```

---

plotUMAP_2D	<i>plotUMAP_2D</i>
-------------	--------------------

---

### Description

Short wrapper for UMAP visualization

### Usage

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

### Arguments

gobject	giotto object
dim_reduction_name	dimension reduction name
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_by	create multiple plots based on cell annotation column
group_by_subset	subset the group_by factor column
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
spat_enr_names	names of spatial enrichment results to include
show_NN_network	show underlying NN network

nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
title	title for plot, defaults to cell_color parameter
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text

axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>

### Details

Description of parameters, see [dimPlot2D](#). For 3D plots see [plotUMAP\\_3D](#)

### Value

ggplot

### Examples

```
plotUMAP_2D(gobject)
```

---

plotUMAP_3D	<i>plotUMAP_3D</i>
-------------	--------------------

---

### Description

Visualize cells according to dimension reduction coordinates

### Usage

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

### Arguments

gobject	giotto object
dim_reduction_name	umap dimension reduction name
default_save_name	default save name for saving, don't change, change save_name in save_param
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim3_to_use	dimension to use on z-axis

show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>

### Details

Description of parameters.

### Value

plotly

### Examples

```
plotUMAP_3D(gobject)
```

---

```
plot_network_layer_ggplot  
    plot_network_layer_ggplot
```

---

### Description

Visualize cells in network layer according to dimension reduction coordinates

### Usage

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

### Arguments

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

### Details

Description of parameters.

### Value

ggplot

### Examples

```
plot_network_layer_ggplot(gobject)
```

---

```
plot_point_layer_ggplot  
    plot_point_layer_ggplot
```

---

### Description

Visualize cells in point layer according to dimension reduction coordinates

**Usage**

```

plot_point_layer_ggplot(
  ggobject,
  annotated_DT_selected,
  annotated_DT_other,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = 0,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_size = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  edge_alpha = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_legend = T
)

```

**Arguments**

annotated_DT_selected	annotated data.table of selected cells
annotated_DT_other	annotated data.table of not selected cells
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
point_size	size of point (cell)



point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_legend	show legend
gobject	giotto object

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
plot_point_layer_ggplot(gobject)
```

---

```
plot_point_layer_ggplot_noFILL
```

```
plot_point_layer_ggplot_noFILL
```

---

**Description**

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

**Usage**

```

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

```

**Arguments**

annotated_DT_selected	annotated data.table of selected cells
annotated_DT_other	annotated data.table of not selected cells
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
point_size	size of point (cell)
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters

center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
edge_alpha	column to use for alpha of the edges
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
show_legend	show legend
gobject	giotto object

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
plot_point_layer_ggplot_noFILL(gobject)
```

---

```
plot_spat_point_layer_ggplot
      plot_spat_point_layer_ggplot
```

---

**Description**

creat ggplot point layer for spatial coordinates

**Usage**

```
plot_spat_point_layer_ggplot(
  ggobject,
  sdimx = NULL,
  sdimy = NULL,
  cell_locations_metadata_selected,
  cell_locations_metadata_other,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
```

```

point_size = 2,
point_border_col = "lightgrey",
point_border_stroke = 0.1,
show_cluster_center = F,
show_center_label = T,
center_point_size = 4,
center_point_border_col = "black",
center_point_border_stroke = 0.1,
label_size = 4,
label_fontface = "bold",
show_other_cells = T,
other_cell_color = "lightgrey",
other_point_size = 1,
show_legend = TRUE
)

```

### Arguments

<code>sdimx</code>	x-axis dimension name (default = 'sdimx')
<code>sdimy</code>	y-axis dimension name (default = 'sdimy')
<code>cell_locations_metadata_selected</code>	annotated location from selected cells
<code>cell_locations_metadata_other</code>	annotated location from non-selected cells
<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_size</code>	size of point (cell)
<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
<code>center_point_size</code>	size of center points

label_size	size of labels
label_fontface	font of labels
show_other_cells	display not selected cells
other_cell_color	color for not selected cells
other_point_size	point size for not selected cells
show_legend	show legend
gobject	giotto object

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
plot_spat_point_layer_ggplot(gobject)
```

---

```
plot_spat_point_layer_ggplot_noFILL
      plot_spat_point_layer_ggplot_noFILL
```

---

**Description**

creat ggplot point layer for spatial coordinates without borders

**Usage**

```
plot_spat_point_layer_ggplot_noFILL(
  ggobject,
  sdimx = NULL,
  sdimy = NULL,
  cell_locations_metadata_selected,
  cell_locations_metadata_other,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_size = 2,
  show_cluster_center = F,
  show_center_label = T,
```

```

    center_point_size = 4,
    label_size = 4,
    label_fontface = "bold",
    show_other_cells = T,
    other_cell_color = "lightgrey",
    other_point_size = 1,
    show_legend = TRUE
  )

```

### Arguments

<code>sdimx</code>	x-axis dimension name (default = 'sdimx')
<code>sdimy</code>	y-axis dimension name (default = 'sdimy')
<code>cell_locations_metadata_selected</code>	annotated location from selected cells
<code>cell_locations_metadata_other</code>	annotated location from non-selected cells
<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_size</code>	size of point (cell)
<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>label_size</code>	size of labels
<code>label_fontface</code>	font of labels
<code>show_other_cells</code>	display not selected cells
<code>other_cell_color</code>	color for not selected cells
<code>other_point_size</code>	point size for not selected cells
<code>show_legend</code>	show legend
<code>gobject</code>	giotto object

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
plot_spat_point_layer_ggplot_noFILL(gobject)
```

---

print.giotto	<i>print method for giotto class</i>
--------------	--------------------------------------

---

**Description**

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

**Usage**

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

**Arguments**

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

---

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

---

**Description**

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

**Usage**

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

**Arguments**

**gobject**                Giotto object  
**sign\_matrix**        Matrix of signature genes for each cell type / process  
**expression\_values**        expression values to use  
**reverse\_log\_scale**        reverse expression values from log scale  
**logbase**            log base to use if reverse\_log\_scale = TRUE  
**output\_enrichment**        how to return enrichment output

**Details**

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

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

**Value**

data.table with enrichment results

**See Also**

[makeSignMatrixRank](#)

**Examples**

```
rankEnrich(gobject)
```

---

rankPermutation

*rankPermutation*

---

**Description**

creates permutation for the rankEnrich test

**Usage**

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

**Examples**

```
rankPermutation()
```



---

rankSpatialCorGroups	<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**

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

**Value**

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

**Examples**

```
rankSpatialCorGroups(gobject)
```

---

rank_binarize	<i>rank_binarize</i>
---------------	----------------------

---

**Description**

create binarized scores using arbitrary rank of top genes

**Usage**

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

---

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**

named vector with giotto instructions

**Examples**

```
replaceGiottoInstructions()
```

---

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 = NULL,  
  return_gobject = TRUE,  
  scale_unit = F,  
  ncp = 200,  
  ...  
)
```

**Arguments**

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

**Details**

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

**Value**

giotto object with updated PCA dimension recuction

**Examples**

```
runPCA(gobject)
```

runtSNE

*runtSNE***Description**

run tSNE

**Usage**

```

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

```

**Arguments**

<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>...</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`
- multiple tSNE results can be stored by changing the *name* of the analysis

## Value

giotto object with updated tSNE dimension reduction

## Examples

```
runtSNE(gobject)
```

---

runUMAP

---

*runUMAP*


---

## Description

run UMAP

## Usage

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

**Arguments**

<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>...</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`
- multiple UMAP results can be stored by changing the *name* of the analysis

**Value**

giotto object with updated UMAP dimension reduction

**Examples**

```
runUMAP(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.

## Details

Description.

## Value

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

## Examples

```
selectPatternGenes(gobject)
```



---

select_expression_values	
	<i>select_expression_values</i>

---

**Description**

helper function to select expression values

**Usage**

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

**Arguments**

gobject	giotto object
values	expression values to extract

**Value**

expression matrix

---

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

---

**Description**

show method for giotto class

**Usage**

```
## S4 method for signature 'giotto'  
show(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**

<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>rotate</code>	rotate dendrogram 90 degrees
<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 <a href="#">all_plots_save_function</a>
<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 parameters for <code>ggdendrogram()</code>

**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 = "showClusterHeatmap",
  ...
)
```

## 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 from <a href="#">all_plots_save_function</a>
<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)
```

---

showCPGscores	<i>showCPGscores</i>
---------------	----------------------

---

Description

visualize Cell Proximity Gene enrichment scores

Usage

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

Arguments

CPGscore	CPGscore, output from getCellProximityGeneScores()
method	visualization method
min_cells	min number of cells threshold
min_fdr	fdr threshold
min_spat_diff	spatial difference threshold
min_log2_fc	min log2 fold-change
keep_int_duplicates	keep both cell_A-cell_B and cell_B-cell_A
direction	up or downregulation or both
cell_color_code	color code for cell types
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

**Details**

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

**Value**

Gene to gene scores in data.table format

**Examples**

```
showCPGscores(CPGscore)
```

---

```
showGeneExpressionProximityScore  
  showGeneExpressionProximityScore
```

---

**Description**

Create heatmap from cell-cell proximity scores

**Usage**

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

**Arguments**

- scores            CPGscore, output from getAverageCellProximityGeneScores()
- selected\_gene    gene to show
- sort\_column      column name to use for sorting

**Details**

Give more details ...

**Value**

ggplot barplot

**Examples**

```
showGeneExpressionProximityScore(scores)
```

---

showGiottoInstructions	<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()
```

---

showGTGscores	<i>showGTGscores</i>
---------------	----------------------

---

**Description**

visualize Cell Proximity Gene enrichment scores

**Usage**

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

**Arguments**

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

**Details**

Give more details ...

**Value**

ggplot

**Examples**

```
showGTGscores(CPGscore)
```

---

```
showIntExpressionProximityScore
```

```
showIntExpressionProximityScore
```

---

**Description**

Create heatmap from cell-cell proximity scores

**Usage**

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

Arguments

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

Details

Give more details ...

Value

ggplot barplot

Examples

```
showIntExpressionProximityScore(scores)
```

---

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

---

Description

show patterns for 2D spatial data

Usage

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

Arguments

gobject	giotto object
spatPatObj	Output from detectSpatialPatterns
dimension	dimension to plot
trim	Trim ends of the PC values.
background_color	background color for plot
grid_border_color	color for grid
show_legend	show legend of ggplot
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
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
show_plot	show plot
return_plot	return ggplot object

save\_plot            directly save the plot [boolean]  
save\_param          list of saving parameters from [all\\_plots\\_save\\_function](#)  
default\_save\_name            default save name for saving, don't change, change save\_name in save\_param

**Value**

ggplot

**Examples**

showPattern2D(gobject)

---

showPattern3D	<i>showPattern3D</i>
---------------	----------------------

---

**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 from <a href="#">all_plots_save_function</a>
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 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>

**Value**

ggplot

**Examples**

```
showPatternGenes(gobject)
```

---

<code>showProcessingSteps</code>	<i>showProcessingSteps</i>
----------------------------------	----------------------------

---

**Description**

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

**Usage**

```
showProcessingSteps(gobject)
```

**Arguments**

<code>gobject</code>	giotto object
----------------------	---------------

**Value**

list of processing steps and names

**Examples**

```
showProcessingSteps(gobject)
```

---

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)
```

---

showTopGeneToGene	<i>showTopGeneToGene</i>
-------------------	--------------------------

---

**Description**

Show enriched/depleted gene-gene enrichments

**Usage**

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

**Arguments**

- GTGscore            GTGscore, output from getGeneToGeneScores()
- top\_interactions    number of top gene-gene enrichments to show
- direction           show top increased or decreased gene-gene enrichments
- complement\_data    include non-enriched gene-gene scores from other cell-cell interactions
- subset\_cell\_ints    subset cell-cell interactions to show
- subset\_genes        subset genes to show

**Details**

Give more details ...

**Value**

ggplot barplot

**Examples**

```
showTopGeneToGene(scores)
```

signPCA

*signPCA***Description**

identify significant principal components (PCs)

**Usage**

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

**Arguments**

<code>gobject</code>	giotto object
<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>genes_to_use</code>	subset of genes to use for PCA
<code>scale_unit</code>	scale features before PCA
<code>ncp</code>	number of principal components to calculate
<code>scree_labels</code>	show labels on scree plot
<code>scree_ylim</code>	y-axis limits on scree plot
<code>jack_iter</code>	number of iterations for jackstraw
<code>jack_threshold</code>	p-value threshold to call a PC significant
<code>jack_verbose</code>	show progress of jackstraw method
<code>show_plot</code>	show plot
<code>return_plot</code>	return ggplot object

save_plot	directly save the plot [boolean]
save_param	list of saving parameters from all_plots_save_function()
default_save_name	default save name for saving, don't change, change save_name in save_param
...	additional parameters for PCA

### Details

Two different methods can be used to assess the number of relevant or significant 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 does not show a significant contribution anymore (= 'elbow method').
2. The Jackstraw method uses the [permutationPA](#) function. By systematically permuting genes it identifies robust, and thus significant, PCs.

multiple PCA results can be stored by changing the *name* parameter

### Value

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

### Examples

```
signPCA(gobject)
```

---

spatCellPlot	<i>spatCellPlot</i>
--------------	---------------------

---

### Description

Visualize cells according to spatial coordinates

### Usage

```
spatCellPlot(
  gobject,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spat_enr_names = NULL,
  cell_annotation_values = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_shape = c("border", "no_border"),
  point_size = 3,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_cluster_center = F,
  show_center_label = F,
  center_point_size = 4,
```



```

center_point_border_col = "black",
center_point_border_stroke = 0.1,
label_size = 4,
label_fontface = "bold",
show_network = F,
spatial_network_name = "spatial_network",
network_color = NULL,
network_alpha = 1,
show_grid = F,
spatial_grid_name = "spatial_grid",
grid_color = NULL,
show_other_cells = T,
other_cell_color = "lightgrey",
other_point_size = 1,
other_cells_alpha = 0.1,
coord_fix_ratio = NULL,
show_legend = T,
legend_text = 8,
legend_symbol_size = 1,
background_color = "white",
axis_text = 8,
axis_title = 8,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatCellPlot"
)

```

### Arguments

<code>gobject</code>	giotto object
<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>	point with border or not (border or no_border)

point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
show_network	show underlying spatial network
spatial_network_name	name of spatial network to use
network_color	color of spatial network
network_alpha	alpha of spatial network
show_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
grid_color	color of spatial grid
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	point size of not selected cells
other_cells_alpha	alpha of not selected cells
coord_fix_ratio	fix ratio between x and y-axis
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

## Details

Description of parameters.

## Value

ggplot

## Examples

```
spatCellPlot(gobject)
```

---

spatCellPlot2D

*spatCellPlot2D*


---

## Description

Visualize cells according to spatial coordinates

## Usage

```
spatCellPlot2D(
  gobject,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spat_enr_names = NULL,
  cell_annotation_values = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_shape = c("border", "no_border"),
  point_size = 3,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_cluster_center = F,
  show_center_label = F,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  show_network = F,
  spatial_network_name = "spatial_network",
  network_color = NULL,
  network_alpha = 1,
  show_grid = F,
  spatial_grid_name = "spatial_grid",
  grid_color = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
```

```

other_point_size = 1,
other_cells_alpha = 0.1,
coord_fix_ratio = NULL,
show_legend = T,
legend_text = 8,
legend_symbol_size = 1,
background_color = "white",
axis_text = 8,
axis_title = 8,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatCellPlot2D"
)

```

### Arguments

<code>gobject</code>	giotto object
<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>	point with border or not (border or no_border)
<code>point_size</code>	size of point (cell)
<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
<code>center_point_size</code>	size of center points

label_size	size of labels
label_fontface	font of labels
show_network	show underlying spatial network
spatial_network_name	name of spatial network to use
network_color	color of spatial network
network_alpha	alpha of spatial network
show_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
grid_color	color of spatial grid
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	point size of not selected cells
other_cells_alpha	alpha of not selected cells
coord_fix_ratio	fix ratio between x and y-axis
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

## Details

Description of parameters.

## Value

ggplot

## Examples

```
spatCellPlot2D(gobject)
```

---

spatDimCellPlot

*spatDimCellPlot*


---

## Description

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

## Usage

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

```

dim_edge_alpha = 0.5,
spat_show_network = F,
spatial_network_name = "spatial_network",
spat_network_color = "red",
spat_network_alpha = 0.5,
spat_show_grid = F,
spatial_grid_name = "spatial_grid",
spat_grid_color = "green",
show_other_cells = TRUE,
other_cell_color = "grey",
dim_other_point_size = 0.5,
spat_other_point_size = 0.5,
spat_other_cells_alpha = 0.5,
coord_fix_ratio = NULL,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_legend = T,
legend_text = 8,
legend_symbol_size = 1,
dim_background_color = "white",
spat_background_color = "white",
axis_text = 8,
axis_title = 8,
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatDimCellPlot"
)

```

### Arguments

<code>gobject</code>	giotto object
<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
<code>gradient_midpoint</code>	midpoint for color gradient

```

gradient_limits
    vector with lower and upper limits
select_cell_groups
    select subset of cells/clusters based on cell_color parameter
select_cells
    select subset of cells based on cell IDs
dim_point_shape
    spatial points with border or not (border or no_border)
dim_point_size
    size of points in dim. reduction space
dim_point_border_col
    border color of points in dim. reduction space
dim_point_border_stroke
    border stroke of points in dim. reduction space
spat_point_shape
    spatial points with border or not (border or no_border)
spat_point_size
    size of spatial points
spat_point_border_col
    border color of spatial points
spat_point_border_stroke
    border stroke of spatial points
dim_show_cluster_center
    show the center of each cluster
dim_show_center_label
    provide a label for each cluster
dim_center_point_size
    size of the center point
dim_center_point_border_col
    border color of center point
dim_center_point_border_stroke
    stroke size of center point
dim_label_size
    size of the center label
dim_label_fontface
    font of the center label
spat_show_cluster_center
    show the center of each cluster
spat_show_center_label
    provide a label for each cluster
spat_center_point_size
    size of the center point
spat_label_size
    size of the center label
spat_label_fontface
    font of the center label
show_NN_network
    show underlying NN network
nn_network_to_use
    type of NN network to use (kNN vs sNN)
nn_network_name
    name of NN network to use, if show_NN_network = TRUE

```



dim_edge_alpha	column to use for alpha of the edges
spat_show_network	show spatial network
spatial_network_name	name of spatial network to use
spat_network_color	color of spatial network
spat_show_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
spat_grid_color	color of spatial grid
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
dim_other_point_size	size of not selected dim cells
spat_other_point_size	size of not selected spat cells
spat_other_cells_alpha	alpha of not selected spat cells
coord_fix_ratio	ratio for coordinates
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
dim_background_color	background color of points in dim. reduction space
spat_background_color	background color of spatial points
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
spatDimCellPlot(gobject)
```

---

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

---

**Description**

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

**Usage**

```
spatDimCellPlot2D(
  gobject,
  plot_alignment = c("vertical", "horizontal"),
  spat_enr_names = NULL,
  cell_annotation_values = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  sdimx = "sdimx",
  sdimy = "sdimy",
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  dim_point_shape = c("border", "no_border"),
  dim_point_size = 1,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  spat_point_shape = c("border", "no_border"),
  spat_point_size = 1,
  spat_point_border_col = "black",
  spat_point_border_stroke = 0.1,
  dim_show_cluster_center = F,
  dim_show_center_label = T,
  dim_center_point_size = 4,
  dim_center_point_border_col = "black",
  dim_center_point_border_stroke = 0.1,
  dim_label_size = 4,
```

```

dim_label_fontface = "bold",
spat_show_cluster_center = F,
spat_show_center_label = F,
spat_center_point_size = 4,
spat_center_point_border_col = "black",
spat_center_point_border_stroke = 0.1,
spat_label_size = 4,
spat_label_fontface = "bold",
show_NN_network = F,
nn_network_to_use = "sNN",
nn_network_name = "sNN.pca",
dim_edge_alpha = 0.5,
spat_show_network = F,
spatial_network_name = "spatial_network",
spat_network_color = "red",
spat_network_alpha = 0.5,
spat_show_grid = F,
spatial_grid_name = "spatial_grid",
spat_grid_color = "green",
show_other_cells = TRUE,
other_cell_color = "grey",
dim_other_point_size = 0.5,
spat_other_point_size = 0.5,
spat_other_cells_alpha = 0.5,
show_legend = T,
legend_text = 8,
legend_symbol_size = 1,
dim_background_color = "white",
spat_background_color = "white",
axis_text = 8,
axis_title = 8,
coord_fix_ratio = NULL,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatDimCellPlot2D"
)

```

### Arguments

<code>gobject</code>	giotto object
<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

dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
sdimx	= spatial dimension to use on x-axis
sdimy	= spatial dimension to use on y-axis
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
dim_point_shape	dim reduction points with border or not (border or no_border)
dim_point_size	size of points in dim. reduction space
dim_point_border_col	border color of points in dim. reduction space
dim_point_border_stroke	border stroke of points in dim. reduction space
spat_point_shape	spatial points with border or not (border or no_border)
spat_point_size	size of spatial points
spat_point_border_col	border color of spatial points
spat_point_border_stroke	border stroke of spatial points
dim_show_cluster_center	show the center of each cluster
dim_show_center_label	provide a label for each cluster
dim_center_point_size	size of the center point
dim_center_point_border_col	border color of center point
dim_center_point_border_stroke	stroke size of center point
dim_label_size	size of the center label
dim_label_fontface	font of the center label
spat_show_cluster_center	show the center of each cluster
spat_show_center_label	provide a label for each cluster

```

    spat_center_point_size      size of the center point
    spat_label_size             size of the center label
    spat_label_fontface         font of the center label
    show_NN_network             show underlying NN network
    nn_network_to_use           type of NN network to use (kNN vs sNN)
    nn_network_name             name of NN network to use, if show_NN_network = TRUE
    dim_edge_alpha              column to use for alpha of the edges
    spat_show_network           show spatial network
    spatial_network_name        name of spatial network to use
    spat_network_color          color of spatial network
    spat_show_grid              show spatial grid
    spatial_grid_name           name of spatial grid to use
    spat_grid_color             color of spatial grid
    show_other_cells            display not selected cells
    other_cell_color            color of not selected cells
    dim_other_point_size        size of not selected dim cells
    spat_other_point_size       size of not selected spat cells
    spat_other_cells_alpha      alpha of not selected spat cells
    show_legend                 show legend
    legend_text                 size of legend text
    legend_symbol_size          size of legend symbols
    dim_background_color        background color of points in dim. reduction space
    spat_background_color       background color of spatial points
    axis_text                   size of axis text
    axis_title                  size of axis title
    coord_fix_ratio             ratio for coordinates
    cow_n_col                   cowplot param: how many columns

```

cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

Examples

spatDimCellPlot2D(gobject)

---

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

---

Description

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

Usage

```
spatDimGenePlot(  
  gobject,  
  expression_values = c("normalized", "scaled", "custom"),  
  plot_alignment = c("vertical", "horizontal"),  
  genes,  
  dim_reduction_to_use = "umap",  
  dim_reduction_name = "umap",  
  dim1_to_use = 1,  
  dim2_to_use = 2,  
  dim_point_shape = c("border", "no_border"),  
  dim_point_size = 1,  
  dim_point_border_col = "black",  
  dim_point_border_stroke = 0.1,  
  show_NN_network = F,  
  show_spatial_network = F,  
  show_spatial_grid = F,  
  nn_network_to_use = "sNN",  
  network_name = "sNN.pca",  
  edge_alpha_dim = NULL,
```

```

scale_alpha_with_expression = FALSE,
spatial_network_name = "spatial_network",
spatial_grid_name = "spatial_grid",
spat_point_shape = c("border", "no_border"),
spat_point_size = 1,
spat_point_border_col = "black",
spat_point_border_stroke = 0.1,
midpoint = 0,
genes_high_color = "red",
genes_mid_color = "white",
genes_low_color = "blue",
show_legend = T,
legend_text = 8,
dim_background_color = "white",
spat_background_color = "white",
axis_text = 8,
axis_title = 8,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatDimGenePlot"
)

```

### Arguments

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

nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
edge_alpha_dim	dim reduction plot: column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
spatial_network_name	name of spatial network to use
spatial_grid_name	name of spatial grid to use
spat_point_shape	spatial points with border or not (border or no_border)
spat_point_size	spatial plot: point size
spat_point_border_col	color of border around points
spat_point_border_stroke	stroke size of border around points
midpoint	size of point (cell)
show_legend	show legend
legend_text	size of legend text
dim_background_color	color of plot background for dimension plot
spat_background_color	color of plot background for spatial plot
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

## Details

Description of parameters.

## Value

ggplot



**See Also**[spatDimGenePlot3D](#)**Examples**

```
spatDimGenePlot(gobject)
```

---

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

---

**Description**

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

**Usage**

```
spatDimGenePlot2D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  plot_alignment = c("vertical", "horizontal"),
  genes,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim_point_shape = c("border", "no_border"),
  dim_point_size = 1,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  show_NN_network = F,
  show_spatial_network = F,
  show_spatial_grid = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  edge_alpha_dim = NULL,
  scale_alpha_with_expression = FALSE,
  spatial_network_name = "spatial_network",
  spatial_grid_name = "spatial_grid",
  spat_point_shape = c("border", "no_border"),
  spat_point_size = 1,
  spat_point_border_col = "black",
  spat_point_border_stroke = 0.1,
  midpoint = 0,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_legend = T,
```

```

    legend_text = 8,
    dim_background_color = "white",
    spat_background_color = "white",
    axis_text = 8,
    axis_title = 8,
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spatDimGenePlot2D"
)

```

### Arguments

<code>gobject</code>	giotto object
<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_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>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>edge_alpha_dim</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>spatial_network_name</code>	name of spatial network to use
<code>spatial_grid_name</code>	name of spatial grid to use
<code>spat_point_shape</code>	spatial points with border or not (border or no_border)
<code>spat_point_size</code>	spatial plot: point size

spat_point_border_col	color of border around points
spat_point_border_stroke	stroke size of border around points
midpoint	size of point (cell)
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_legend	show legend
legend_text	size of legend text
dim_background_color	color of plot background for dimension plot
spat_background_color	color of plot background for spatial plot
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

## Details

Description of parameters.

## Value

ggplot

## See Also

[spatDimGenePlot3D](#)

## Examples

```
spatDimGenePlot2D(gobject)
```

---

spatDimGenePlot3D	<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 = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  label_size = 16,
  genes_low_color = "blue",
  genes_mid_color = "white",
  genes_high_color = "red",
  dim_point_size = 3,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  network_color = "lightgray",
  spatial_network_alpha = 0.5,
  show_spatial_grid = F,
  spatial_grid_name = "spatial_grid",
  spatial_grid_color = NULL,
  spatial_grid_alpha = 0.5,
  spatial_point_size = 3,
  legend_text_size = 12,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
```

```

    z_ticks = NULL,
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spatDimGenePlot3D"
)

```

## Arguments

<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>genes</code>	genes to show
<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>dim_point_size</code>	dim reduction plot: point size
<code>spatial_network_name</code>	name of spatial network to use
<code>spatial_grid_name</code>	name of spatial grid to use
<code>spatial_point_size</code>	spatial plot: point size
<code>show_plot</code>	show plots
<code>return_plot</code>	return plotly object
<code>save_plot</code>	directly save the plot [boolean]
<code>save_param</code>	list of saving parameters from <a href="#">all_plots_save_function</a>
<code>default_save_name</code>	default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code>
<code>edge_alpha_dim</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>point_size</code>	size of point (cell)
<code>show_legend</code>	show legend

**Details**

Description of parameters.

**Value**

plotly

**Examples**

```
spatDimGenePlot3D(gobject)
```

---

spatDimPlot	<i>spatDimPlot</i>
-------------	--------------------

---

**Description**

Visualize cells according to spatial AND dimension reduction coordinates 2D

**Usage**

```
spatDimPlot(  
  gobject,  
  plot_alignment = c("vertical", "horizontal"),  
  dim_reduction_to_use = "umap",  
  dim_reduction_name = "umap",  
  dim1_to_use = 1,  
  dim2_to_use = 2,  
  sdimx = "sdimx",  
  sdimy = "sdimy",  
  spat_enr_names = NULL,  
  cell_color = NULL,  
  color_as_factor = T,  
  cell_color_code = NULL,  
  cell_color_gradient = c("blue", "white", "red"),  
  gradient_midpoint = NULL,  
  gradient_limits = NULL,  
  select_cell_groups = NULL,  
  select_cells = NULL,  
  dim_point_shape = c("border", "no_border"),  
  dim_point_size = 1,  
  dim_point_border_col = "black",  
  dim_point_border_stroke = 0.1,  
  spat_point_shape = c("border", "no_border"),  
  spat_point_size = 1,  
  spat_point_border_col = "black",  
  spat_point_border_stroke = 0.1,  
  dim_show_cluster_center = F,  
  dim_show_center_label = T,  
  dim_center_point_size = 4,  
  dim_center_point_border_col = "black",  
  dim_center_point_border_stroke = 0.1,  
)
```

```

dim_label_size = 4,
dim_label_fontface = "bold",
spat_show_cluster_center = F,
spat_show_center_label = F,
spat_center_point_size = 4,
spat_label_size = 4,
spat_label_fontface = "bold",
show_NN_network = F,
nn_network_to_use = "sNN",
network_name = "sNN.pca",
nn_network_alpha = 0.05,
show_spatial_network = F,
spat_network_name = "spatial_network",
spat_network_color = "blue",
spat_network_alpha = 0.5,
show_spatial_grid = F,
spat_grid_name = "spatial_grid",
spat_grid_color = "blue",
show_other_cells = T,
other_cell_color = "lightgrey",
dim_other_point_size = 1,
spat_other_point_size = 1,
spat_other_cells_alpha = 0.5,
dim_show_legend = F,
spat_show_legend = F,
legend_text = 8,
legend_symbol_size = 1,
dim_background_color = "white",
spat_background_color = "white",
axis_text = 8,
axis_title = 8,
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatDimPlot"
)

```

### Arguments

<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>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

cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
cell_color_gradient	vector with 3 colors for numeric data
gradient_midpoint	midpoint for color gradient
gradient_limits	vector with lower and upper limits
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
dim_point_shape	point with border or not (border or no_border)
dim_point_size	size of points in dim. reduction space
dim_point_border_col	border color of points in dim. reduction space
dim_point_border_stroke	border stroke of points in dim. reduction space
spat_point_shape	point with border or not (border or no_border)
spat_point_size	size of spatial points
spat_point_border_col	border color of spatial points
spat_point_border_stroke	border stroke of spatial points
dim_show_cluster_center	show the center of each cluster
dim_show_center_label	provide a label for each cluster
dim_center_point_size	size of the center point
dim_center_point_border_col	border color of center point
dim_center_point_border_stroke	stroke size of center point
dim_label_size	size of the center label
dim_label_fontface	font of the center label
spat_show_cluster_center	show the center of each cluster
spat_show_center_label	provide a label for each cluster
spat_center_point_size	size of the center point



spat_label_size	size of the center label
spat_label_fontface	font of the center label
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
nn_network_alpha	column to use for alpha of the edges
show_spatial_network	show spatial network
spat_network_name	name of spatial network to use
spat_network_color	color of spatial network
show_spatial_grid	show spatial grid
spat_grid_name	name of spatial grid to use
spat_grid_color	color of spatial grid
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
dim_other_point_size	size of not selected dim cells
spat_other_point_size	size of not selected spat cells
spat_other_cells_alpha	alpha of not selected spat cells
dim_show_legend	show legend of dimension reduction plot
spat_show_legend	show legend of spatial plot
legend_text	size of legend text
legend_symbol_size	size of legend symbols
dim_background_color	background color of points in dim. reduction space
spat_background_color	background color of spatial points
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

**Details**

Description of parameters.

**Value**

ggplot

**See Also**

[spatDimPlot2D](#) and [spatDimPlot3D](#) for 3D visualization.

**Examples**

```
spatDimPlot(gobject)
```

---

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

---

**Description**

Visualize cells according to spatial AND dimension reduction coordinates 2D

**Usage**

```
spatDimPlot2D(  
  gobject,  
  plot_alignment = c("vertical", "horizontal"),  
  dim_reduction_to_use = "umap",  
  dim_reduction_name = "umap",  
  dim1_to_use = 1,  
  dim2_to_use = 2,  
  sdimx = "sdimx",  
  sdimy = "sdimy",  
  spat_enr_names = NULL,  
  cell_color = NULL,  
  color_as_factor = T,  
  cell_color_code = NULL,  
  cell_color_gradient = c("blue", "white", "red"),  
  gradient_midpoint = NULL,  
  gradient_limits = NULL,  
  select_cell_groups = NULL,  
  select_cells = NULL,  
  dim_point_shape = c("border", "no_border"),  
  dim_point_size = 1,  
  dim_point_border_col = "black",  
  dim_point_border_stroke = 0.1,  
  spat_point_shape = c("border", "no_border"),  
  spat_point_size = 1,  
  spat_point_border_col = "black",  
  spat_point_border_stroke = 0.1,  
  dim_show_cluster_center = F,
```

```

dim_show_center_label = T,
dim_center_point_size = 4,
dim_center_point_border_col = "black",
dim_center_point_border_stroke = 0.1,
dim_label_size = 4,
dim_label_fontface = "bold",
spat_show_cluster_center = F,
spat_show_center_label = F,
spat_center_point_size = 4,
spat_label_size = 4,
spat_label_fontface = "bold",
show_NN_network = F,
nn_network_to_use = "sNN",
network_name = "sNN.pca",
nn_network_alpha = 0.05,
show_spatial_network = F,
spat_network_name = "spatial_network",
spat_network_color = "blue",
spat_network_alpha = 0.5,
show_spatial_grid = F,
spat_grid_name = "spatial_grid",
spat_grid_color = "blue",
show_other_cells = T,
other_cell_color = "lightgrey",
dim_other_point_size = 1,
spat_other_point_size = 1,
spat_other_cells_alpha = 0.5,
dim_show_legend = F,
spat_show_legend = F,
legend_text = 8,
legend_symbol_size = 1,
dim_background_color = "white",
spat_background_color = "white",
axis_text = 8,
axis_title = 8,
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatDimPlot2D"
)

```

### Arguments

<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>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
<code>dim_point_border_col</code>	border color of points in dim. reduction space
<code>dim_point_border_stroke</code>	border stroke of points in dim. reduction space
<code>spat_point_shape</code>	point with border or not ( <code>border</code> or <code>no_border</code> )
<code>spat_point_size</code>	size of spatial points
<code>spat_point_border_col</code>	border color of spatial points
<code>spat_point_border_stroke</code>	border stroke of spatial points
<code>dim_show_cluster_center</code>	show the center of each cluster
<code>dim_show_center_label</code>	provide a label for each cluster
<code>dim_center_point_size</code>	size of the center point
<code>dim_center_point_border_col</code>	border color of center point
<code>dim_center_point_border_stroke</code>	stroke size of center point
<code>dim_label_size</code>	size of the center label
<code>dim_label_fontface</code>	font of the center label
<code>spat_show_cluster_center</code>	show the center of each cluster

```

    spat_show_center_label
                        provide a label for each cluster
    spat_center_point_size
                        size of the center point
    spat_label_size
                        size of the center label
    spat_label_fontface
                        font of the center label
    show_NN_network
                        show underlying NN network
    nn_network_to_use
                        type of NN network to use (kNN vs sNN)
    network_name
        name of NN network to use, if show_NN_network = TRUE
    nn_network_alpha
                        column to use for alpha of the edges
    show_spatial_network
                        show spatial network
    spat_network_name
                        name of spatial network to use
    spat_network_color
                        color of spatial network
    show_spatial_grid
                        show spatial grid
    spat_grid_name
        name of spatial grid to use
    spat_grid_color
                        color of spatial grid
    show_other_cells
                        display not selected cells
    other_cell_color
                        color of not selected cells
    dim_other_point_size
                        size of not selected dim cells
    spat_other_point_size
                        size of not selected spat cells
    spat_other_cells_alpha
                        alpha of not selected spat cells
    dim_show_legend
                        show legend of dimension reduction plot
    spat_show_legend
                        show legend of spatial plot
    legend_text
        size of legend text
    legend_symbol_size
                        size of legend symbols
    dim_background_color
                        background color of points in dim. reduction space
    spat_background_color
                        background color of spatial points
    axis_text
        size of axis text

```

axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

Details

Description of parameters.

Value

ggplot

See Also

[spatDimPlot3D](#)

Examples

spatDimPlot2D(gobject)

---

spatDimPlot3D	<i>spatDimPlot3D</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",  
  show_NN_network = F,  
  nn_network_to_use = "sNN",  
  network_name = "sNN.pca",  
  show_cluster_center = F,  
  show_center_label = T,  
  center_point_size = 4,
```

```

    label_size = 16,
    select_cell_groups = NULL,
    select_cells = NULL,
    show_other_cells = T,
    other_cell_color = "lightgrey",
    other_point_size = 1.5,
    cell_color = NULL,
    color_as_factor = T,
    cell_color_code = NULL,
    dim_point_size = 3,
    nn_network_alpha = 0.5,
    show_spatial_network = F,
    spatial_network_name = "spatial_network",
    network_color = "lightgray",
    spatial_network_alpha = 0.5,
    show_spatial_grid = F,
    spatial_grid_name = "spatial_grid",
    spatial_grid_color = NULL,
    spatial_grid_alpha = 0.5,
    spatial_point_size = 3,
    axis_scale = c("cube", "real", "custom"),
    custom_ratio = NULL,
    x_ticks = NULL,
    y_ticks = NULL,
    z_ticks = NULL,
    legend_text_size = 12,
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spatDimPlot3D"
)

```

### Arguments

<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>show_NN_network</code>	
	show underlying NN network
<code>nn_network_to_use</code>	
	type of NN network to use (kNN vs sNN)

network_name	name of NN network to use, if show_NN_network = TRUE
show_cluster_center	show the center of each cluster
show_center_label	provide a label for each cluster
center_point_size	size of the center point
label_size	size of the center label
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	size of not selected cells
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
dim_point_size	size of points in dim. reduction space
nn_network_alpha	column to use for alpha of the edges
show_spatial_network	show spatial network
spatial_network_name	name of spatial network to use
spatial_network_alpha	alpha of spatial network
show_spatial_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
spatial_grid_color	color of spatial grid
spatial_point_size	size of spatial points
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
dim_point_border_col	border color of points in dim. reduction space



dim\_point\_border\_stroke  
border stroke of points in dim. reduction space

spatial\_network\_color  
color of spatial network

spatial\_other\_point\_size  
size of not selected spatial points

spatial\_other\_cells\_alpha  
alpha of not selected spatial points

dim\_other\_point\_size  
size of not selected dim. reduction points

show\_legend show legend

**Details**

Description of parameters.

**Value**

plotly

**Examples**

spatDimPlot3D(gobject)

---

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

---

**Description**

Visualize cells and gene expression according to spatial coordinates

**Usage**

```
spatGenePlot(  
  gobject,  
  expression_values = c("normalized", "scaled", "custom"),  
  genes,  
  genes_high_color = "darkred",  
  genes_mid_color = "white",  
  genes_low_color = "darkblue",  
  show_network = F,  
  network_color = NULL,  
  spatial_network_name = "spatial_network",  
  edge_alpha = NULL,  
  show_grid = F,  
  grid_color = NULL,  
  spatial_grid_name = "spatial_grid",  
  midpoint = 0,  
  scale_alpha_with_expression = FALSE,  
  point_shape = c("border", "no_border"),  
  point_size = 1,
```

```

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

```

### Arguments

<code>gobject</code>	giotto object
<code>expression_values</code>	gene expression values to use
<code>genes</code>	genes to show
<code>genes_high_color</code>	color represents high gene expression
<code>genes_mid_color</code>	color represents middle gene expression
<code>genes_low_color</code>	color represents low gene expression
<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>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>	point with border or not (border or no_border)
<code>point_size</code>	size of point (cell)
<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

legend_text	size of legend text
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for cowplot::save_plot()

Details

Description of parameters.

Value

ggplot

See Also

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

Examples

spatGenePlot(gobject)

---

spatGenePlot2D	<i>spatGenePlot2D</i>
----------------	-----------------------

---

Description

Visualize cells and gene expression according to spatial coordinates

**Usage**

```

spatGenePlot2D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes,
  genes_high_color = "darkred",
  genes_mid_color = "white",
  genes_low_color = "darkblue",
  show_network = F,
  network_color = NULL,
  spatial_network_name = "spatial_network",
  edge_alpha = NULL,
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  midpoint = 0,
  scale_alpha_with_expression = FALSE,
  point_shape = c("border", "no_border"),
  point_size = 1,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_legend = T,
  legend_text = 8,
  background_color = "white",
  axis_text = 8,
  axis_title = 8,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_plot = NA,
  return_plot = NA,
  save_plot = NA,
  save_param = list(),
  default_save_name = "spatGenePlot2D"
)

```

**Arguments**

<code>gobject</code>	giotto object
<code>expression_values</code>	gene expression values to use
<code>genes</code>	genes to show
<code>genes_high_color</code>	color represents high gene expression
<code>genes_mid_color</code>	color represents middle gene expression
<code>genes_low_color</code>	color represents low gene expression
<code>show_network</code>	show underlying spatial network
<code>network_color</code>	color of spatial network

spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
midpoint	expression midpoint
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
legend_text	size of legend text
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
...	parameters for cowplot::save_plot()

**Details**

Description of parameters.

**Value**

ggplot

**See Also**

[spatGenePlot3D](#)

**Examples**

```
spatGenePlot2D(gobject)
```

---

spatGenePlot3D

*spatGenePlot3D*


---

## Description

Visualize cells and gene expression according to spatial coordinates

## Usage

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

## Arguments

<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

spatial_network_name	name of spatial network to use
show_grid	show spatial grid
genes_high_color	color represents high gene expression
genes_mid_color	color represents middle gene expression
genes_low_color	color represents low gene expression
spatial_grid_name	name of spatial grid to use
point_size	size of point (cell)
show_legend	show legend
show_plot	show plots
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
grid_color	color of spatial grid
midpoint	expression midpoint
scale_alpha_with_expression	scale expression with ggplot alpha parameter
...	parameters for cowplot::save_plot()

Details

Description of parameters.

Value

ggplot

Examples

```
spatGenePlot3D(gobject)
```

---

spatialAEH	<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

Examples

```
spatialAEH(gobject)
```

---

spatialDE	<i>spatialDE</i>
-----------	------------------

---

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 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**

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

**Value**

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

**Examples**

```
spatialDE(gobject)
```

---

Spatial_AEH	<i>Spatial_AEH</i>
-------------	--------------------

---

**Description**

calculate automatic expression histology with spatialDE method

**Usage**

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

**Arguments**

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

**Details**

Description.

**Value**

a list or a dataframe of SVs

**Examples**

```
Spatial_AEH(gobject)
```

---

Spatial\_DE

*Spatial\_DE*


---

**Description**

calculate spatial variable genes with spatialDE method

**Usage**

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

**Arguments**

<code>gobject</code>	Giotto object
<code>show_plot</code>	show FSV plot
<code>python_path</code>	specify specific path to python if required

**Details**

Description.

**Value**

a list or a dataframe of SVs

**Examples**

```
Spatial_DE(gobject)
```

---

spatNetwDistributions *spatNetwDistributionsDistance*


---

**Description**

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

**Usage**

```

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

```

**Arguments**

<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 <a href="#">all_plots_save_function</a>
<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 <a href="#">all_plots_save_function</a>
<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 <a href="#">all_plots_save_function</a>
<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(
  gobject,
  group_by = NULL,
  group_by_subset = NULL,
  sdimx = "sdimx",
  sdimy = "sdimy",
  spat_enr_names = NULL,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  cell_color_gradient = c("blue", "white", "red"),
  gradient_midpoint = NULL,
  gradient_limits = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  point_shape = c("border", "no_border"),
  point_size = 3,
  point_border_col = "black",
  point_border_stroke = 0.1,
  show_cluster_center = F,
  show_center_label = F,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
  show_network = F,
  spatial_network_name = "spatial_network",
  network_color = NULL,
  network_alpha = 1,
  show_grid = F,
  spatial_grid_name = "spatial_grid",
  grid_color = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 1,
  other_cells_alpha = 0.1,
  coord_fix_ratio = NULL,
  title = NULL,
  show_legend = T,
  legend_text = 8,
  legend_symbol_size = 1,
```

```

background_color = "white",
axis_text = 8,
axis_title = 8,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatPlot"
)

```

### Arguments

<code>gobject</code>	giotto object
<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>	point with border or not (border or no_border)
<code>point_size</code>	size of point (cell)
<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
<code>center_point_size</code>	size of center points



label_size	size of labels
label_fontface	font of labels
show_network	show underlying spatial network
spatial_network_name	name of spatial network to use
network_color	color of spatial network
network_alpha	alpha of spatial network
show_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
grid_color	color of spatial grid
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	point size of not selected cells
other_cells_alpha	alpha of not selected cells
coord_fix_ratio	fix ratio between x and y-axis
title	title of plot
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_by	create multiple plots based on cell annotation column

## Details

Description of parameters.

Value

ggplot

See Also

[spatPlot3D](#)

Examples

```
spatPlot(gobject)
```

---

spatPlot2D	<i>spatPlot2D</i>
------------	-------------------

---

Description

Visualize cells according to spatial coordinates

Usage

```
spatPlot2D(  
  gobject,  
  group_by = NULL,  
  group_by_subset = NULL,  
  sdimx = "sdimx",  
  sdimy = "sdimy",  
  spat_enr_names = NULL,  
  cell_color = NULL,  
  color_as_factor = T,  
  cell_color_code = NULL,  
  cell_color_gradient = c("blue", "white", "red"),  
  gradient_midpoint = NULL,  
  gradient_limits = NULL,  
  select_cell_groups = NULL,  
  select_cells = NULL,  
  point_shape = c("border", "no_border"),  
  point_size = 3,  
  point_border_col = "black",  
  point_border_stroke = 0.1,  
  show_cluster_center = F,  
  show_center_label = F,  
  center_point_size = 4,  
  center_point_border_col = "black",  
  center_point_border_stroke = 0.1,  
  label_size = 4,  
  label_fontface = "bold",  
  show_network = F,  
  spatial_network_name = "spatial_network",  
  network_color = NULL,  
  network_alpha = 1,  
  show_grid = F,
```

```

    spatial_grid_name = "spatial_grid",
    grid_color = NULL,
    show_other_cells = T,
    other_cell_color = "lightgrey",
    other_point_size = 1,
    other_cells_alpha = 0.1,
    coord_fix_ratio = NULL,
    title = NULL,
    show_legend = T,
    legend_text = 8,
    legend_symbol_size = 1,
    background_color = "white",
    axis_text = 8,
    axis_title = 8,
    cow_n_col = 2,
    cow_rel_h = 1,
    cow_rel_w = 1,
    cow_align = "h",
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spatPlot2D"
  )

```

### Arguments

<code>gobject</code>	giotto object
<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>	point with border or not (border or no_border)
<code>point_size</code>	size of point (cell)

point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
show_network	show underlying spatial network
spatial_network_name	name of spatial network to use
network_color	color of spatial network
network_alpha	alpha of spatial network
show_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
grid_color	color of spatial grid
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	point size of not selected cells
other_cells_alpha	alpha of not selected cells
coord_fix_ratio	fix ratio between x and y-axis
title	title of plot
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plot	show plot

return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param
groub_by	create multiple plots based on cell annotation column

**Details**

Description of parameters.

**Value**

ggplot

**See Also**

[spatPlot3D](#)

**Examples**

```
spatPlot2D(gobject)
```

---

spatPlot2D_single	<i>spatPlot2D_single</i>
-------------------	--------------------------

---

**Description**

Visualize cells according to spatial coordinates

**Usage**

```
spatPlot2D_single(  
  gobject,  
  sdimx = "sdimx",  
  sdimy = "sdimy",  
  spat_enr_names = NULL,  
  cell_color = NULL,  
  color_as_factor = T,  
  cell_color_code = NULL,  
  cell_color_gradient = c("blue", "white", "red"),  
  gradient_midpoint = NULL,  
  gradient_limits = NULL,  
  select_cell_groups = NULL,  
  select_cells = NULL,  
  point_shape = c("border", "no_border"),  
  point_size = 3,  
  point_border_col = "black",  
  point_border_stroke = 0.1,  
  show_cluster_center = F,  
  show_center_label = F,
```

```

center_point_size = 4,
center_point_border_col = "black",
center_point_border_stroke = 0.1,
label_size = 4,
label_fontface = "bold",
show_network = F,
spatial_network_name = "spatial_network",
network_color = NULL,
network_alpha = 1,
show_grid = F,
spatial_grid_name = "spatial_grid",
grid_color = NULL,
show_other_cells = T,
other_cell_color = "lightgrey",
other_point_size = 1,
other_cells_alpha = 0.1,
coord_fix_ratio = NULL,
title = NULL,
show_legend = T,
legend_text = 8,
legend_symbol_size = 1,
background_color = "white",
axis_text = 8,
axis_title = 8,
show_plot = NA,
return_plot = NA,
save_plot = NA,
save_param = list(),
default_save_name = "spatPlot2D_single"
)

```

### Arguments

<code>gobject</code>	giotto object
<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

point_shape	point with border or not (border or no_border)
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
label_fontface	font of labels
show_network	show underlying spatial network
spatial_network_name	name of spatial network to use
network_color	color of spatial network
network_alpha	alpha of spatial network
show_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
grid_color	color of spatial grid
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
other_point_size	point size of not selected cells
other_cells_alpha	alpha of not selected cells
coord_fix_ratio	fix ratio between x and y-axis
title	title of plot
show_legend	show legend
legend_text	size of legend text
legend_symbol_size	size of legend symbols
background_color	color of plot background
axis_text	size of axis text
axis_title	size of axis title
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

**Details**

Description of parameters.

**Value**

ggplot

**See Also**

[spatPlot3D](#)

**Examples**

```
spatPlot2D_single(gobject)
```

---

spatPlot3D

*spatPlot3D*


---

**Description**

Visualize cells according to spatial coordinates

**Usage**

```
spatPlot3D(
  gobject,
  sdimx = "sdimx",
  sdimy = "sdimy",
  sdimz = "sdimz",
  point_size = 3,
  cell_color = NULL,
  cell_color_code = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_network = F,
  network_color = NULL,
  network_alpha = 1,
  other_cell_alpha = 0.5,
  spatial_network_name = "spatial_network",
  show_grid = F,
  grid_color = NULL,
  spatial_grid_name = "spatial_grid",
  title = "",
  show_legend = T,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
```



```

    z_ticks = NULL,
    show_plot = NA,
    return_plot = NA,
    save_plot = NA,
    save_param = list(),
    default_save_name = "spat3D"
)

```

## Arguments

<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>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>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>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>title</code>	title of plot
<code>show_legend</code>	show legend
<code>axis_scale</code>	the way to scale the axis
<code>custom_ratio</code>	customize the scale of the plot
<code>x_ticks</code>	set the number of ticks on the x-axis
<code>y_ticks</code>	set the number of ticks on the y-axis
<code>z_ticks</code>	set the number of ticks on the z-axis
<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 <a href="#">all_plots_save_function</a>
<code>default_save_name</code>	default save name for saving, don't change, change <code>save_name</code> in <code>save_param</code>

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

spatPlot3D(gobject)

---

spat_fish_func	<i>spat_fish_func</i>
----------------	-----------------------

---

**Description**

performs fisher exact test

**Usage**

spat\_fish\_func(gene, bin\_matrix, spat\_mat)

---

spat_OR_func	<i>spat_OR_func</i>
--------------	---------------------

---

**Description**

calculate odds-ratio

**Usage**

spat\_OR\_func(gene, bin\_matrix, spat\_mat)

---

```
specificCellCellcommunicationScores
      specificCellCellcommunicationScores
```

---

## Description

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

## Usage

```
specificCellCellcommunicationScores(
  gobject,
  spatial_network_name = "spatial_network",
  cluster_column = "cell_types",
  random_iter = 100,
  cell_type_1 = "astrocyte",
  cell_type_2 = "endothelial",
  gene_set_1,
  gene_set_2,
  log2FC_addendum = 0.1,
  min_observations = 2,
  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>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.. More details will follow soon.

**Value**

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

**Examples**

```
specificCellCellcommunicationScores(gobject)
```

---

```
split_dendrogram_in_two
```

```
split_dendrogram_in_two
```

---

**Description**

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

**Usage**

```
split_dendrogram_in_two(dend)
```

**Arguments**

dend                      dendrogram object

**Value**

list of two dendrograms and height of node

**Examples**

```
split_dendrogram_in_two(dend)
```

---

```
stitchFieldCoordinates
```

```
stitchFieldCoordinates
```

---

**Description**

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

**Usage**

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

Arguments

location\_file    location dataframe with X and Y coordinates  
offset\_file      dataframe that describes the offset for each field (see details)  
cumulate\_offset\_x  
                  (boolean) Do the x-axis offset values need to be cumulated?  
cumulate\_offset\_y  
                  (boolean) Do the y-axis offset values need to be cumulated?  
field\_col        column that indicates the field within the location\_file  
X\_coord\_col      column that indicates the x coordinates  
Y\_coord\_col      column that indicates the x coordinates  
reverse\_final\_x  
                  (boolean) Do the final x coordinates need to be reversed?  
reverse\_final\_y  
                  (boolean) Do the final y coordinates need to be reversed?

Details

Stitching of fields:

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

Value

Updated location dataframe with new X ['X\_final'] and Y ['Y\_final'] coordinates

Examples

```
stitchFieldCoordinates(gobject)
```

---

subClusterCells	<i>subClusterCells</i>
-----------------	------------------------

---

Description

subcluster cells

Usage

```
subClusterCells(  
  gobject,  
  name = "sub_clus",  
  cluster_method = c("leiden", "louvain_community", "louvain_multinet"),  
  cluster_column = NULL,  
  selected_clusters = NULL,  
  hvg_param = list(reverse_log_scale = T, difference_in_variance = 1, expression_values  
    = "normalized"),
```

```

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

```

## Arguments

<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>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	<i>subsetGiotto</i>
--------------	---------------------

---

## 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	<i>subsetGiottoLocs</i>
------------------	-------------------------

---

## 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

## Details

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

## Value

giotto object

## Examples

```
subsetGiottoLocs(gobject)
```



---

trendSceek	<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 <a href="#">trendsceek_test</a> function

## Details

This function is a wrapper for the `trendsceek_test` method implemented in the `trendsceek` package

## Value

data.frame with trendsceek spatial genes results

## Examples

```
trendSceek(gobject)
```

---

viewHMRFresults	<i>viewHMRFresults</i>
-----------------	------------------------

---

## Description

View results from doHMRF.

## Usage

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

## Arguments

gobject	giotto object
HMRFoutput	HMRF output from doHMRF
k	number of HMRF domains
betas_to_view	results from different betas that you want to view
...	paramters to visPlot()

## Details

Description ...

## Value

spatial plots with HMRF domains

## See Also

[visPlot](#)

## Examples

```
viewHMRFresults(gobject)
```

---

viewHMRFresults2D	<i>viewHMRFresults2D</i>
-------------------	--------------------------

---

## Description

View results from doHMRF.

## Usage

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

## Arguments

gobject	giotto object
HMRFoutput	HMRF output from doHMRF
k	number of HMRF domains
betas_to_view	results from different betas that you want to view
...	paramters to visPlot()

## Details

Description ...

## Value

spatial plots with HMRF domains

## See Also

[spatPlot2D](#)

## Examples

```
viewHMRFresults2D(gobject)
```

---

viewHMRFresults3D	<i>viewHMRFresults3D</i>
-------------------	--------------------------

---

## Description

View results from doHMRF.

## Usage

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

## Arguments

gobject	giotto object
HMRFoutput	HMRF output from doHMRF
k	number of HMRF domains
betas_to_view	results from different betas that you want to view
...	paramters to visPlot()

## Details

Description ...

## Value

spatial plots with HMRF domains

## See Also

[spatPlot3D](#)

## Examples

```
viewHMRFresults3D(gobject)
```

---

violinPlot

*violinPlot*


---

## Description

Creates violinplot for selected clusters

## Usage

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

## Arguments

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

save_plot	directly save the plot [boolean]
save_param	list of saving parameters from <a href="#">all_plots_save_function</a>
default_save_name	default save name for saving, don't change, change save_name in save_param

### Value

ggplot

### Examples

```
violinPlot(gobject)
```

---

visDimGenePlot	<i>visDimGenePlot</i>
----------------	-----------------------

---

### Description

Visualize cells and gene expression according to dimension reduction coordinates

### Usage

```
visDimGenePlot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  network_color = "lightgray",
  edge_alpha = NULL,
  scale_alpha_with_expression = FALSE,
  point_size = 1,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  point_border_col = "black",
  point_border_stroke = 0.1,
  midpoint = 0,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_legend = T,
  plot_method = c("ggplot", "plotly"),
  show_plots = F
)
```

**Arguments**

<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>dim3_to_use</code>	dimension to use on z-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>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_size</code>	size of point (cell)
<code>point_border_col</code>	color of border around points
<code>point_border_stroke</code>	stroke size of border around points
<code>midpoint</code>	size of point (cell)
<code>cow_n_col</code>	cowplot param: how many columns
<code>cow_rel_h</code>	cowplot param: relative height
<code>cow_rel_w</code>	cowplot param: relative width
<code>cow_align</code>	cowplot param: how to align
<code>show_legend</code>	show legend
<code>show_plots</code>	show plots

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
visDimGenePlot(gobject)
```

---

```
visDimGenePlot_2D_ggplot
      visDimGenePlot_2D_ggplot
```

---

## Description

Visualize cells and gene expression according to dimension reduction coordinates

## Usage

```
visDimGenePlot_2D_ggplot(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  network_color = "lightgray",
  edge_alpha = NULL,
  scale_alpha_with_expression = FALSE,
  point_size = 1,
  genes_high_color = "red",
  genes_mid_color = "white",
  genes_low_color = "blue",
  point_border_col = "black",
  point_border_stroke = 0.1,
  midpoint = 0,
  cow_n_col = 2,
  cow_rel_h = 1,
  cow_rel_w = 1,
  cow_align = "h",
  show_legend = T,
  show_plots = F
)
```

## Arguments

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



dim2_to_use	dimension to use on y-axis
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
edge_alpha	column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
midpoint	size of point (cell)
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_legend	show legend
show_plots	show plots

## Details

Description of parameters.

## Value

ggplot

## Examples

```
visDimGenePlot_2D_ggplot(gobject)
```

---

```
visDimGenePlot_3D_plotly
visDimGenePlot_3D_plotly
```

---

## Description

Visualize cells and gene expression according to dimension reduction coordinates

**Usage**

```
visDimGenePlot_3D_plotly(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  genes = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = 3,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  network_color = "lightgray",
  edge_alpha = NULL,
  point_size = 1,
  genes_high_color = NULL,
  genes_mid_color = "white",
  genes_low_color = "blue",
  show_legend = T,
  show_plots = F
)
```

**Arguments**

<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>dim3_to_use</code>	dimension to use on z-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>edge_alpha</code>	column to use for alpha of the edges
<code>point_size</code>	size of point (cell)
<code>show_legend</code>	show legend
<code>show_plots</code>	show plots

**Details**

Description of parameters.

Value

ggplot

Examples

```
visDimGenePlot_3D_plotly(gobject)
```

---

visDimPlot	<i>visDimPlot</i>
------------	-------------------

---

Description

Visualize cells according to dimension reduction coordinates

Usage

```
visDimPlot(  
  gobject,  
  dim_reduction_to_use = "umap",  
  dim_reduction_name = "umap",  
  dim1_to_use = 1,  
  dim2_to_use = 2,  
  dim3_to_use = NULL,  
  show_NN_network = F,  
  nn_network_to_use = "sNN",  
  network_name = "sNN.pca",  
  cell_color = NULL,  
  color_as_factor = T,  
  cell_color_code = NULL,  
  select_cell_groups = NULL,  
  select_cells = NULL,  
  show_other_cells = T,  
  other_cell_color = "lightgrey",  
  other_point_size = 0.5,  
  show_cluster_center = F,  
  show_center_label = T,  
  center_point_size = 4,  
  center_point_border_col = "black",  
  center_point_border_stroke = 0.1,  
  label_size = 4,  
  label_fontface = "bold",  
  edge_alpha = NULL,  
  point_size = 3,  
  point_border_col = "black",  
  point_border_stroke = 0.1,  
  plot_method = c("ggplot", "plotly"),  
  show_legend = T,  
  show_plot = F,  
  return_plot = TRUE,  
  save_plot = F,  
  save_dir = NULL,
```

```

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

```

### Arguments

<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>dim3_to_use</code>	dimension to use on z-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>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>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>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_size</code>	size of point (cell)
<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>show_plot</code>	show plot
<code>return_plot</code>	return ggplot object
<code>save_plot</code>	directly save the plot [boolean]
<code>save_dir</code>	directory to save the plot

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

## Details

Description of parameters.

## Value

ggplot or plotly

## Examples

```
visDimPlot(gobject)
```

---

visDimPlot_2D_ggplot	<i>visDimPlot_2D_ggplot</i>
----------------------	-----------------------------

---

## Description

Visualize cells according to dimension reduction coordinates

## Usage

```
visDimPlot_2D_ggplot(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  center_point_border_col = "black",
  center_point_border_stroke = 0.1,
  label_size = 4,
  label_fontface = "bold",
```

```

    edge_alpha = NULL,
    point_size = 1,
    point_border_col = "black",
    point_border_stroke = 0.1,
    show_legend = T,
    show_plot = F,
    return_plot = TRUE,
    save_plot = F,
    save_dir = NULL,
    save_folder = NULL,
    save_name = NULL,
    save_format = NULL,
    show_saved_plot = F,
    ...
)

```

### Arguments

<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>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>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

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

### Details

Description of parameters.

### Value

ggplot

### Examples

```
visDimPlot_2D_ggplot(gobject)
```

---

visDimPlot\_2D\_plotly    *visDimPlot\_2D\_plotly*

---

### Description

Visualize cells according to dimension reduction coordinates

### Usage

```
visDimPlot_2D_plotly(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  color_as_factor = T,
  cell_color = NULL,
  cell_color_code = NULL,
  show_cluster_center = F,
  show_center_label = T,
```

```

    center_point_size = 4,
    label_size = 4,
    edge_alpha = NULL,
    point_size = 5
  )

```

### Arguments

<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>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>color_as_factor</code>	convert color column to factor
<code>cell_color</code>	color for cells (see details)
<code>cell_color_code</code>	named vector with colors
<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>label_size</code>	size of labels
<code>edge_alpha</code>	column to use for alpha of the edges
<code>point_size</code>	size of point (cell)

### Details

Description of parameters.

### Value

plotly

### Examples

```
visDimPlot_2D_plotly(gobject)
```



---

visDimPlot\_3D\_plotly    *visDimPlot\_3D\_plotly*


---

## Description

Visualize cells according to dimension reduction coordinates

## Usage

```
visDimPlot_3D_plotly(
  gobject,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = 3,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  color_as_factor = T,
  cell_color = NULL,
  cell_color_code = NULL,
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 4,
  edge_alpha = NULL,
  point_size = 1
)
```

## Arguments

<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>dim3_to_use</code>	dimension to use on z-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)

network_name	name of NN network to use, if show_NN_network = TRUE
color_as_factor	convert color column to factor
cell_color	color for cells (see details)
cell_color_code	named vector with colors
show_cluster_center	plot center of selected clusters
show_center_label	plot label of selected clusters
center_point_size	size of center points
label_size	size of labels
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)

### Details

Description of parameters.

### Value

plotly

### Examples

```
visDimPlot_3D_plotly(gobject)
```

---

visForceLayoutPlot	<i>visForceLayoutPlot</i>
--------------------	---------------------------

---

### Description

Visualize cells according to forced layout algorithm coordinates

### Usage

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

```

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

```

### Arguments

gobject	giotto object
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	NN network to use
layout_name	name of layout to use
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
show_NN_network	show underlying NN network
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
edge_alpha	column to use for alpha of the edges
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_dir	directory to save the plot
save_folder	(optional) folder in directory to save the plot
save_name	name of plot
save_format	format of plot (e.g. tiff, png, pdf, ...)
show_saved_plot	load & display the saved plot

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
visForceLayoutPlot(gobject)
```

---

visGenePlot	<i>visGenePlot</i>
-------------	--------------------

---

**Description**

Visualize cells and gene expression according to spatial coordinates

**Usage**

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

**Arguments**

<code>gobject</code>	giotto object
<code>expression_values</code>	gene expression values to use
<code>genes</code>	genes to show
<code>genes_high_color</code>	color represents high gene expression
<code>genes_mid_color</code>	color represents middle gene expression
<code>genes_low_color</code>	color represents low gene expression
<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>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_size</code>	size of point (cell)
<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>cow_n_col</code>	cowplot param: how many columns
<code>cow_rel_h</code>	cowplot param: relative height
<code>cow_rel_w</code>	cowplot param: relative width
<code>cow_align</code>	cowplot param: how to align
<code>axis_scale</code>	three mode to adjust axis scale
<code>x_ticks</code>	number of ticks on x axis
<code>y_ticks</code>	number of ticks on y axis
<code>z_ticks</code>	number of ticks on z axis
<code>plot_method</code>	two methods of plot
<code>show_plots</code>	show plots

**Details**

Description of parameters.

**Value**

ggplot or plotly

**Examples**

```
visGenePlot(gobject)
```

---

```
visGenePlot_2D_ggplot  visGenePlot_2D_ggplot
```

---

**Description**

Visualize cells and gene expression according to spatial coordinates

**Usage**

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

**Arguments**

<code>gobject</code>	giotto object
<code>expression_values</code>	gene expression values to use
<code>genes</code>	genes to show
<code>genes_high_color</code>	color represents high gene expression
<code>genes_mid_color</code>	color represents middle gene expression

genes_low_color	color represents low gene expression
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
midpoint	expression midpoint
scale_alpha_with_expression	scale expression with ggplot alpha parameter
point_size	size of point (cell)
point_border_col	color of border around points
point_border_stroke	stroke size of border around points
show_legend	show legend
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_plots	show plots

**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
visGenePlot_2D_ggplot(gobject)
```

---

visGenePlot\_3D\_plotly    *visGenePlot\_3D\_plotly*

---

**Description**

Visualize cells and gene expression according to spatial coordinates

**Usage**

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

**Arguments**

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



z_ticks	number of ticks on z axis
show_plots	show plots
grid_color	color of spatial grid
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align

Details

Description of parameters.

Value

plotly

Examples

```
visGenePlot_3D_plotly(gobject)
```

---

visPlot	<i>visPlot</i>
---------	----------------

---

Description

Visualize cells according to spatial coordinates

Usage

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

```

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

```

### Arguments

<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 = 'sdimz')
<code>point_size</code>	size of point (cell)
<code>point_border_col</code>	color of border around points
<code>point_border_stroke</code>	stroke size of border around points
<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>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>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

show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
coord_fix_ratio	fix ratio between x and y-axis
title	title of plot
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_dir	directory to save the plot
save_folder	(optional) folder in directory to save the plot
save_name	name of plot
save_format	format of plot (e.g. tiff, png, pdf, ...)
show_saved_plot	load & display the saved plot

### Details

Description of parameters.

### Value

ggplot

### Examples

```
visPlot(gobject)
```

---

visPlot_2D_ggplot	<i>visPlot_2D_ggplot</i>
-------------------	--------------------------

---

### Description

Visualize cells according to spatial coordinates

### Usage

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

```

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

```

### Arguments

<code>gobject</code>	giotto object
<code>sdimx</code>	x-axis dimension name (default = 'sdimx')
<code>sdimy</code>	y-axis dimension name (default = 'sdimy')
<code>point_size</code>	size of point (cell)
<code>point_border_col</code>	color of border around points
<code>point_border_stroke</code>	stroke size of border around points
<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>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
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
spatial_grid_name	name of spatial grid to use
coord_fix_ratio	fix ratio between x and y-axis
title	title of plot
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_dir	directory to save the plot
save_folder	(optional) folder in directory to save the plot
save_name	name of plot
save_format	format of plot (e.g. tiff, png, pdf, ...)
show_saved_plot	load & display the saved plot

## Details

Description of parameters.

## Value

ggplot

## Examples

```
visPlot_2D_ggplot(gobject)
```

---

visPlot_2D_plotly	<i>visPlot_2D_plotly</i>
-------------------	--------------------------

---

## Description

Visualize cells according to spatial coordinates

## Usage

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

## Arguments

<code>gobject</code>	giotto object
<code>sdimx</code>	x-axis dimension name (default = 'sdimx')
<code>sdimy</code>	y-axis dimension name (default = 'sdimy')
<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>color_as_factor</code>	convert color column to factor

select_cell_groups	select a subset of the groups from cell_color
show_network	show underlying spatial network
network_color	color of spatial network
spatial_network_name	name of spatial network to use
show_grid	show spatial grid
grid_color	color of spatial grid
grid_alpha	alpha of spatial grid
spatial_grid_name	name of spatial grid to use
show_legend	show legend
show_plot	show plot

**Details**

Description of parameters.

**Value**

plotly

**Examples**

```
visPlot_2D_plotly(gobject)
```

---

visPlot_3D_plotly	<i>visPlot_3D_plotly</i>
-------------------	--------------------------

---

**Description**

Visualize cells according to spatial coordinates

**Usage**

```
visPlot_3D_plotly(
  gobject,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  point_size = 3,
  cell_color = NULL,
  cell_color_code = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  other_point_size = 0.5,
  show_network = F,
```

```

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

```

### Arguments

<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 = 'sdimz')
<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 a subset of the groups from <code>cell_color</code>
<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>spatial_grid_name</code>	name of spatial grid to use
<code>title</code>	title of plot
<code>show_legend</code>	show legend
<code>show_plot</code>	show plot
<code>point_border_col</code>	color of border around points
<code>point_border_stroke</code>	stroke size of border around points
<code>color_as_factor</code>	convert color column to factor
<code>show_grid</code>	show spatial grid
<code>grid_color</code>	color of spatial grid
<code>coord_fix_ratio</code>	fix ratio between x and y-axis



**Details**

Description of parameters.

**Value**

ggplot

**Examples**

```
visPlot_3D_plotly(gobject)
```

---

visSpatDimGenePlot	<i>visSpatDimGenePlot</i>
--------------------	---------------------------

---

**Description**

integration of visSpatDimGenePlot\_2D(ggplot) and visSpatDimGenePlot\_3D(plotly)

**Usage**

```
visSpatDimGenePlot(
  gobject,
  plot_method = c("ggplot", "plotly"),
  expression_values = c("normalized", "scaled", "custom"),
  plot_alignment = c("horizontal", "vertical"),
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  genes,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  edge_alpha_dim = NULL,
  scale_alpha_with_expression = FALSE,
  label_size = 16,
  genes_low_color = "blue",
  genes_mid_color = "white",
  genes_high_color = "red",
  dim_point_size = 3,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  network_color = "lightgray",
  spatial_network_alpha = 0.5,
```

```

show_spatial_grid = F,
spatial_grid_name = "spatial_grid",
spatial_grid_color = NULL,
spatial_grid_alpha = 0.5,
spatial_point_size = 3,
spatial_point_border_col = "black",
spatial_point_border_stroke = 0.1,
legend_text_size = 12,
axis_scale = c("cube", "real", "custom"),
custom_ratio = NULL,
x_ticks = NULL,
y_ticks = NULL,
z_ticks = NULL,
midpoint = 0,
point_size = 1,
cow_n_col = 2,
cow_rel_h = 1,
cow_rel_w = 1,
cow_align = "h",
show_legend = T,
show_plots = F
)

```

### Arguments

<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>	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>genes</code>	genes to show
<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>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>

edge_alpha_dim	dim reduction plot: column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
label_size	size for the label
genes_low_color	color to represent low expression of gene
genes_high_color	color to represent high expression of gene
dim_point_size	dim reduction plot: point size
spatial_network_name	name of spatial network to use
spatial_grid_name	name of spatial grid to use
spatial_point_size	spatial plot: point size
spatial_point_border_col	color of border around points
spatial_point_border_stroke	stroke size of border around points
legend_text_size	the size of the text in legend
axis_scale	three modes to adjust axis scale ratio
custom_ratio	set the axis scale ratio on custom
x_ticks	number of ticks on x axis
y_ticks	number of ticks on y axis
z_ticks	number of ticks on z axis
midpoint	size of point (cell)
point_size	size of point (cell)
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_legend	show legend
show_plot	show plot

## Details

Description of parameters.

## Value

ggplot or plotly

## Examples

```
visSpatDimGenePlot(gobject)
```

---

visSpatDimGenePlot\_2D    *visSpatDimGenePlot\_2D*


---

### Description

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

### Usage

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

### Arguments

gobject                      giotto object

expression_values	gene expression values to use
plot_alignment	direction to align plot
genes	genes to show
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
point_size	size of point (cell)
dim_point_border_col	color of border around points
dim_point_border_stroke	stroke size of border around points
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
edge_alpha_dim	dim reduction plot: column to use for alpha of the edges
scale_alpha_with_expression	scale expression with ggplot alpha parameter
spatial_network_name	name of spatial network to use
spatial_grid_name	name of spatial grid to use
spatial_point_size	spatial plot: point size
spatial_point_border_col	color of border around points
spatial_point_border_stroke	stroke size of border around points
midpoint	size of point (cell)
cow_n_col	cowplot param: how many columns
cow_rel_h	cowplot param: relative height
cow_rel_w	cowplot param: relative width
cow_align	cowplot param: how to align
show_legend	show legend
dim_point_size	dim reduction plot: point size
show_plot	show plot

## Details

Description of parameters.

**Value**

ggplot

**Examples**

```
visSpatDimGenePlot_2D(gobject)
```

---

```
visSpatDimGenePlot_3D  visSpatDimGenePlot_3D
```

---

**Description**

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

**Usage**

```
visSpatDimGenePlot_3D(
  gobject,
  expression_values = c("normalized", "scaled", "custom"),
  plot_alignment = c("horizontal", "vertical"),
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  genes,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  label_size = 16,
  genes_low_color = "blue",
  genes_mid_color = "white",
  genes_high_color = "red",
  dim_point_size = 3,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  network_color = "lightgray",
  spatial_network_alpha = 0.5,
  show_spatial_grid = F,
  spatial_grid_name = "spatial_grid",
  spatial_grid_color = NULL,
  spatial_grid_alpha = 0.5,
  spatial_point_size = 3,
  legend_text_size = 12,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
```

```

    y_ticks = NULL,
    z_ticks = NULL
)

```

### Arguments

gobject	giotto object
plot_alignment	direction to align plot
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim3_to_use	dimension to use on z-axis
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
genes_low_color	color represent high gene expression (see details)
genes_high_color	color represent high gene expression (see details)
nn_network_alpha	column to use for alpha of the edges
show_spatial_network	show spatial network
spatial_network_name	name of spatial network to use
network_color	color of spatial/nn network
spatial_network_alpha	alpha of spatial network
show_spatial_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
spatial_grid_color	color of spatial grid
spatial_grid_alpha	alpha of spatial grid
legend_text_size	text size of legend
show_legend	show legend
show_plot	show plot

### Details

Description of parameters.

**Value**

plotly

**Examples**

```
visSpatDimPlot_3D(gobject)
```

---

visSpatDimPlot

*visSpatDimPlot*


---

**Description**

integration of visSpatDimPlot\_2D and visSpatDimPlot\_3D

**Usage**

```
visSpatDimPlot(
  gobject,
  plot_method = c("ggplot", "plotly"),
  plot_alignment = NULL,
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  sdims = NULL,
  sdims = NULL,
  sdims = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = NULL,
  label_fontface = "bold",
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  select_cell_groups = NULL,
  select_cells = NULL,
  show_other_cells = T,
  other_cell_color = "lightgrey",
  dim_point_size = 3,
  dim_point_border_col = "black",
  dim_point_border_stroke = 0.1,
  nn_network_alpha = NULL,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  network_color = "lightgray",
  spatial_network_alpha = 0.5,
```



```

    show_spatial_grid = F,
    spatial_grid_name = "spatial_grid",
    spatial_grid_color = NULL,
    spatial_grid_alpha = 0.5,
    spatial_point_size = 3,
    legend_text_size = 12,
    spatial_point_border_col = "black",
    spatial_point_border_stroke = 0.1,
    show_legend = T,
    axis_scale = c("cube", "real", "custom"),
    custom_ratio = NULL,
    x_ticks = NULL,
    y_ticks = NULL,
    z_ticks = NULL,
    show_plot = F
  )

```

### Arguments

<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>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>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>nn_network_alpha</code>	column to use for alpha of the edges
<code>show_spatial_network</code>	show spatial network

```

spatial_network_name
    name of spatial network to use
spatial_network_alpha
    alpha of spatial network
show_spatial_grid
    show spatial grid
spatial_grid_name
    name of spatial grid to use
spatial_grid_color
    color of spatial grid
spatial_grid_alpha
    alpha of spatial grid
legend_text_size
    text size of legend
show_legend
    show legend
show_plot
    show plot
plot_mode
    choose the mode to draw plot : ggplot or plotly
spatial_network_color
    color of spatial network

```

### Details

Description of parameters.

### Value

ggplot or plotly

### Examples

```
visSpatDimPlot(gobject)
```

---

visSpatDimPlot_2D	<i>visSpatDimPlot_2D</i>
-------------------	--------------------------

---

### Description

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

### Usage

```

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

```

```

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

```

### Arguments

<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>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)

color_as_factor	convert color column to factor
cell_color_code	named vector with colors
select_cell_groups	select subset of cells/clusters based on cell_color parameter
select_cells	select subset of cells based on cell IDs
show_other_cells	display not selected cells
other_cell_color	color of not selected cells
nn_network_alpha	column to use for alpha of the edges
show_spatial_network	show spatial network
spatial_network_name	name of spatial network to use
spatial_network_color	color of spatial network
show_spatial_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
spatial_grid_color	color of spatial grid
show_legend	show legend
show_plot	show plot
return_plot	return ggplot object
save_plot	directly save the plot [boolean]
save_dir	directory to save the plot
save_folder	(optional) folder in directory to save the plot
save_name	name of plot
save_format	format of plot (e.g. tiff, png, pdf, ...)
show_saved_plot	load & display the saved plot

### Details

Description of parameters.

### Value

ggplot

### Examples

```
visSpatDimPlot_2D(gobject)
```

---

visSpatDimPlot_3D	<i>visSpatDimPlot_3D</i>
-------------------	--------------------------

---

## Description

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

## Usage

```
visSpatDimPlot_3D(
  gobject,
  plot_alignment = c("horizontal", "vertical"),
  dim_reduction_to_use = "umap",
  dim_reduction_name = "umap",
  dim1_to_use = 1,
  dim2_to_use = 2,
  dim3_to_use = NULL,
  sdimx = NULL,
  sdimy = NULL,
  sdimz = NULL,
  show_NN_network = F,
  nn_network_to_use = "sNN",
  network_name = "sNN.pca",
  show_cluster_center = F,
  show_center_label = T,
  center_point_size = 4,
  label_size = 16,
  cell_color = NULL,
  color_as_factor = T,
  cell_color_code = NULL,
  dim_point_size = 3,
  nn_network_alpha = 0.5,
  show_spatial_network = F,
  spatial_network_name = "spatial_network",
  network_color = "lightgray",
  spatial_network_alpha = 0.5,
  show_spatial_grid = F,
  spatial_grid_name = "spatial_grid",
  spatial_grid_color = NULL,
  spatial_grid_alpha = 0.5,
  spatial_point_size = 3,
  axis_scale = c("cube", "real", "custom"),
  custom_ratio = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  z_ticks = NULL,
  legend_text_size = 12
)
```

## Arguments

gobject                  giotto object

plot_alignment	direction to align plot
dim_reduction_to_use	dimension reduction to use
dim_reduction_name	dimension reduction name
dim1_to_use	dimension to use on x-axis
dim2_to_use	dimension to use on y-axis
dim3_to_use	dimension to use on z-axis
show_NN_network	show underlying NN network
nn_network_to_use	type of NN network to use (kNN vs sNN)
network_name	name of NN network to use, if show_NN_network = TRUE
cell_color	color for cells (see details)
color_as_factor	convert color column to factor
cell_color_code	named vector with colors
nn_network_alpha	column to use for alpha of the edges
show_spatial_network	show spatial network
spatial_network_name	name of spatial network to use
spatial_network_alpha	alpha of spatial network
show_spatial_grid	show spatial grid
spatial_grid_name	name of spatial grid to use
spatial_grid_color	color of spatial grid
spatial_grid_alpha	alpha of spatial grid
legend_text_size	text size of legend
spatial_network_color	color of spatial network
show_legend	show legend
show_plot	show plot

## Details

Description of parameters.

## Value

plotly

**Examples**

```
visSpatDimPlot_3D(gobject)
```

---

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)
```

---

write_giotto_viewer_annotation	<i>write_giotto_viewer_annotation</i>
--------------------------------	---------------------------------------

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

---

```
write_giotto_viewer_dim_reduction
      write_giotto_viewer_dim_reduction
```

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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



---

```
write_giotto_viewer_numeric_annotation  
    write_giotto_viewer_numeric_annotation
```

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

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