Package ‘Voyager’

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Type Package

Title From geospatial to spatial omics

Version 1.4.0

Description SpatialFeatureExperiment (SFE) is a new S4 class for working with spatial single-cell genomics data. The voyager package implements basic exploratory spatial data analysis (ESDA) methods for SFE. Univariate methods include univariate global spatial ESDA methods such as Moran's I, permutation testing for Moran's I, and correlograms. Bivariate methods include Lee's L and cross variogram. Multivariate methods include MULTISPATI PCA and multivariate local Geary's C recently developed by Anselin. The Voyager package also implements plotting functions to plot SFE data and ESDA results.

Imports BiocParallel, bluster, ggbiascale, ggplot2 (>= 3.4.0), grDevices, grid, lifecycle, Matrix, matrixStats, methods, patchwork, rlang, RSpectra, S4Vectors, scales, scico, sf, SingleCellExperiment, SpatialExperiment, SpatialFeatureExperiment (>= 1.2.1), spdep, stats, SummarizedExperiment, terra, utils

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BugReports https://github.com/pachterlab/voyager/issues
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geom_spi.R' 'gstat.R' 'listSFEMethods.R' 'multivariate.R'
'plot-non-spatial.R' 'plot-univar-downstream.R' 'plot.R'
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Author Lambda Moses [aut, cre] (<https://orcid.org/0000-0002-7092-9427>),
Kayla Jackson [aut] (<https://orcid.org/0000-0001-6483-0108>),
Laura Luebbert [aut] (<https://orcid.org/0000-0003-1379-2927>),
Lior Pachter [aut, rev] (<https://orcid.org/0000-0002-9164-6231>)

Maintainer Lambda Moses <dlu2@caltech.edu>

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calculateBivariate

Bivariate spatial statistics

Description
These functions perform bivariate spatial analysis. In this version, the bivariate global method supported are `lee`, `lee.mc`, and `lee.test` from spdep, and cross variograms from gstat (use `cross_variogram` and `cross_variogram_map` for type argument, see `variogram-internal`). Global Lee statistic is computed by my own implementation that is much faster than that in spdep. Bivariate local methods supported are `lee` (use `locallee` for type argument) and `localmoran_bv` a bivariate version of Local Moran in spdep.

Usage

```r
## S4 method for signature 'ANY'
calculateBivariate(
  x,
  y = NULL,
  type,
  listw = NULL,
  coords_df = NULL,
  BPPARAM = SerialParam(),
  zero.policy = NULL,
  returnDF = TRUE,
  p.adjust.method = "BH",
  name = NULL,
  ...
)

## S4 method for signature 'SpatialFeatureExperiment'
calculateBivariate(
  x,
  type,
  feature1,
```

```
calculateBivariate

feature2 = NULL,
colGraphName = 1L,
colGeometryName = 1L,
sample_id = "all",
exprs_values = "logcounts",
BPPARAM = SerialParam(),
zero.policy = NULL,
returnDF = TRUE,
p.adjust.method = "BH",
swap_rownames = NULL,
name = NULL,

)

runBivariate(
  x,
type,
feature1,
feature2 = NULL,
colGraphName = 1L,
colGeometryName = 1L,
sample_id = "all",
exprs_values = "logcounts",
BPPARAM = SerialParam(),
swap_rownames = NULL,
name = NULL,
overwrite = FALSE,

)

Arguments

x A numeric matrix whose rows are features/genes, or a numeric vector (then y must be specified), or a SpatialFeatureExperiment (SFE) object with such a matrix in an assay.

y A numeric matrix whose rows are features/genes, or a numeric vector. Bivariate statics will be computed for all pairwise combinations of row names of x and row names of y, except in cross variogram where combinations within x and y are also computed.

type An SFEMethod object, or a string matching the name of an SFEMethod object. The methods mentioned above correspond to SFEMethod objects already implemented in the Voyager package. Use listSFEMethods to see which methods are available. You can implement new SFEMethod objects to apply Voyager functions to other spatial analysis methods. This is in part inspired by the caret, parsnip, and BiocSingular packages.

listw Weighted neighborhood graph as a spdep listw object. Not used when the
method specified in type does not use a spatial neighborhood graph, such as the variogram.

coords_df
A sf data frame specifying location of each cell. Not used when the method specified in type uses a spatial neighborhood graph. Must be specified otherwise.

BPPARAM
A BiocParallelParam object specifying whether and how computing the metric for numerous genes shall be parallelized.

zero.policy
default NULL, use global option value; if TRUE assign zero to the lagged value of zones without neighbours, if FALSE assign NA

returnDF
Logical, when the results are not added to a SFE object, whether the results should be formatted as a DataFrame.

p.adjust.method
Method to correct for multiple testing, passed to p.adjustSP. Methods allowed are in p.adjust.methods.

name
Name to use to store the results, defaults to the name in the SFEMethod object passed to argument type. Can be set to distinguish between results from the same method but with different parameters.

...
Other arguments passed to S4 method (for convenience wrappers like calculateMoransI) or method used to compute metrics as specified by the argument type (as in more general functions like calculateUnivariate). See documentation of functions with the same name as specified in type in the spdep package for the method specific arguments. For variograms, see .variogram.

feature1
ID or symbol of the first genes in SFE object, for the argument x.

feature2
ID or symbol of the second genes in SFE object, for the argument x. Mandatory if length of feature1 is 1.

colGraphName
Name of the listw graph in the SFE object that corresponds to entities represented by columns of the gene count matrix. Use colGraphNames to look up names of the available graphs for cells/spots. Note that for multiple sample_ids, it is assumed that all of them have a graph of this same name.

colGeometryName
Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots. In the SFE method of calculateUnivariate, this is to specify location of cells for methods that don’t take a spatial neighborhood graph such as the variogram. If the geometry is not of type POINT, then spatialCoords(x) is used instead.

sample_id
Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.

exprs_values
Integer scalar or string indicating which assay of x contains the expression values.

swap_rownames
Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.

overwrite
Logical, whether to overwrite existing results with the same name. Defaults to FALSE.
calculateMultivariate

Value

The calculateBivariate function returns a correlation matrix for global Lee, and the results for the each pair of genes for other methods. Global results are not stored in the SFE object. Some methods return one result for each pair of genes, while some return pairwise results for more than 2 genes jointly. Local results are stored in the localResults field in the SFE object, with name the concatenation the two gene names separated by two underscores (_-)_.

Examples

```r
library(SFEData)
library(scater)
library(scran)
library(SpatialFeatureExperiment)
library(SpatialExperiment)
sfe <- McKellarMuscleData()
sfe <- sfe[,sfe$in_tissue]
sfe <- logNormCounts(sfe)
gs <- modelGeneVar(sfe)
hvgs <- getTopHVGs(gs, fdr.threshold = 0.01)
g <- colGraph(sfe, "visium") <- findVisiumGraph(sfe)

# Matrix method
mat <- logcounts(sfe)[hvgs[1:5],]
mat <- logcounts(sfe)[hvgs[1:5],]
df <- df2sf(spatialCoords(sfe), spatialCoordsNames(sfe))
out <- calculateBivariate(mat, type = "lee", listw = g)
out <- calculateBivariate(mat, type = "cross_variogram", coords_df = df)

# SFE method
out <- calculateBivariate(sfe, type = "lee",
feature1 = c("Myh1", "Myh2", "Csrp3"), swap_rownames = "symbol")
out2 <- calculateBivariate(sfe, type = "lee.test", feature1 = "Myh1",
feature2 = "Myh2", swap_rownames = "symbol")
sfe <- runBivariate(sfe, type = "locallee", feature1 = "Myh1",
feature2 = "Myh2", swap_rownames = "symbol")
```

calculateMultivariate  Multivariate spatial data analysis

Description

These functions perform multivariate spatial data analysis, usually spatially informed dimension reduction.

Usage

```r
## S4 method for signature 'ANY,SFEMethod'
calculateMultivariate(
x,
type,
```
calculateMultivariate

```r
listw = NULL,
transposed = FALSE,
zero.policy = TRUE,
p.adjust.method = "BH",
...
)
```

## S4 method for signature 'ANY,character'
calculateMultivariate(x, type, listw = NULL, transposed = FALSE, ...)

## S4 method for signature 'SpatialFeatureExperiment,ANY'
calculateMultivariate(
  x,
  type,
  colGraphName = 1L,
  subset_row = NULL,
  exprs_values = "logcounts",
  sample_action = c("joint", "separate"),
  BPPARAM = SerialParam(),
  ...
)

runMultivariate(
  x,
  type,
  colGraphName = 1L,
  subset_row = NULL,
  exprs_values = "logcounts",
  sample_action = c("joint", "separate"),
  BPPARAM = SerialParam(),
  name = NULL,
  dest = c("reducedDim", "colData"),
  ...
)

Arguments

- **x**  A numeric matrix whose rows are features/genes, or a SpatialFeatureExperiment (SFE) object with such a matrix in an assay.
- **type**  An SFEMethod object, or a string matching the name of an SFEMethod object. The methods mentioned above correspond to SFEMethod objects already implemented in the Voyager package. Use `listSFEMethods` to see which methods are available. You can implement new SFEMethod objects to apply Voyager functions to other spatial analysis methods. This is in part inspired by the caret, parsnip, and BiocSingular packages.
- **listw**  Weighted neighborhood graph as a spdep listw object. Not used when the method specified in type does not use a spatial neighborhood graph, such as the variogram.
transposed Logical, whether the matrix has genes in columns and cells in rows.

zero.policy default NULL, use global option value; if TRUE assign zero to the lagged value of zones without neighbours, if FALSE assign NA

p.adjust.method Method to correct for multiple testing, passed to `p.adjustSP`. Methods allowed are in `p.adjust.methods`.

... Extra arguments passed to the specific multivariate method. For example, see `multispati_rsp` for arguments for MULTISPATI PCA. See `localC` for arguments for "localC_multi" and "localC_perm_multi".

colGraphName Name of the listw graph in the SFE object that corresponds to entities represented by columns of the gene count matrix. Use `colGraphNames` to look up names of the available graphs for cells/spots. Note that for multiple sample_ids, it is assumed that all of them have a graph of this same name.

subset_row Vector specifying the subset of features to use for dimensionality reduction. This can be a character vector of row names, an integer vector of row indices or a logical vector.

exprs_values Integer scalar or string indicating which assay of x contains the expression values.

sample_action Character, either "joint" or "separate". Spatial methods depend on the spatial coordinates and/or spatial neighborhood graph, which is why `SpatialExperiment` uses sample_id to keep coordinates from different samples separate. Some spatial methods can be sensibly run jointly for multiple samples. In this case, "joint" will run the method jointly for all samples, and "separate" will run the method separately for each sample and concatenate the results.

BPPARAM A `BiocParallelParam` object specifying whether and how computing the metric for numerous genes shall be parallelized. This is to parallelize computation across multiple samples when there are a large number of samples. Be cautious if using an optimized BLAS for matrix operations that supports multithreading.

name Name to use to store the results, defaults to the name in the SFEMethod object passed to argument `type`. Can be set to distinguish between results from the same method but with different parameters.

dest Character, either "reducedDim" or "colData". If the output of the multivariate method is a matrix or array, as in spatially informed dimension reduction, then the only option is "reducedDim", so the results will be stored in `reducedDim` of the SFE object. If the output is a vector, as in the multivariate version of `localC`, then it will be stored in `colData`. Data frame output, such as from `localC_perm`, can be stored in either `reducedDim` or `colData`.

Details

For the argument `type`, this package supports "multispati" for MULTISPATI PCA, "localC_multi" for a multivariate generalization of Geary’s C, "localC_perm_multi" for the multivariate Geary’s C with permutation testing, and "gwpca" for geographically weighted PCA.
**calculateUnivariate**

**Value**

In `calculateMultivariate`, a matrix for cell embeddings whose attributes include loadings and eigenvalues if relevant, ready to be added to the SFE object with `reducedDim` setter. For `run*`, a `SpatialFeatureExperiment` object with the results added. See Details for where the results are stored.

**References**


**Examples**

```r
# example code
library(SFEDA)
library(scater)
library(scran)
sfe <- McKellarMuscleData()
sfe <- logNormCounts(sfe)
gvs <- modelGeneVar(sfe)
hvgs <- getTopHVGS(gvs, fdr.threshold = 0.05)
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
sfe <- runMultivariate(sfe, "multispati", subset_row = hvgs)
```

---

**calculateUnivariate**  
*Univariate spatial statistics*

**Description**

These functions compute univariate spatial statistics, both global and local, on matrices, data frames, and SFE objects. For SFE objects, the statistics can be computed for numeric columns of `colData`, `colGeometries`, and `annotGeometries`, and the results are stored within the SFE object. `calculateMoransI` and `runMoransI` are convenience wrappers for `calculateUnivariate` and `runUnivariate` respectively.

**Usage**

```r
## S4 method for signature 'ANY,SFEMethod'
calculateUnivariate(
  x,
  type,
  listw = NULL,
  coords_df = NULL,
  BPPARAM = SerialParam(),
  zero.policy = NULL,
)```

calculateUnivariate

returnDF = TRUE,
p.adjust.method = "BH",
name = NULL,
...

## S4 method for signature 'ANY,character'
calculateUnivariate(
x,
type,
listw = NULL,
coords_df = NULL,
BPPARAM = SerialParam(),
zero.policy = NULL,
returnDF = TRUE,
p.adjust.method = "BH",
name = NULL,
...
)

## S4 method for signature 'SpatialFeatureExperiment,ANY'
calculateUnivariate(
x,
type,
features = NULL,
colGraphName = 1L,
colGeometryName = 1L,
sample_id = "all",
exprs_values = "logcounts",
BPPARAM = SerialParam(),
zero.policy = NULL,
returnDF = TRUE,
include_self = FALSE,
p.adjust.method = "BH",
swap_rownames = NULL,
name = NULL,
...
)

## S4 method for signature 'ANY'
calculateMoransI(
x,
...
BPPARAM = SerialParam(),
zero.policy = NULL,
name = "moran"
)
calculateUnivariate

## S4 method for signature 'SpatialFeatureExperiment'
calculateMoransI(
  x,
  features = NULL,
  colGraphName = 1L,
  colGeometryName = 1L,
  sample_id = "all",
  exprs_values = "logcounts",
  BPPARAM = SerialParam(),
  zero.policy = NULL,
  returnDF = TRUE,
  include_self = FALSE,
  p.adjust.method = "BH",
  swap_rownames = NULL,
  name = NULL,
  ...
)

colDataUnivariate(
  x,
  type,
  features,
  colGraphName = 1L,
  sample_id = "all",
  BPPARAM = SerialParam(),
  zero.policy = NULL,
  include_self = FALSE,
  p.adjust.method = "BH",
  name = NULL,
  ...
)

colDataMoransI(
  x,
  features,
  colGraphName = 1L,
  sample_id = "all",
  BPPARAM = SerialParam(),
  zero.policy = NULL,
  include_self = FALSE,
  p.adjust.method = "BH",
  name = NULL,
  ...
)

colGeometryUnivariate(
  x,
  type,
calculateUnivariate

features,
        colGeometryName = 1L,
        colGraphName = 1L,
        sample_id = "all",
        BPPARAM = SerialParam(),
        zero.policy = NULL,
        include_self = FALSE,
        p.adjust.method = "BH",
        name = NULL,
        ...
    )

colGeometryMoransI(
    x,
    features,
        colGeometryName = 1L,
        colGraphName = 1L,
        sample_id = "all",
        BPPARAM = SerialParam(),
        zero.policy = NULL,
        include_self = FALSE,
        p.adjust.method = "BH",
        name = NULL,
        ...
    )

annotGeometryUnivariate(
    x,
    type,
    features,
        annotGeometryName = 1L,
        annotGraphName = 1L,
        sample_id = "all",
        BPPARAM = SerialParam(),
        zero.policy = NULL,
        include_self = FALSE,
        p.adjust.method = "BH",
        name = NULL,
        ...
    )

annotGeometryMoransI(
    x,
    features,
        annotGeometryName = 1L,
        annotGraphName = 1L,
        sample_id = "all",
        BPPARAM = SerialParam(),
calculateUnivariate

zero.policy = NULL,
include_self = FALSE,
p.adjust.method = "BH",
name = NULL,
...
)
runUnivariate(
  x,
type,
features = NULL,
colGraphName = 1L,
colGeometryName = 1L,
sample_id = "all",
exprs_values = "logcounts",
BPPARAM = SerialParam(),
swap_rownames = NULL,
zero.policy = NULL,
include_self = FALSE,
p.adjust.method = "BH",
name = NULL,
overwrite = FALSE,
...
)
runMoransI(
  x,
features = NULL,
colGraphName = 1L,
colGeometryName = 1L,
sample_id = "all",
exprs_values = "logcounts",
BPPARAM = SerialParam(),
swap_rownames = NULL,
zero.policy = NULL,
include_self = FALSE,
p.adjust.method = "BH",
name = NULL,
...
)
reducedDimUnivariate(
  x,
type,
dimred = 1L,
components = 1L,
colGraphName = 1L,
sample_id = "all",
...
BPPARAM = SerialParam(),
zero.policy = NULL,
include_self = FALSE,
p.adjust.method = "BH",
name = NULL,
...)

reducedDimMoransI(
x,
dimred = 1L,
components = 1L,
colGraphName = 1L,
sample_id = "all",
BPPARAM = SerialParam(),
zero.policy = NULL,
include_self = FALSE,
p.adjust.method = "BH",
name = NULL,
...)

Arguments

x A numeric matrix whose rows are features/genes, or a SpatialFeatureExperiment (SFE) object with such a matrix in an assay.
type An SFEMethod object, or a string matching the name of an SFEMethod object. The methods mentioned above correspond to SFEMethod objects already implemented in the Voyager package. Use listSFEMethods to see which methods are available. You can implement new SFEMethod objects to apply Voyager functions to other spatial analysis methods. This is in part inspired by the caret, parsnip, and BiocSingular packages.
listw Weighted neighborhood graph as a spdep listw object. Not used when the method specified in type does not use a spatial neighborhood graph, such as the variogram.
coords_df A sf data frame specifying location of each cell. Not used when the method specified in type uses a spatial neighborhood graph. Must be specified otherwise.
BPPARAM A BiocParallelParam object specifying whether and how computing the metric for numerous genes shall be parallelized.
zero.policy default NULL, use global option value; if TRUE assign zero to the lagged value of zones without neighbours, if FALSE assign NA
returnDF Logical, when the results are not added to a SFE object, whether the results should be formatted as a DataFrame.
p.adjust.method Method to correct for multiple testing, passed to p.adjustSP. Methods allowed are in p.adjust.methods.
**calculateUnivariate**

- **name**: Name to use to store the results, defaults to the name in the SFEMethod object passed to argument type. Can be set to distinguish between results from the same method but with different parameters.

- **features**: Genes (calculate* SFE method and run*) or numeric columns of colData(x) (colData*) or any colGeometry (colGeometry*) or annotGeometry (annotGeometry*) for which the univariate metric is to be computed. Default to NULL. When NULL, then the metric is computed for all genes with the values in the assay specified in the argument exprs_values. This can be parallelized with the argument BPPARAM. For genes, if the row names of the SFE object are Ensembl IDs, then the gene symbol can be used and converted to IDs behind the scene with a column in rowData can be specified in swap_rownames. However, if one symbol matches multiple IDs, a warning will be given and the first match will be used. Internally, the results are always stored by the Ensembl ID rather than symbol.

- **colGraphName**: Name of the listw graph in the SFE object that corresponds to entities represented by columns of the gene count matrix. Use colGraphNames to look up names of the available graphs for cells/spots. Note that for multiple sample_ids, it is assumed that all of them have a graph of this same name.

- **colGeometryName**: Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots. In the SFE method of calculateUnivariate, this is to specify location of cells for methods that don’t take a spatial neighborhood graph such as the variogram. If the geometry is not of type POINT, then spatialCoords(x) is used instead.

- **sample_id**: Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.

- **exprs_values**: Integer scalar or string indicating which assay of x contains the expression values.

- **include_self**: Logical, whether the spatial neighborhood graph should include edges from each location to itself. This is for Getis-Ord Gi* as in localG and localG_perm, not to be used for any other method.

- **swap_rownames**: Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.

- **annotGeometryName**: Name of a annotGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use annotGeometryNames to look up names of the sf data frames associated with annotations.

- **annotGraphName**: Name of the listw graph in the SFE object that corresponds to the annotGeometry of interest. Use annotGraphNames to look up names of available annotation graphs.
overwrite Logical, whether to overwrite existing results with the same name. Defaults to FALSE.

dimred Name of a dimension reduction, can be seen in reducedDimNames.

components Numeric vector of which components in the dimension reduction to compute spatial statistics on.

Details

Most univariate methods in the package spdep are supported here. These methods are global, meaning returning one result for all spatial locations in the dataset: moran, geary, moran.mc, geary.mc, moran.test, geary.test, globalG.test, sp.correlogram. The variogram and variogram map from the gstat package are also supported.

The following methods are local, meaning each location has its own results: moran.plot, localmoran, localmoran_perm, localC, localC_perm, localG, localG_perm, LOSH, LOSH.mc, LOSH.cs. The GWmodel::gwss method will be supported soon, but is not supported yet.

Global results for genes are stored in rowData. For colGeometry and annotGeometry, the results are added to an attribute of the data frame called featureData, which is a DataFrame analogous to rowData for the gene count matrix, and can be accessed with the geometryFeatureData function. New column names in featureData would follow the same rules as in rowData. For colData, the results can be accessed with the colFeatureData function.

Local results are stored in the field localResults field of the SFE object, which can be accessed with localResults or localResult. If the results have p-values, then -log10 p and adjusted -log10 p are added. Note that in the multiple testing correction, p.adjustSP is used.

When the results are stored in the SFE object, parameters used to compute the results as well as to construct the spatial neighborhood graph are also added. For localResults, the parameters are added to the metadata field params of the localResults sorted by name, which defaults to the name in the SFEMethod object as specified in the type argument. For global methods, parameters for results for genes are in the metadata of rowData(x), organized by name (metadata(rowData(x))$params[[name]]). For colData, the global method parameters are stored in metadata of colData in the field params (metadata(colData(x))$params[[name]]). For geometries, the global method parameters are in an attribute named "params" of the corresponding sf data frame (attr(df, "params")[[name]]).

Value

In calculateUnivariate, if returnDF = TRUE, then a DataFrame, otherwise a list each element of which is the results for each feature. For run*, a SpatialFeatureExperiment object with the results added. See Details for where the results are stored.

References


Examples

library(SpatialFeatureExperiment)
library(SingleCellExperiment)
library(SFEData)
sfe <- McKellarMuscleData("small")
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
features_use <- rownames(sfe)[1:5]

# Moran's I
moran_results <- calculateMoransI(sfe,
    features = features_use,
    colGraphName = "visium",
    exprs_values = "counts"
)

# This does not advocate for computing Moran's I on raw counts.
# Just an example for function usage.
sfe <- runMoransI(sfe,
    features = features_use, colGraphName = "visium",
    exprs_values = "counts"
)

# Look at the results
head(rowData(sfe))

# Local Moran's I
sfe <- runUnivariate(sfe,
    type = "localmoran", features = features_use,
    colGraphName = "visium", exprs_values = "counts"
)
head(localResult(sfe, "localmoran", features_use[1]))

# For colData
sfe <- colDataUnivariate(sfe,
    type = "localmoran", features = "nCounts",
    colGraphName = "visium"
)
head(localResult(sfe, "localmoran", "nCounts"))

# For annotGeometries
annotGraph(sfe, "myofiber_tri2nb") <- 
    findSpatialNeighbors(sfe,
        type = "myofiber_simplified", MARGIN = 3L,
        method = "tri2nb", dist_type = "idw",
        zero.policy = TRUE
    )
sfe <- annotGeometryUnivariate(sfe,
    type = "localG", features = "area",
    annotGraphName = "myofiber_tri2nb",
    annotGeometryName = "myofiber_simplified",
    zero.policy = TRUE
)
head(localResult(sfe, "localG", "area",  
annotGeometryName = "myofiber_simplified")
)

clusterCorrelograms  
Find clusters of correlogram patterns

Description
Cluster the correlograms to find patterns in length scales of spatial autocorrelation. All the correlograms clustered must be computed with the same method and have the same number of lags. Correlograms are clustered jointly across samples.

Usage
clusterCorrelograms(
  sfe,  
  features,  
  BLUSPARAM,  
  sample_id = "all",  
  method = "I",  
  colGeometryName = NULL,  
  annotGeometryName = NULL,  
  reducedDimName = NULL,  
  swap_rownames = NULL,  
  name = "sp.correlogram"
)

Arguments
sfe A SpatialFeatureExperiment object with correlograms computed for features of interest.
features Features whose correlograms to cluster.
BLUSPARAM A BlusterParam object specifying the algorithm to use.
sample_id Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.
method "corr" for correlation, "I" for Moran's I, "C" for Geary's C
colGeometryName Name of colGeometry from which to look for features.
annotGeometryName Name of annotGeometry from which to look for features.
reducedDimName Name of a dimension reduction, can be seen in reducedDimNames, colGeometryName and annotGeometryName have precedence over reducedDimName.
swap_rownames Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.
named Name under which the correlogram results are stored, which is by default "sp.correlogram".
Value

A data frame with 3 columns: feature for the features, cluster a factor for cluster membership of the features within each sample, and sample_id for the sample.

Examples

```r
library(SpatialFeatureExperiment)
library(SFEData)
library(bluster)
sfe <- McKellarMuscleData("small")
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
inds <- c(1, 3, 4, 5)
sfe <- runUnivariate(sfe,
  type = "sp.correlogram",
  features = rownames(sfe)[inds],
  exprs_values = "counts", order = 5
)
clust <- clusterCorrelograms(sfe,
  features = rownames(sfe)[inds],
  BLUSPARAM = KmeansParam(2)
)
```

Description

The Moran plot plots the value at each location on the x axis, and the average of the neighbors of each locations on the y axis. Sometimes clusters can be seen on the Moran plot, indicating different types of neighborhoods.

Usage

```r
clusterMoranPlot(
  sfe, features, BLUSPARAM,
  sample_id = "all",
  colGeometryName = NULL, annotGeometryName = NULL,
  swap_rownames = NULL
)
```

Arguments

- **sfe** | A SpatialFeatureExperiment object with Moran plot computed for the feature of interest. If the Moran plot for that feature has not been computed for that feature in this sample_id, it will be calculated and stored in rowData. See `calculateUnivariate`.
features

Features whose Moran plot are to be cluster. Features whose Moran plots have not been computed will be skipped, with a warning.

BLUSPARAM

A BlusterParam object specifying the algorithm to use.

sample_id

Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.

colGeometryName

Name of colGeometry from which to look for features.

annotGeometryName

Name of annotGeometry from which to look for features.

swap_rownames

Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.

Value

A data frame each column of which is a factor for cluster membership of each feature. The column names are the features.

Examples

library(SpatialFeatureExperiment)
library(SingleCellExperiment)
library(SFEData)
library(bluster)
sfe <- McKellarMuscleData("small")
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
# Compute moran plot
sfe <- runUnivariate(sfe,
  type = "moran.plot", features = rownames(sfe)[1],
  exprs_values = "counts"
)
clusts <- clusterMoranPlot(sfe, rownames(sfe)[1],
  BLUSPARAM = KmeansParam(2)
)

---

clusterVariograms

Cluster variograms of multiple features

Description

This function clusters variograms of features across samples to find patterns in decays in spatial autocorrelation. The fitted variograms are clustered as different samples can have different distance bins.
clusterVariograms

Usage

classclusterVariograms(
  sfe,
  features,
  BLUSPARAM,
  n = 20,
  sample_id = "all",
  colGeometryName = NULL,
  annotGeometryName = NULL,
  reducedDimName = NULL,
  swap_rownames = NULL,
  name = "variogram"
)

Arguments

sfe A SpatialFeatureExperiment object with correlograms computed for features of interest.
features Features whose correlograms to cluster.
BLUSPARAM A BlusterParam object specifying the algorithm to use.
n Number of points on the fitted variogram line.
sample_id Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.
colGeometryName Name of colGeometry from which to look for features.
annotGeometryName Name of annotGeometry from which to look for features.
reducedDimName Name of a dimension reduction, can be seen in reducedDimNames. colGeometryName and annotGeometryName have precedence over reducedDimName.
swap_rownames Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.
name Name under which the correlogram results are stored, which is by default "sp.correlogram".

Value

A data frame with 3 columns: feature for the features, cluster a factor for cluster membership of the features within each sample, and sample_id for the sample.

Examples

library(SFEData)
library(scater)
library(bluster)
library(Matrix)
sfe <- McKellarMuscleData()
sfe <- logNormCounts(sfe)  
# Just the highly expressed genes
gs <- order(Matrix::rowSums(counts(sfe)), decreasing = TRUE)[1:10]
gen <- rownames(sfe)[gs]

sfe <- runUnivariate(sfe, "variogram", features = genes)
clusts <- clusterVariograms(sfe, genes, BLUSPARAM = HclustParam(),
swap_rownames = "symbol")

# Plot the clustering
plotVariogram(sfe, genes, color_by = clusts, group = "feature",
use_lty = FALSE, swap_rownames = "symbol", show_np = FALSE)

---

### colFeatureData

Get metadata of colData, rowData, and geometries

#### Description

Results of spatial analyses on columns in colData, rowData, and geometries are stored in their metadata, which can be accessed by the `metadata` function. The `colFeatureData` function allows the users to more directly access these results.

#### Usage

```r
colFeatureData(sfe)
rowFeatureData(sfe)
geometryFeatureData(sfe, type, MARGIN = 2L)
reducedDimFeatureData(sfe, dimred)
```

#### Arguments

- `sfe`: An SFE object.
- `type`: Which geometry, can be name (character) or index (integer)
- `dimred`: Name of a dimension reduction, can be seen in `reducedDimNames`.

#### Value

A DataFrame.

#### See Also

getParams
Examples

library(SpatialFeatureExperiment)
library(SingleCellExperiment)
library(SFEData)
sfe <- McKellarMuscleData("small")
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
# Moran's I for colData
sfe <- colDataMoransI(sfe, "nCounts")
colFeatureData(sfe)

ditto_colors

Colorblind friendly palette from dittoSeq

Description

Just to get the palette without having to install all those dependencies of dittoSeq.

Usage

ditto_colors

Format

A character vector of hex colors of the palette. There are 40 colors.

Source

The dittoSeq package.

ElbowPlot

Plot the elbow plot or scree plot for PCA

Description

Apparently, there is no apparent way to plot the PC elbow plot other than extracting the variance explained attribute of the dimred slot, because even the OSCA book makes the elbow plot this way, which I find kind of cumbersome compared to Seurat. So I’m writing this function to make the elbow plot with SCE less cumbersome.
Usage

```r
ElbowPlot(
  sce,
  ndims = 20,
  nfnega = 0,
  reduction = "PCA",
  sample_id = "all",
  facet = FALSE,
  ncol = NULL
)
```

Arguments

- **sce**: A `SingleCellExperiment` object, or anything that inherits from `SingleCellExperiment`.
- **ndims**: Number of components with positive eigenvalues, such as PCs in non-spatial PCA.
- **nfnega**: Number of nega eigenvalues and their eigenvectors to compute. These indicate negative spatial autocorrelation.
- **reduction**: Name of the dimension reduction to use. It must have an attribute called either "percentVar" or "eig" for eigenvalues. Defaults to "PCA".
- **sample_id**: Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.
- **facet**: Logical, whether to facet by samples when multiple samples are present. This is relevant when spatial PCA is run separately for each sample, which gives different results from running jointly for all samples.
- **ncol**: Number of columns of facets if facetting.

Value

A `ggplot` object. The y axis is eigenvalues or percentage of variance explained if relevant.

Examples

```r
library(SFEData)
library(scater)
sfe <- McKellarMuscleData("small")
sfe <- runPCA(sfe, ncomponents = 10, exprs_values = "counts")
ElbowPlot(sfe, ndims = 10)
```

getDivergeRange

Get beginning and end of palette to center a divergent palette

Description

This function is no longer used internally as it's unnecessary for scico divergent palettes. But it can be useful when using divergent palettes outside scico where one must specify beginning and end but not midpoint, to override the default palette.
getParams

Usage

getDivergeRange(values, diverge_center = 0)

Arguments

values Numeric vector to be colored.
diverge_center Value to center on, defaults to 0.

Value

A numeric vector of length 2, the first element is for beginning, and the second for end. The values are between 0 and 1.

Examples

v <- rnorm(10)
geetDivergeRange(v, diverge_center = 0)

getParams

Get parameters used in spatial methods

Description

The getParams function allows users to access the parameters used to compute the results that may be stored in colFeatureData.

Usage

getParams(
  sfe,
  name,
  local = FALSE,
  colData = FALSE,
  colGeometryName = NULL,
  annotGeometryName = NULL,
  reducedDimName = NULL
)

Arguments

sfe A SpatialFeatureExperiment object.
name Name used to store the results.
local Logical, whether the results of interest come from a local spatial method.
colData Logical, whether the results were computed for a column of colData(sfe).
colGeometryName To get results for a colGeometry.
annotGeometryName  To get results for an annotGeometry; colGeometry has precedence so this argument is ignored if colGeometryName is specified.

reducedDimName  Name of a dimension reduction, can be seen in reducedDimNames. colGeometryName and annotGeometryName have precedence over reducedDimName.

Value
A named list showing the parameters

Examples
library(SFEData)
library(scater)
sfe <- McKellarMuscleData("small")
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
sfe <- colDataMoransI(sfe, "nCounts")
getParams(sfe, "moran", colData = TRUE)

listSFEMethods  List all spatial methods in Voyager package

Description
This package ships with many spatial statistics methods as SFEMethod objects. The user can adapt the uniform user interface of this package to other spatial methods by creating new SFEMethod objects. This function lists the names of all methods within Voyager, to use for the type argument in calculateUnivariate, calculateBivariate, and calculateMultivariate.

Usage
listSFEMethods(variate = c("uni", "bi", "multi"), scope = c("global", "local"))

Arguments
variate       Uni-, bi-, or multi-variate.
scope         whether it’s local or global.

Value
A data frame with a column for the name and another for a brief description.

Examples
listSFEMethods("uni", "local")
listw2sparse

Convert listw into sparse adjacency matrix

Description

Edge weights are used in the adjacency matrix. Because most elements of the matrix are 0, using sparse matrix greatly reduces memory use.

Usage

listw2sparse(listw)

Arguments

listw

A listw object for spatial neighborhood graph.

Value

A sparse dgCMatrix, whose row represents each cell or spot and whose columns represent the neighbors. The matrix does not have to be symmetric. If region.id is present in the listw object, then it will be the row and column names of the output matrix.

Examples

library(SFEData)
sfe <- McKellarMuscleData("small")
g <- findVisiumGraph(sfe)
mat <- listw2sparse(g)

moranBounds

Compute the bounds of Moran’s I given spatial neighborhood graph

Description

Values Moran’s I can take depends on the spatial neighborhood graph. The bounds of Moran’s I given the graph, C, are given by the minimum and maximum eigenvalues of the double centered – i.e. subtracting column means and row means – adjacency matrix \((I - \bar{\mathbf{v}}\bar{\mathbf{v}}^T/n)C(I - \bar{\mathbf{v}}\bar{\mathbf{v}}^T/n)\), where \(\mathbf{v}\) is a vector of all 1’s. This implementation follows the implementation in ade4spatial and uses the RSpectra package to more quickly find only the minimum and maximum eigenvalues without performing unnecessary work to find the full spectrum as done in base R’s eigen.

Usage

moranBounds(listw)
Arguments

listw A listw object for spatial neighborhood graph.

Value

A numeric vector of minimum and maximum Moran’s I given the spatial neighborhood graph.

Note

After double centering, the adjacency matrix is no longer sparse, so this function can take up a lot of memory for larger datasets.

References


Examples

# example code
library(SFEData)
sfe <- McKellarMuscleData("small")
g <- findVisiumGraph(sfe)
moranBounds(g)

moranPlot

Use ggplot to plot the moran.plot results

Description

This function uses ggplot2 to plot the Moran plot. The plot would be more aesthetically pleasing than the base R version implemented in spdep. In addition, contours are plotted to show point density on the plot, and the points can be colored by a variable, such as clusters. The contours may also be filled and only influential points plotted. When filled, the viridis E option is used.

Usage

moranPlot(
  sfe,
  feature,
  graphName = 1L,
  sample_id = "all",
  contour_color = "cyan",
  color_by = NULL,
  colGeometryName = NULL,
  annotGeometryName = NULL,
  plot_singletons = TRUE,
  binned = FALSE,
filled = FALSE,
divergent = FALSE,
diverge_center = NULL,
swap_rownames = NULL,
bins = 100,
binwidth = NULL,
hex = FALSE,
plot_influential = TRUE,
bins_contour = NULL,
name = "moran.plot",
...)

Arguments

sfe A SpatialFeatureExperiment object.

feature Name of one variable to show on the plot. It will be converted to sentence case on the x axis and lower case in the y axis appended after "Spatially lagged". One feature at a time since the colors in color_by may be specific to this feature (e.g. from clusterMoranPlot).

graphName Name of the colGraph or annotGraph, the spatial neighborhood graph used to compute the Moran plot. This is to determine which points are singletons to plot differently on this plot.

sample_id One sample_id for the sample whose graph to plot.

contour_color Color of the point density contours, which can be changed so the contours stand out from the points.

color_by Variable to color the points by. It can be the name of a column in colData, a gene, or the name of a column in the colGeometry specified in colGeometryName. Or it can be a vector of the same length as the number of cells/spots in the sample_id of interest.

colGeometryName Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots.

annotGeometryName Name of a annotGeometry of the SFE object, to annotate the gene expression plot.

plot_singletons Logical, whether to plot items that don’t have spatial neighbors.

binned Logical, whether to plot 2D histograms. This argument has precedence to filled.

filled Logical, whether to plot filled contours for the non-influential points and only plot influential points as points.

divergent Logical, whether a divergent palette should be used.

diverge_center If divergent = TRUE, the center from which the palette should diverge. If NULL, then not centering.
Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.

If binning the colGeometry in space due to large number of cells or spots, the number of bins, passed to geom_bin2d or geom_hex. If NULL (default), then the colGeometry is plotted without binning. If binning, a point geometry is recommended. If the geometry is not point, then the centroids will be used.

Width of bins, passed to geom_bin2d or geom_hex.

Logical, whether to use geom_hex. Note that geom_hex is broken in ggplot2 version 3.4.0. Please update ggplot2 if you are getting horizontal stripes when hex = TRUE.

Logical, whether to plot influential points with different palette if binned = TRUE.

Number of bins in the point density contour. Use a smaller number to make sparser contours.

Name under which the Moran plot results are stored. By default "moran.plot".

Other arguments to pass to geom_density2d.

A ggplot object.

library(SpatialFeatureExperiment)
library(SingleCellExperiment)
library(SFEData)
library(bluster)
library(scater)
sfe <- McKellarMuscleData("full")
sfe <- sfe[, colData(sfe)$in_tissue]
sfe <- logNormCounts(sfe)
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
sfe <- runUnivariate(sfe, type = "moran.plot", features = "Myh1",
  swap_rownames = "symbol")
clust <- clusterMoranPlot(sfe, "Myh1", BLUSPARAM = KmeansParam(2),
  swap_rownames = "symbol")
moranPlot(sfe, "Myh1", graphName = "visium", color_by = clust[, 1],
  swap_rownames = "symbol")

multispati_rsp A faster implementation of MULTISPATI PCA
Description

This implementation uses the RSpectra package to efficiently compute a small subset of eigenvalues and eigenvectors, as a small subset is typically used. Hence it’s much faster and memory efficient than the original implementation in adespatial. However, this implementation here does not support row and column weighting other than the standard ones for PCA, so the adespatial implementation is more general.

Usage

```r
multispati_rsp(x, listw, nfposi = 30L, nfnega = 30L, scale = TRUE)
```

Arguments

- `x`: A matrix whose columns are features and rows are cells.
- `listw`: A listw object, a spatial neighborhood graph for the cells in `x`. The length must be equal to the number of row of `x`.
- `nfposi`: Number of positive eigenvalues and their eigenvectors to compute.
- `nfnega`: Number of negative eigenvalues and their eigenvectors to compute. These indicate negative spatial autocorrelation.
- `scale`: Logical, whether to scale the data.

Value

A matrix for the cell embeddings in each spatial PC, with attribute `loading` for the eigenvectors or `gene loadings`, and attribute `eig` for the eigenvalues.

Note

Eigen decomposition will fail if any feature has variance zero leading to NaN in the scaled matrix.

References


Examples

```r
library(SFEData)
library(scater)
sfe <- McKellarMuscleData("small")
sfe <- sfe[,sfe$in_tissue]
sfe <- logNormCounts(sfe)
inds <- order(rowSums(logcounts(sfe)), decreasing = TRUE)[1:50]
mat <- logcounts(sfe)[inds,]
g <- findVisiumGraph(sfe)
out <- multispati_rsp(t(mat), listw = g, nfposi = 10, nfnega = 10)
```
**multi_listw2sparse**  
*Convert multiple listw graphs into a single sparse adjacency matrix*

**Description**

Each sample in the SFE object has a separate spatial neighborhood graph. Spatial analyses performed jointly on multiple samples require a combined spatial neighborhood graph from the different samples, where the different samples would be disconnected components of the graph. This combined adjacency matrix can be used in MULTISPATI PCA.

**Usage**

```r
multi_listw2sparse(listws)
```

**Arguments**

- `listws`  
  A list of `listw` objects.

**Value**

A sparse `dgCMatrix` of the combined spatial neighborhood graph, with the original spatial neighborhood graphs of the samples on the diagonal. When the input is an SFE object, the rows and columns will match the column names of the SFE object.

**Examples**

```r
# example code
```

---

**plotCellBin2D**  
*Plot cell density as 2D histogram*

**Description**

This function plots cell density in histological space as 2D histograms, especially helpful for larger smFISH-based datasets.

**Usage**

```r
plotCellBin2D(
    sfe,
    sample_id = "all",
    bins = 200,
    binwidth = NULL,
    hex = FALSE,
    ncol = NULL,
    bbox = NULL
)
```
**plotColDataFreqpoly**

Plot frequency polygons for colData and rowData columns

**Description**

This function is recommended instead of `plotColDataHistogram` when coloring by multiple categories and log transforming the y axis, which causes problems in stacked histograms.

**Usage**

```r
plotColDataFreqpoly(
  sce,
  feature,
  color_by = NULL,
  subset = NULL,
)```

**Arguments**

- `sfe`: A SpatialFeatureExperiment object.
- `sample_id`: Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.
- `bins`: Number of bins. Can be a vector of length 2 to specify for x and y axes separately.
- `binwidth`: Width of bins, passed to `geom_bin2d` or `geom_hex`.
- `hex`: Logical, whether to use hexagonal bins.
- `ncol`: Number of columns if plotting multiple features. Defaults to `NULL`, which means using the same logic as `facet_wrap`, which is used by patchwork's `wrap_plots` by default.
- `bbox`: A bounding box to specify a smaller region to plot, useful when the dataset is large. Can be a named numeric vector with names "xmin", "xmax", "ymin", and "ymax", in any order. If plotting multiple samples, it should be a matrix with sample IDs as column names and "xmin", "ymin", "xmax", and "ymax" as row names. If multiple samples are plotted but `bbox` is a vector rather than a matrix, then the same bounding box will be used for all samples. You may see points at the edge of the geometries if the intersection between the bounding box and a geometry happens to be a point there. If `NULL`, then the entire tissue is plotted.

**Value**

A ggplot object.

**Examples**

```r
library(SFEData)
sfe <- HeNSCLCData()
plotCellBin2D(sfe)
```
plotColDataFreqpoly(bins = 100, binwidth = NULL, linewidth = 1.2, scales = "free", ncol = 1, position = "identity")

plotRowDataFreqpoly(sce, feature, color_by = NULL, subset = NULL, bins = 100, binwidth = NULL, linewidth = 1.2, scales = "free", ncol = 1, position = "identity")

Arguments

sce A SingleCellExperiment object.
feature Names of columns in colData orrowData to plot. When multiple features are specified, they will be plotted in separate facets.
color_by Name of a categorical column in colData or rowData to color the polygons.
subset Name of a logical column to only plot a subset of the data.
bins Number of bins. Overridden by binwidth. Defaults to 30.
binwidth The width of the bins. Can be specified as a numeric value or as a function that calculates width from unscaled x. Here, "unscaled x" refers to the original x values in the data, before application of any scale transformation. When specifying a function along with a grouping structure, the function will be called once per group. The default is to use the number of bins in bins, covering the range of the data. You should always override this value, exploring multiple widths to find the best to illustrate the stories in your data.
The bin width of a date variable is the number of days in each time; the bin width of a time variable is the number of seconds.
linewidth Line width of the polygons, defaults to a thicker 1.2.
scales Should scales be fixed ("fixed", the default), free ("free"), or free in one dimension ("free_x", "free_y")?
ncol Number of columns in the facetting.
position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
plotColDataHistogram

See Also

plotColDataHistogram

Examples

library(SFEData)
sfe <- McKellarMuscleData()
plotColDataFreqpoly(sfe, c("nCounts", "nGenes"), color_by = "in_tissue",
                   bins = 50)
plotColDataFreqpoly(sfe, "nCounts", subset = "in_tissue")
sfe2 <- sfe[, sfe$in_tissue]
plotColDataFreqpoly(sfe2, c("nCounts", "nGenes"), bins = 50)

plotColDataHistogram  Plot histograms for colData and rowData columns

Description

Plot histograms for colData and rowData columns

Usage

plotColDataHistogram(
  sce,
  feature,
  fill_by = NULL,
  facet_by = NULL,
  subset = NULL,
  bins = 100,
  binwidth = NULL,
  scales = "free",
  ncol = 1,
  position = "stack",
  ...
)

plotRowDataHistogram(
  sce,
  feature,
  fill_by = NULL,
  facet_by = NULL,
  subset = NULL,
  bins = 100,
  binwidth = NULL,
  scales = "free",
  ncol = 1,
  position = "stack",
  ...
Arguments

sce
A SingleCellExperiment object.

feature
Names of columns in colData orrowData to plot. When multiple features are specified, they will be plotted in separate facets.

fill_by
Name of a categorical column in colData orrowData to fill the histogram.

facet_by
Column in colData orrowData to facet with. When multiple features are plotted, the features will be in different facets. In this case, setting facet_by will call facet_grid so the features are in rows and categories in facet_by will be in columns.

subset
Name of a logical column to only plot a subset of the data.

bins
Numeric vector giving number of bins in both vertical and horizontal directions. Set to 100 by default.

binwidth
The width of the bins. Can be specified as a numeric value or as a function that calculates width from unscaled x. Here, "unscaled x" refers to the original x values in the data, before application of any scale transformation. When specifying a function along with a grouping structure, the function will be called once per group. The default is to use the number of bins in bins, covering the range of the data. You should always override this value, exploring multiple widths to find the best to illustrate the stories in your data.

The bin width of a date variable is the number of days in each time; the bin width of a time variable is the number of seconds.

scales
Should scales be fixed ("fixed", the default), free ("free"), or free in one dimension ("free_x", "free_y")?

ncol
Number of columns in the facetting.

position
Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

Value
A ggplot object

See Also
plotColDataFreqpoly
plotColGraph

Examples

library(SFEData)
sfe <- McKellarMuscleData()
plotColDataHistogram(sfe, c("nCounts", "nGenes"), fill_by = "in_tissue",
                      bins = 50, position = "stack")
plotColDataHistogram(sfe, "nCounts", subset = "in_tissue")
sfe2 <- sfe[, sfe$in_tissue]
plotColDataHistogram(sfe2, c("nCounts", "nGenes"), bins = 50)

plotColGraph  

Description

A ggplot version of spdep::plot.nb, reducing boilerplate for SFE objects.

Usage

plotColGraph(
  sfe,
  colGraphName = 1L,
  colGeometryName = 1L,
  sample_id = "all",
  weights = FALSE,
  segment_size = 0.5,
  geometry_size = 0.5,
  ncol = NULL,
  bbox = NULL
)

plotAnnotGraph(
  sfe,
  annotGraphName = 1L,
  annotGeometryName = 1L,
  sample_id = "all",
  weights = FALSE,
  segment_size = 0.5,
  geometry_size = 0.5,
  ncol = NULL,
  bbox = NULL
)

Arguments

sfe          A SpatialFeatureExperiment object.
colGraphName Name of graph associated with columns of the gene count matrix to be plotted.
colGeometryName

Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots.

sample_id

Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.

weights

Whether to plot weights. If TRUE, then transparency (alpha) of the segments will represent edge weights.

segment_size

Thickness of the segments that represent graph edges.

gometry_size

Point size (for POINT geometries) or line thickness (for LINestring and POLYGON) to plot the geometry in the background.

ncol

Number of columns if plotting multiple features. Defaults to NULL, which means using the same logic as facet_wrap, which is used by patchwork’s wrap_plots by default.

bbox

A bounding box to specify a smaller region to plot, useful when the dataset is large. Can be a named numeric vector with names "xmin", "xmax", "ymin", and "ymax", in any order. If plotting multiple samples, it should be a matrix with sample IDs as column names and "xmin", "ymin", "xmax", and "ymax" as row names. If multiple samples are plotted but bbox is a vector rather than a matrix, then the same bounding box will be used for all samples. You may see points at the edge of the geometries if the intersection between the bounding box and a geometry happens to be a point there. If NULL, then the entire tissue is plotted.

annotGraphName

Name of the annotation graph to plot.

annotGeometryName

Name of the annotGeometry, which is associated with the graph specified with annotGraphName, for spatial coordinates of the graph nodes and for context.

Value

A ggplot2 object.

Examples

library(SpatialFeatureExperiment)
library(SFEData)
library(sf)
sfe <- McKellarMuscleData("small")
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
plotColGraph(sfe, colGraphName = "visium", colGeometryName = "spotPoly")
# Make the myofiber segmentations a valid POLYGON geometry
ag <- annotGeometry(sfe, "myofiber_simplified")
ag <- st_buffer(ag, 0)
ag <- ag[!st_is_empty(ag), ]
annotGeometry(sfe, "myofiber_simplified") <- ag
annotGraph(sfe, "myofibers") <-
findSpatialNeighbors(sfe,
    type = "myofiber_simplified", MARGIN = 3,
    method = "tri2nb", dist_type = "idw"
)
plotCorrelogram

Description

Use ggplot2 to plot correlograms computed by runUnivariate, pulling results from rowData. Correlograms of multiple genes with error bars can be plotted, and they can be colored by any numeric or categorical column in rowData or a vector with the same length as nrow of the SFE object. The coloring is useful when the correlograms are clustered to show types of length scales or patterns of decay of spatial autocorrelation. For method = "I", the error bars are twice the standard deviation of the estimated Moran’s I value.

Usage

plotCorrelogram(
  sfe, 
  features, 
  sample_id = "all", 
  method = "I", 
  color_by = NULL, 
  facet_by = c("sample_id", "features"), 
  ncol = NULL, 
  colGeometryName = NULL, 
  annotGeometryName = NULL, 
  reducedDimName = NULL, 
  plot_signif = TRUE, 
  p_adj_method = "BH", 
  divergent = FALSE, 
  diverge_center = NULL, 
  swap_rownames = NULL, 
  name = "sp.correlogram" 
)

Arguments

sfe A SpatialFeatureExperiment object.
features Features to plot, must be in rownames of the gene count matrix, colnames of colData or a colGeometry, colnames of cell embeddings in reducedDim, or numeric indices of dimension reduction components.
**plotCorrelogram**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>sample_id</code></td>
<td>Sample(s) in the SFE object whose cells/spots to use. Can be &quot;all&quot; to compute metric for all samples; the metric is computed separately for each sample.</td>
</tr>
<tr>
<td><code>method</code></td>
<td>&quot;corr&quot; for correlation, &quot;I&quot; for Moran’s I, &quot;C&quot; for Geary’s C</td>
</tr>
<tr>
<td><code>color_by</code></td>
<td>Name of a column in rowData(sfe) or in the featureData of colData (see colFeatureData), colGeometry, or annotGeometry by which to color the correlogram of each feature. Alternatively, a vector of the same length as features, or a data frame from clusterCorrelograms.</td>
</tr>
<tr>
<td><code>facet_by</code></td>
<td>Whether to facet by sample_id (default) or features. If facetting by sample_id, then different features will be plotted in the same facet for comparison. If facetting by features, then different samples will be compared for each feature. Ignored if only one sample is specified.</td>
</tr>
<tr>
<td><code>ncol</code></td>
<td>Number of columns if facetting.</td>
</tr>
<tr>
<td><code>colGeometryName</code></td>
<td>Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots.</td>
</tr>
<tr>
<td><code>annotGeometryName</code></td>
<td>Name of a annotGeometry of the SFE object, to annotate the gene expression plot.</td>
</tr>
<tr>
<td><code>reducedDimName</code></td>
<td>Name of a dimension reduction, can be seen in reducedDimNames. colGeometryName and annotGeometryName have precedence over reducedDimName.</td>
</tr>
<tr>
<td><code>plot_signif</code></td>
<td>Logical, whether to plot significance symbols: p &lt; 0.001: ***, p &lt; 0.01: **, p &lt; 0.05 * , p &lt; 0.1: ., otherwise no symbol. The p-values are two sided, based on the assumption that the estimated Moran’s I is normally distributed with mean from a randomized version of the data. The mean and variance come from moran.test for Moran’s I and geary.test for Geary’s C. Take the results with a grain of salt if the data is not normally distributed.</td>
</tr>
<tr>
<td><code>p_adj_method</code></td>
<td>Multiple testing correction method as in p.adjust, to correct for multiple testing (number of lags times number of features) in the Moran’s I estimates if plot_signif = TRUE.</td>
</tr>
<tr>
<td><code>divergent</code></td>
<td>Logical, whether a divergent palette should be used.</td>
</tr>
<tr>
<td><code>diverge_center</code></td>
<td>If divergent = TRUE, the center from which the palette should diverge. If NULL, then not centering.</td>
</tr>
<tr>
<td><code>swap_rownames</code></td>
<td>Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.</td>
</tr>
<tr>
<td><code>name</code></td>
<td>Name under which the correlogram results are stored, which is by default &quot;sp.correlogram&quot;.</td>
</tr>
</tbody>
</table>

**Value**

A ggplot object.
Examples

```r
library(SpatialFeatureExperiment)
library(SFEData)
library(bluster)
library(scater)
sfe <- McKellarMuscleData("small")
sfe <- logNormCounts(sfe)
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
inds <- c(1, 3, 4, 5)
features <- rownames(sfe)[inds]
sfe <- runUnivariate(sfe, 
  type = "sp.correlogram", features = features, 
  exprs_values = "counts", order = 5
)
clust <- clusterCorrelograms(sfe, 
  features = features,
  BLUSPARAM = KmeansParam(2)
)
# Color by features
plotCorrelogram(sfe, features)
# Color by something else
plotCorrelogram(sfe, features, color_by = clust$cluster)
# Facet by features
plotCorrelogram(sfe, features, facet_by = "features")
```

Description

Equivalent to `gstat::plot.gstatVariogram`, but using ggplot2 to be more customizable.

Usage

```r
plotCrossVariogram(res, show_np = TRUE)
```

Arguments

- `res` Cross variogram results for one sample, from `calculateBivariate`. Global bivariate results are not stored in the SFE object.
- `show_np` Logical, whether to show number of pairs of cells at each distance bin.

Value

A ggplot object. Unfortunately I haven’t figured out a way to collect all the facet labels to the top of the entire plot.
plotCrossVariogramMap

See Also

plotCrossVariogramMap

Examples

library(SFEData)
library(scater)
sfe <- McKellarMuscleData()
sfe <- sfe[,sfe$in_tissue]
sfe <- logNormCounts(sfe)

res <- calculateBivariate(sfe, type = "cross_variogram",
 feature1 = c("Myh1", "Myh2", "Csrp3"), swap_rownames = "symbol")
plotCrossVariogram(res)

plotCrossVariogramMap  Plot cross variogram map

Description

Equivalent to gstat::plot.gstatVariogram, but using ggplot2 to be more customizable.

Usage

plotCrossVariogramMap(res, plot_np = FALSE)

Arguments

res  Cross variogram results for one sample, from calculateBivariate. Global
     bivariate results are not stored in the SFE object.

plot_np  Logical, whether to plot the number of pairs in each distance bin instead of the
     variance.

Value

A ggplot object.

See Also

plotCrossVariogram
Examples

```r
library(SFEData)
library(scater)
sfe <- McKellarMuscleData()
sfe <- sfe[,sfe$in_tissue]
sfe <- logNormCounts(sfe)

res <- calculateBivariate(sfe, type = "cross_variogram_map",
feature1 = c("Myh1", "Myh2", "Csrp3"), swap_rownames = "symbol",
width = 500, cutoff = 2000)
plotCrossVariogramMap(res)
```

Description

Just like Seurat’s VizDimLoadings function. I haven’t found an equivalent for SCE but find it useful. But I’m not trying to reproduce that Seurat function exactly. For instance, I don’t like it when Seurat imposes a ggplot theme, and I don’t like the cowplot theme. Maybe I should rewrite it in base R but for now I’m using Tidyverse.

Usage

```r
plotDimLoadings(
  sce,
  dims = 1:4,
  nfeatures = 10,
  swap_rownames = NULL,
  reduction = "PCA",
  balanced = TRUE,
  ncol = 2,
  sample_id = "all"
)
```

Arguments

- **sce**: A `SingleCellExperiment` object, or anything that inherits from `SingleCellExperiment`.
- **dims**: Numeric vector specifying which PCs to plot. For MULTISPATI, PCs with negative eigenvalues are in the right most columns of the embedding and loading matrices. See the `ElbowPlot`.
- **nfeatures**: Number of genes to plot.
- **swap_rownames**: Column name of `rowData(object)` to be used to identify features instead of `rownames(object)` when labeling plot elements. If not found in `rowData`, then rownames of the gene count matrix will be used.
reduction Name of the dimension reduction to use. It must have an attribute called either "percentVar" or "eig" for eigenvalues. Defaults to "PCA".

balanced Return an equal number of genes with + and - scores. If FALSE, returns the top genes ranked by the scores absolute values.

ncol Number of columns in the facetted plot.

sample_id Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.

Value

A ggplot object. Loadings for different PCs are plotted in different facets so one ggplot object is returned.

Examples

library(SFEData)
library(scater)
sfe <- McKellarMuscleData("small")
sfe <- runPCA(sfe, ncomponents = 10, exprs_values = "counts")
plotDimLoadings(sfe, dims = 1:2)

plotGeometry

Plot geometries without coloring

Description

Different samples are plotted in separate facets.

Usage

plotGeometry(
  sfe,
  type,
  MARGIN = 2L,
  sample_id = "all",
  ncol = NULL,
  bbox = NULL,
  image_id = NULL,
  maxcell = 5e+05
)

Arguments

sfe A SpatialFeatureExperiment object.
type Name of the geometry associated with the MARGIN of interest for which to compute the graph.
plotLocalResult

MARGIN

Just like in `apply`, where 1 stands for row, 2 stands for column. Here, in addition, 3 stands for annotation, to query the `annotGeometries`, such as nuclei segmentation in a Visium data.

sample_id

Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.

ncol

Number of columns if plotting multiple features. Defaults to `NULL`, which means using the same logic as `facet_wrap`, which is used by patchwork’s `wrap_plots` by default.

bbox

A bounding box to specify a smaller region to plot, useful when the dataset is large. Can be a named numeric vector with names "xmin", "xmax", "ymin", and "ymax", in any order. If plotting multiple samples, it should be a matrix with sample IDs as column names and "xmin", "ymin", "xmax", and "ymax" as row names. If multiple samples are plotted but `bbox` is a vector rather than a matrix, then the same bounding box will be used for all samples. You may see points at the edge of the geometries if the intersection between the bounding box and a geometry happens to be a point there. If `NULL`, then the entire tissue is plotted.

image_id

ID of the image to plot behind the geometries. If `NULL`, then not plotting images. Use `imgData` to see image IDs present.

maxcell

Maximum number of pixels to plot in the image. If the image is larger, it will be resampled so it have less than this number of pixels to save memory and for faster plotting. We recommend reducing this number when plotting multiple facets.

Value

A `ggplot` object.

Examples

```r
library(SFEData)
sfe1 <- McKellarMuscleData("small")
sfe2 <- McKellarMuscleData("small2")
sfe <- cbind(sfe1, sfe2)
sfe <- removeEmptySpace(sfe)
plotGeometry(sfe, "spotPoly")
plotGeometry(sfe, "myofiber_simplified", MARGIN = 3)
```

Description

Plot results of local spatial analyses in space, such as local Getis-Ord Gi* values.
Usage

plotLocalResult(
  sfe,
  name,
  features,
  attribute = NULL,
  sample_id = "all",
  colGeometryName = NULL,
  annotGeometryName = NULL,
  ncol = NULL,
  ncol_sample = NULL,
  annot_aes = list(),
  annot_fixed = list(),
  bbox = NULL,
  image_id = NULL,
  maxcell = 5e+05,
  aes_use = c("fill", "color", "shape", "linetype"),
  divergent = FALSE,
  diverge_center = NULL,
  annot_divergent = FALSE,
  annot_diverge_center = NULL,
  size = 0.5,
  shape = 16,
  linewidth = 0,
  linetype = 1,
  alpha = 1,
  color = "black",
  fill = "gray80",
  swap_rownames = NULL,
  scattermore = FALSE,
  pointsize = 0,
  bins = NULL,
  summary_fun = sum,
  hex = FALSE,
  dark = FALSE,
  type = name,
  ...
)

Arguments

sfe A SpatialFeatureExperiment object.

name Which local spatial results. Use localResultNames to see which types of results have already been calculated.

features Character vector of vectors. To see which features have the results of a given type, see localResultFeatures.

attribute Which field in the local results of the type and features. If the result of each feature is a vector, the this argument is ignored. But if the result is a data frame
or a matrix, then this is the column name of the result, such as "Ii" for local Moran's I. For each local spatial analysis method, there's a default attribute. See Details. Use `localResultAttrs`.

**sample_id**
Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.

**colGeometryName**
Name of a `colGeometry` sf data frame whose numeric columns of interest are to be used to compute the metric. Use `colGeometryNames` to look up names of the sf data frames associated with cells/spots.

**annotGeometryName**
Name of a `annotGeometry` of the SFE object, to annotate the gene expression plot.

**ncol**
Number of columns if plotting multiple features. Defaults to NULL, which means using the same logic as `facet_wrap`, which is used by `patchwork`'s `wrap_plots` by default.

**ncol_sample**
If plotting multiple samples as facets, how many columns of such facets. This is distinct from `ncols`, which is for multiple features. When plotting multiple features for multiple samples, then the result is a multi-panel plot each panel of which is a plot for each feature faceted by samples.

**annot_aes**
A named list of plotting parameters for the annotation sf data frame. The names are which geom (as in ggplot2, such as color and fill), and the values are column names in the annotation sf data frame. Tidyeval is NOT supported.

**annot_fixed**
Similar to `annot_aes`, but for fixed aesthetic settings, such as `color = "gray"`. The defaults are the same as the relevant defaults for this function.

**bbox**
A bounding box to specify a smaller region to plot, useful when the dataset is large. Can be a named numeric vector with names "xmin", "xmax", "ymin", and "ymax", in any order. If plotting multiple samples, it should be a matrix with sample IDs as column names and "xmin", "ymin", "xmax", and "ymax" as row names. If multiple samples are plotted but bbox is a vector rather than a matrix, then the same bounding box will be used for all samples. You may see points at the edge of the geometries if the intersection between the bounding box and a geometry happens to be a point there. If NULL, then the entire tissue is plotted.

**image_id**
ID of the image to plot behind the geometries. If NULL, then not plotting images. Use `imgData` to see image IDs present.

**maxcell**
Maximum number of pixels to plot in the image. If the image is larger, it will be resampled so it have less than this number of pixels to save memory and for faster plotting. We recommend reducing this number when plotting multiple facets.

**aes_use**
Aesthetic to use for discrete variables. For continuous variables, it's always "fill" for polygons and point shapes 21-25. For discrete variables, it can be fill, color, shape, or linetype, whenever applicable. The specified value will be changed to the applicable equivalent. For example, if the geometry is point but "linetype" is specified, then "shaped" will be used instead.

**divergent**
Logical, whether a divergent palette should be used.
diverge_center  If divergent = TRUE, the center from which the palette should diverge. If NULL, then not centering.
annot_divergent  Just as divergent, but for the annotGeometry in case it’s different.
annot_diverge_center  Just as diverge_center, but for the annotGeometry in case it’s different.
size  Fixed size of points. For points defaults to 0.5. Ignored if size_by is specified.
shape  Fixed shape of points, ignored if shape_by is specified and applicable.
linewidth  Width of lines, including outlines of polygons. For polygons, this defaults to 0, meaning no outlines.
linetype  Fixed line type, ignored if linetype_by is specified and applicable.
alpha  Transparency.
color  Fixed color for colGeometry if color_by is not specified or not applicable, or for annotGeometry if annot_color_by is not specified or not applicable.
fill  Similar to color, but for fill.
swap_rownames  Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.
scattermore  Logical, whether to use the scattermore package to greatly speed up plotting numerous points. Only used for POINT colGeometries. If the geometry is not POINT, then the centroids are used. Recommended for plotting hundreds of thousands or more cells where the cell polygons can’t be seen when plotted due to the large number of cells and small plot size such as when plotting multiple panels for multiple features.
pointsize  Radius of rasterized point in scattermore. Default to 0 for single pixels (fastest).
bins  If binning the colGeometry in space due to large number of cells or spots, the number of bins, passed to geom_bin2d or geom_hex. If NULL (default), then the colGeometry is plotted without binning. If binning, a point geometry is recommended. If the geometry is not point, then the centroids will be used.
summary_fun  Function to summarize the feature value when the colGeometry is binned.
hex  Logical, whether to use geom_hex. Note that geom_hex is broken in ggplot2 version 3.4.0. Please update ggplot2 if you are getting horizontal stripes when hex = TRUE.
dark  Logical, whether to use dark theme. When using dark theme, the palette will have lighter color represent higher values as if glowing in the dark. This is intended for plotting gene expression on top of fluorescent images.
type  An SFEMethod object or a string corresponding to the name of one of such objects in the environment. If the localResult of interest was manually added outside runUnivariate and runBivariate, so the method is not recorded, then the type argument can be used to specify the method to properly get the title and labels. By default, this argument is set to be the same as argument name. If the method parameters are recorded, then the type argument is ignored.
...  Other arguments passed to wrap_plots.
Details

Many local spatial analyses return a data frame or matrix as the results, whose columns can be the statistic of interest at each location, its variance, expected value from permutation, p-value, and etc. The attribute argument specifies which column to use when there are multiple columns. Below are the defaults for each local method supported by this package what they mean:

localmoran and localmoran_perm Ii, local Moran’s I statistic at each location.
localC_perm localC, the local Geary C statistic at each location.
localG and localG_perm localG, the local Getis-Ord Gi or Gi* statistic. If include_self = TRUE when calculateUnivariate or runUnivariate was called, then it would be Gi*. Otherwise it’s Gi.
LOSH and LOSH.mc Hi, local spatial heteroscedasticity
moran.plot wx, the average of the value of each neighbor of each location. Moran plot is best plotted as a scatter plot of wx vs x. See moranPlot.

Other local methods not listed above return vectors as results. For instance, localC returns a vector by default, which is the local Geary’s C statistic.

Value

A ggplot2 object if plotting one feature. A patchwork object if plotting multiple features.

Note

While this function shares internals with plotSpatialFeature, there are some important differences. In plotSpatialFeature, the annotGeometry is indeed only used for annotation and the protagonist is the colGeometry, since it’s easy to directly use ggplot2 to plot the data in annotGeometry sf data frames while overlaying annotGeometry and colGeometry involves more complicated code. In contrast, in this function, local results for annotGeometry can be plotted separately without anything related to colGeometry. Note that when annotGeometry local results are plotted without colGeometry, the annot_* arguments are ignored. Use the other arguments for aesthetics as if it’s for colGeometry.

Examples

library(SpatialFeatureExperiment)
library(SFEData)
library(scater)
sfe <- McKellarMuscleData("small")
sfe <- sfe[,sfe$in_tissue]
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
feature_use <- rownames(sfe)[1]
sfe <- logNormCounts(sfe)
sfe <- runUnivariate(sfe, "localmoran", feature_use)
# Which types of results are available?
localResultNames(sfe)
# Which features for localmoran?
localResultFeatures(sfe, "localmoran")
# Which columns does the localmoran results have?
localResultAttrs(sfe, "localmoran", feature_use)
plotLocalResult(sfe, "localmoran", feature_use, "Ii",
    colGeometryName = "spotPoly"
)

# For annotGeometry
# Make sure it's type POLYGON
annotGeometry(sfe, "myofiber_simplified") <-
    sf::st_buffer(annotGeometry(sfe, "myofiber_simplified"), 0)
annotGraph(sfe, "poly2nb_myo") <-
    findSpatialNeighbors(sfe,
        type = "myofiber_simplified", MARGIN = 3,
        method = "poly2nb", zero.policy = TRUE
    )
sfe <- annotGeometryUnivariate(sfe, "localmoran",
    features = "area",
    annotGraphName = "poly2nb_myo",
    annotGeometryName = "myofiber_simplified",
    zero.policy = TRUE
)
plotLocalResult(sfe, "localmoran", "area", "Ii",
    annotGeometryName = "myofiber_simplified",
    size = 0.3, color = "cyan"
)
plotLocalResult(sfe, "localmoran", "area", "Z.Ii",
    annotGeometryName = "myofiber_simplified"
)
# don't use annot_* arguments when annotGeometry is plotted without colGeometry

---

**plotMoranMC**

*Plot Moran/Geary Monte Carlo results*

**Description**

Plot the simulations as a density plot or histogram compared to the observed Moran's I or Geary's C, with ggplot2 so it looks nicer. Unlike the plotting function in spdep, this function can also plot the same feature in different samples as facets or plot different features or samples together for comparison.

**Usage**

```r
plotMoranMC(
    sfe, features, sample_id = "all",
    facet_by = c("sample_id", "features"),
    ncol = NULL, colGeometryName = NULL,
    annotGeometryName = NULL,
)```
Arguments

sfe A SpatialFeatureExperiment object.
features Features to plot, must be in rownames of the gene count matrix, colnames of colData or a colGeometry, colnames of cell embeddings in reducedDim, or numeric indices of dimension reduction components.
sample_id Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.
facet_by Whether to facet by sample_id (default) or features. If facetting by sample_id, then different features will be plotted in the same facet for comparison. If facetting by features, then different samples will be compared for each feature. Ignored if only one sample is specified.
ncol Number of columns if facetting.
colGeometryName Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots.
annotGeometryName Name of a annotGeometry of the SFE object, to annotate the gene expression plot.
reducedDimName Name of a dimension reduction, can be seen in reducedDimNames. colGeometryName and annotGeometryName have precedence over reducedDimName.
ptype Plot type, one of "density", "histogram", or "freqpoly".
swap_rownames Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.
name Name under which the Monte Carlo results are stored, which defaults to "moran.mc". For Geary's C Monte Carlo, the default is "geary.mc".
... Other arguments passed to geom_density, geom_histogram, or geom_freqpoly, depending on ptype.

Value

A ggplot2 object.

Examples

library(SpatialFeatureExperiment)
library(SFEData)
plotSpatialFeature

Plot gene expression in space

Description

Unlike Seurat and ggspavis, plotting functions in this package uses geom_sf whenever applicable.

Usage

plotSpatialFeature(
  sfe,
  features,
  colGeometryName = 1L,
  sample_id = "all",
  ncol = NULL,
  ncol_sample = NULL,
  annotGeometryName = NULL,
  annot_aes = list(),
  annot_fixed = list(),
  exprs_values = "logcounts",
  bbox = NULL,
  image_id = NULL,
  maxcell = 5e+05,
  aes_use = c("fill", "color", "shape", "linetype"),
  divergent = FALSE,
  diverge_center = NA,
  annot_divergent = FALSE,
  annot_diverge_center = NA,
  size = 0.5,
  shape = 16,
  linewidth = 0,
  linetype = 1,
  alpha = 1,
  color = "black",
  fill = "gray80",
  swap_rownames = NULL,
  scattermore = FALSE,
  pointsize = 0,
  bins = NULL,
  summary_fun = sum,
  hex = FALSE,
  dark = FALSE,
)
Arguments

sfe  A SpatialFeatureExperiment object.
features  Features to plot, must be in rownames of the gene count matrix, colnames of colData or a colGeometry.

colGeometryName  Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots.
sample_id  Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.
ncol  Number of columns if plotting multiple features. Defaults to NULL, which means using the same logic as facet_wrap, which is used by patchwork’s wrap_plots by default.
ncol_sample  If plotting multiple samples as facets, how many columns of such facets. This is distinct from ncol, which is for multiple features. When plotting multiple features for multiple samples, then the result is a multi-panel plot each panel of which is a plot for each feature faceted by samples.
annotGeometryName  Name of a annotGeometry of the SFE object, to annotate the gene expression plot.
annot_aes  A named list of plotting parameters for the annotation sf data frame. The names are which geom (as in ggplot2, such as color and fill), and the values are column names in the annotation sf data frame. Tidyeval is NOT supported.
annot_fixed  Similar to annot_aes, but for fixed aesthetic settings, such as color = "gray". The defaults are the same as the relevant defaults for this function.
exprs_values  Integer scalar or string indicating which assay of x contains the expression values.
bbox  A bounding box to specify a smaller region to plot, useful when the dataset is large. Can be a named numeric vector with names "xmin", "xmax", "ymin", and "ymax", in any order. If plotting multiple samples, it should be a matrix with sample IDs as column names and "xmin", "ymin", "xmax", and "ymax" as row names. If multiple samples are plotted but bbox is a vector rather than a matrix, then the same bounding box will be used for all samples. You may see points at the edge of the geometries if the intersection between the bounding box and a geometry happens to be a point there. If NULL, then the entire tissue is plotted.
image_id  ID of the image to plot behind the geometries. If NULL, then not plotting images. Use imgData to see image IDs present.
maxcell  Maximum number of pixels to plot in the image. If the image is larger, it will be resampled so it have less than this number of pixels to save memory and for faster plotting. We recommend reducing this number when plotting multiple facets.
aes_use Aesthetic to use for discrete variables. For continuous variables, it's always "fill" for polygons and point shapes 21-25. For discrete variables, it can be fill, color, shape, or linetype, whenever applicable. The specified value will be changed to the applicable equivalent. For example, if the geometry is point but "linetype" is specified, then "shaped" will be used instead.

divergent Logical, whether a divergent palette should be used.

diverge_center If divergent = TRUE, the center from which the palette should diverge. If NULL, then not centering.

annot_divergent Just as divergent, but for the annotGeometry in case it’s different.

annot_diverge_center Just as diverge_center, but for the annotGeometry in case it’s different.

size Fixed size of points. For points defaults to 0.5. Ignored if size_by is specified.

shape Fixed shape of points, ignored if shape_by is specified and applicable.

linewidth Width of lines, including outlines of polygons. For polygons, this defaults to 0, meaning no outlines.

linetype Fixed line type, ignored if linetype_by is specified and applicable.

alpha Transparency.

color Fixed color for colGeometry if color_by is not specified or not applicable, or for annotGeometry if annot_color_by is not specified or not applicable.

fill Similar to color, but for fill.

swap_rownames Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.

scattermore Logical, whether to use the scattermore package to greatly speed up plotting numerous points. Only used for POINT colGeometries. If the geometry is not POINT, then the centroids are used. Recommended for plotting hundreds of thousands or more cells where the cell polygons can’t be seen when plotted due to the large number of cells and small plot size such as when plotting multiple panels for multiple features.

pointsize Radius of rasterized point in scattermore. Default to 0 for single pixels (fastest).

bins If binning the colGeometry in space due to large number of cells or spots, the number of bins, passed to geom_bin2d or geom_hex. If NULL (default), then the colGeometry is plotted without binning. If binning, a point geometry is recommended. If the geometry is not point, then the centroids will be used.

summary_fun Function to summarize the feature value when the colGeometry is binned.

hex Logical, whether to use geom_hex. Note that geom_hex is broken in ggplot2 version 3.4.0. Please update ggplot2 if you are getting horizontal stripes when hex = TRUE.

dark Logical, whether to use dark theme. When using dark theme, the palette will have lighter color represent higher values as if glowing in the dark. This is intended for plotting gene expression on top of fluorescent images.

... Other arguments passed to wrap_plots.
Details

In the documentation of this function, a "feature" can be a gene (or whatever entity that corresponds to rows of the gene count matrix), a column in colData, or a column in the colGeometry sf data frame specified in the colGeometryName argument.

In the light theme, for continuous variables, the Blues palette from colorbrewer is used if divergent = FALSE, and the roma palette from the scico package if divergent = TRUE. In the dark theme, the nuuk palette from scico is used if divergent = FALSE, and the berlin palette from scico is used if divergent = TRUE. For discrete variables, the dittoSeq palette is used.

For annotation, the YlOrRd colorbrewer palette is used for continuous variables in the light theme. In the dark theme, the acton palette from scico is used when divergent = FALSE and the vanimo palette from scico is used when divergent = FALSE. The other end of the dittoSeq palette is used for discrete variables.

Each individual palette should be colorblind friendly, but when plotting continuous variables coloring a colGeometry and a annotGeometry simultaneously, the combination of the two palettes is not guaranteed to be colorblind friendly.

In addition, when plotting an image behind the geometries, the colors of the image may distort color perception of the values of the geometries.

theme_void is used for all spatial plots in this package, because the units in the spatial coordinates are often arbitrary. This can be overridden to show the axes by using a different theme as normally done in ggplot2.

Value

A ggplot2 object if plotting one feature. A patchwork object if plotting multiple features.

Examples

library(SFEDData)
library(sf)
sfe <- McKellarMuscleData("small")
# features can be genes or colData or colGeometry columns
plotSpatialFeature(sfe, c("nCounts", rownames(sfe)[1]),
  exprs_values = "counts",
  colGeometryName = "spotPoly",
  annotGeometryName = "tissueBoundary"
)
# Change fixed aesthetics
plotSpatialFeature(sfe, "nCounts",
  colGeometryName = "spotPoly",
  annotGeometryName = "tissueBoundary",
  annot_fixed = list(color = "blue", size = 0.3, fill = NA),
  alpha = 0.7
)
# Make the myofiber segmentations a valid POLYGON geometry
ag <- annotGeometry(sfe, "myofiber_simplified")
ag <- st_buffer(ag, 0)
ag <- ag[!st_is_empty(ag), ]
annotGeometry(sfe, "myofiber_simplified") <- ag
# Also plot an annotGeometry variable
plotVariogram(sfe, "nCounts",
  colGeometryName = "spotPoly",
  annotGeometryName = "myofiber_simplified",
  annot_aes = list(fill = "area")
)

# Use a bounding box to zoom in
bbox <- c(xmin = 5500, ymin = 13500, xmax = 6000, ymax = 14000)
plotSpatialFeature(sfe, "nCounts", colGeometryName = "spotPoly",
  annotGeometry = "myofiber_simplified",
  bbox = bbox, annot_fixed = list(linewidth = 0.3))

---

**plotVariogram**

**Plot variogram**

---

### Description

This function plots the variogram of a feature and its fitted variogram models, showing the nugget, range, and sill of the model. Unlike the plotting functions in package automap that uses lattice, this function uses ggplot2 to make prettier and more customizable plots.

### Usage

```r
plotVariogram(
  sfe,
  features,
  sample_id = "all",
  color_by = NULL,
  group = c("none", "sample_id", "features", "angles"),
  use_lty = TRUE,
  show_np = TRUE,
  ncol = NULL,
  colGeometryName = NULL,
  annotGeometryName = NULL,
  reducedDimName = NULL,
  divergent = FALSE,
  diverge_center = NULL,
  swap_rownames = NULL,
  name = "variogram"
)
```

### Arguments

- **sfe**  
  A SpatialFeatureExperiment object.

- **features**  
  Features to plot, must be in rownames of the gene count matrix, colnames of colData or a colGeometry, colnames of cell embeddings in reducedDim, or numeric indices of dimension reduction components.

- **sample_id**  
  Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.
plotVariogram

- **color_by**: Name of a column in rowData(sfe) or in the featureData of colData (see colFeatureData), colGeometry, or annotGeometry by which to color the correlogram of each feature. Alternatively, a vector of the same length as features, or a data frame from clusterCorrelograms.

- **group**: Which of samples, features, and angles to show in the same facet for comparison when there are multiple. Default to "none", meaning each facet will contain one variogram. When grouping multiple variograms in the same facet, the text with model, nugget, sill, and range of the variograms will not be shown.

- **use_lty**: Logical, whether to use linetype or point shape to distinguish between the different features or samples in the same facet. If FALSE, then the different features or samples are not distinguished and the patterns are shown only.

- **show_np**: Logical, whether to show number of pairs of cells at each distance bin.

- **ncol**: Number of columns if facetting.

- **colGeometryName**: Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots.

- **annotGeometryName**: Name of a annotGeometry of the SFE object, to annotate the gene expression plot.

- **reducedDimName**: Name of a dimension reduction, can be seen in reducedDimNames. colGeometryName and annotGeometryName have precedence over reducedDimName.

- **divergent**: Logical, whether a divergent palette should be used.

- **diverge_center**: If divergent = TRUE, the center from which the palette should diverge. If NULL, then not centering.

- **swap_rownames**: Column name of rowData(object) to be used to identify features instead of rownames(object) when labeling plot elements. If not found in rowData, then rownames of the gene count matrix will be used.

- **name**: Name under which the correlogram results are stored, which is by default "sp.correlogram".

**Value**

A ggplot object. The empirical variogram at each distance bin is plotted as points, and the fitted variogram model is plotted as a line for each feature. The number next to each point is the number of pairs of cells in that distance bin.

**See Also**

plotVariogramMap

**Examples**

```r
library(SFEData)
sfe <- McKellarMuscleData()
sfe <- colDataUnivariate(sfe, "variogram", features = "nCounts", model = "Sph")
plotVariogram(sfe, "nCounts")
```
# Anisotropy, will get a message
sfe <- colDataUnivariate(sfe, "variogram", features = "nCounts",
model = "Sph", alpha = c(30, 90, 150), name = "variogram_anis")
# Facet by angles by default
plotVariogram(sfe, "nCounts", name = "variogram_anis")
# Plot angles with different colors
plotVariogram(sfe, "nCounts", group = "angles", name = "variogram_anis")

---

**plotVariogramMap**  
*Plot variogram maps*

**Description**

Plot variogram maps that show the variogram in all directions in a grid of distances in x and y coordinates.

**Usage**

```r
plotVariogramMap(
  sfe,
  features,
  sample_id = "all",
  plot_np = FALSE,
  ncol = NULL,
  colGeometryName = NULL,
  annotGeometryName = NULL,
  reducedDimName = NULL,
  swap_rownames = NULL,
  name = "variogram_map"
)
```

**Arguments**

- **sfe**  
  A SpatialFeatureExperiment object.
- **features**  
  Features to plot, must be in rownames of the gene count matrix, colnames of colData or a colGeometry, colnames of cell embeddings in reducedDim, or numeric indices of dimension reduction components.
- **sample_id**  
  Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.
- **plot_np**  
  Logical, whether to plot the number of pairs in each distance bin instead of the variance.
- **ncol**  
  Number of columns if facetting.
- **colGeometryName**  
  Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use `colGeometryNames` to look up names of the sf data frames associated with cells/spots.
**SFEMethod**

**annotGeometryName**
Name of a annotGeometry of the SFE object, to annotate the gene expression plot.

**reducedDimName**
Name of a dimension reduction, can be seen in `reducedDimNames`. `colGeometryName` and `annotGeometryName` have precedence over `reducedDimName`.

**swap_rownames**
Column name of `rowData(object)` to be used to identify features instead of `rownames(object)` when labeling plot elements. If not found in `rowData`, then `rownames` of the gene count matrix will be used.

**name**
Name under which the correlogram results are stored, which is by default "sp.correlogram".

**Value**
A ggplot object.

**See Also**
`plotVariogram`

**Examples**

```r
library(SFEData)
sfe <- McKellarMuscleData()
sfe <- colDataUnivariate(sfe, "variogram_map", features = "nCounts",
width = 500, cutoff = 5000)
plotVariogramMap(sfe, "nCounts")
```

---

**SFEMethod**  
**SFEMethod class**

**Description**

This S4 class is used to wrap spatial analysis methods, taking inspiration from the caret and tidymodels packages.

**Usage**

```r
SFEMethod(
    name,  
    fun,  
    reorganize_fun,  
    package,  
    variate = c("uni", "bi", "multi"),  
    scope = c("global", "local"),  
    title = NULL,  
    default_attr = NA,  
    args_not_check = NA,  
    joint = FALSE,
```

```
use_graph = TRUE,
use_matrix = FALSE,
dest = c("reducedDim", "colData")
)

## S4 method for signature 'SFEMethod'
info(x, type)

## S4 method for signature 'SFEMethod'
is_local(x)

## S4 method for signature 'SFEMethod'
fun(x)

## S4 method for signature 'SFEMethod'
reorganize_fun(x)

## S4 method for signature 'SFEMethod'
args_not_check(x)

## S4 method for signature 'SFEMethod'
is_joint(x)

## S4 method for signature 'SFEMethod'
use_graph(x)

## S4 method for signature 'SFEMethod'
use_matrix(x)

### Arguments

- **name**: Name of the method, used by user-facing functions to specify the method to use, such as "moran" for Moran's I.
- **fun**: Function to run the method. See Details.
- **reorganize_fun**: Function to reorganize results to add to the SFE object. See Details.
- **package**: Name of the package whose implementation of the method is used here, used to check if the package is installed.
- **variate**: How many variables this method works with, must be one of "uni" for univariate, "bi" for bivariate, or "multi" for multivariate.
- **scope**: Either "global", returning one result for the entire dataset, or "local", returning one result for each spatial location. For multivariate methods, this is irrelevant.
- **title**: Descriptive title to show when plotting the results.
- **default_attr**: For local methods that return multiple fields, such as local Moran values and their p-values, the default field to use when plotting.
- **args_not_check**: A character vector indicating which argument are not to be checked when comparing parameters in with those of a previous run.
**joint** Logical, whether it makes sense to run this method to multiple samples jointly. If TRUE, then `fun` must be able to handle an adjacency matrix for the `listw` argument because there’s no straightforward way to concatenate `listw` objects from multiple samples.

**use_graph** Logical, to indicate whether the method uses a spatial neighborhood graph because unifying the user-facing functions have an argument asking for the graph as most though not all methods require the graph.

**use_matrix** Logical, whether the function in slot `fun` takes a matrix as input. The argument is only used for bivariate methods.

**dest** Whether the results are more appropriate for `reducedDim` or `colData`. Only used for multivariate methods. This overrides the "local" field in `info`.

**x** A `SFEMethod` object

**type** One of the names of the `info` slot, see slot documentation.

**Details**

The `fun` slot should be specified as such:

For all methods, there must be arguments `x` for a vector, `listw` for a `listw` object specifying the spatial neighborhood graph, `zero.policy` specifying what to do with cells without neighbors (default NULL, use global option value; if TRUE assign zero to the lagged value of zones without neighbours, if FALSE assign NA), and optionally other method specific arguments and ... to pass to the underlying imported function. If the original function implementing the method in the package has different argument names or orders, write a thin wrapper to rearrange and/or rename the arguments.

For univariate methods that use a spatial neighborhood graph, the first two arguments must be `x` and `listw`. For univariate methods that don’t use a spatial neighborhood graph, such as the variogram, the first two arguments must be `x` for a numeric vector and `coords_df` for a `sf` data frame with cell locations and optionally other regressors. The `formula` argument is optional and can have defaults specifying regressors to use.

For bivariate methods, the first three arguments must be `x`, `y`, and `listw`.

For multivariate methods, the argument `x` is mandatory, for the matrix input. These arguments must be present but can be optional by having defaults: `listw` and `ncomponents` to set the number of dimensions in the output.

The `reorganize_fun` slot should be specified as such:

Univariate methods are meant to be run separately for each gene, so the input to `reorganize_fun` in the argument `out` should be a list of outputs; each element of the list corresponds to the output of a gene.

For univariate global methods, different fields of the result should be columns of a data frame with one row so results for multiple features will be a data frame. The arguments should be `out`, and `name` to rename the primary field if a more informative name is needed, and ... for other arguments specific to methods. The output of `reorganize_fun` should be a `DataFrame` whose rows correspond to the genes and columns correspond to fields in the output.

For univariate local methods, the arguments should be `out`, `nb` for a neighborhood list used for multiple testing correction, and `p.adjust.method` for a method to correct for multiple testing as in `p.adjust`, and .... The output of `reorganize_fun` should be a list of reorganized output. Each
element of the list corresponds to a gene, and the reorganized content of the element can be a vector, matrix, or data frame, but they must all have the same dimensions for all genes. Each element of the vector, or each row of the matrix or data frame corresponds to a cell.

For multivariate methods whose results go into `reducedDim`, `reorganize_fun` should have one argument out for the raw output. The output of `reorganize_fun` should be the cell embedding matrix ready to be added to `reducedDim`. Other relevant information such as gene loadings and eigenvalues should be added to the attributes of the cell embedding matrix.

For multivariate methods whose results can go into `colData`, the arguments should be `out`, `nb`, and `p.adjust.method`. Unlike the univariate local counterpart, `out` takes the raw output instead of a list of outputs. The output of `reorganize_fun` is a vector or a data frame ready to be added to `colData`.

**Value**

The constructor returns a `SFEMethod` object. The getters return the content of the corresponding slots.

**Slots**

- `info` A named character vector specifying information about the method.
- `fun` The function implementing the method. See Details.
- `reorganize_fun` Function to convert output from `fun` into a format to store in the SFE object. See Details.
- `misc` Miscellaneous information on how the method interacts with the rest of the package. This should be a named list.

**Examples**

```r
moran <- SFEMethod(  
  name = "moran", title = "Moran's I", package = "spdep", variate = "uni",  
  scope = "global",  
  fun = function(x, listw, zero.policy = NULL)  
    spdep::moran(x, listw, n = length(listw$neighbours), S0 = spdep::Szero(listw),  
                 zero.policy = zero.policy),  
  reorganize_fun = Voyager:::.moran2df
)
```

**spatialReducedDim**

*Plot dimension reduction components in space*

**Description**

Such as plotting the value of projection of gene expression of each cell to a principal component in space. At present, this function does not work for the 3D array of geographically weighted PCA (GWPCA), but a future version will deal with GWPCA results.
spatialReducedDim

Usage

spatialReducedDim(
  sfe,
  dimred,
  ncomponents = NULL,
  components = ncomponents,
  colGeometryName = 1L,
  sample_id = "all",
  ncol = NULL,
  ncol_sample = NULL,
  annotGeometryName = NULL,
  annot_aes = list(),
  annot_fixed = list(),
  exprs_values = "logcounts",
  bbox = NULL,
  image_id = NULL,
  maxcell = 5e+05,
  aes_use = c("fill", "color", "shape", "linetype"),
  divergent = FALSE,
  diverge_center = NULL,
  annot_divergent = FALSE,
  annot_diverge_center = NULL,
  size = 0,
  shape = 16,
  linewidth = 0,
  linetype = 1,
  alpha = 1,
  color = NA,
  fill = "gray80",
  scattermore = FALSE,
  pointsize = 0,
  bins = NULL,
  summary_fun = sum,
  hex = FALSE,
  dark = FALSE,
...
)

Arguments

sfe A SpatialFeatureExperiment object.
dimred A string or integer scalar indicating the reduced dimension result in reducedDim(sfe) to plot.
ncomponents A numeric scalar indicating the number of dimensions to plot, starting from the first dimension. Alternatively, a numeric vector specifying the dimensions to be plotted.
components A numeric scalar or vector specifying which dimensions to be plotted. Use this instead of ncomponents when plotting only one dimension.
colGeometryName
Name of a colGeometry sf data frame whose numeric columns of interest are to be used to compute the metric. Use colGeometryNames to look up names of the sf data frames associated with cells/spots.

sample_id
Sample(s) in the SFE object whose cells/spots to use. Can be "all" to compute metric for all samples; the metric is computed separately for each sample.

ncol
Number of columns if plotting multiple features. Defaults to NULL, which means using the same logic as facet_wrap, which is used by patchwork’s wrap_plots by default.

ncol_sample
If plotting multiple samples as facets, how many columns of such facets. This is distinct from ncolS, which is for multiple features. When plotting multiple features for multiple samples, then the result is a multi-panel plot each panel of which is a plot for each feature faceted by samples.

annotGeometryName
Name of a annotGeometry of the SFE object, to annotate the gene expression plot.

annot_aes
A named list of plotting parameters for the annotation sf data frame. The names are which geom (as in ggplot2, such as color and fill), and the values are column names in the annotation sf data frame. Tidyeval is NOT supported.

annot_fixed
Similar to annot_aes, but for fixed aesthetic settings, such as color = "gray". The defaults are the same as the relevant defaults for this function.

eprs_values
Integer scalar or string indicating which assay of x contains the expression values.

bbox
A bounding box to specify a smaller region to plot, useful when the dataset is large. Can be a named numeric vector with names "xmin", "xmax", "ymin", and "ymax", in any order. If plotting multiple samples, it should be a matrix with sample IDs as column names and "xmin", "ymin", "xmax", and "ymax" as row names. If multiple samples are plotted but bbox is a vector rather than a matrix, then the same bounding box will be used for all samples. You may see points at the edge of the geometries if the intersection between the bounding box and a geometry happens to be a point there. If NULL, then the entire tissue is plotted.

image_id
ID of the image to plot behind the geometries. If NULL, then not plotting images. Use imgData to see image IDs present.

maxcell
Maximum number of pixels to plot in the image. If the image is larger, it will be resampled so it have less than this number of pixels to save memory and for faster plotting. We recommend reducing this number when plotting multiple facets.

aes_use
Aesthetic to use for discrete variables. For continuous variables, it’s always "fill" for polygons and point shapes 21-25. For discrete variables, it can be fill, color, shape, or linetype, whenever applicable. The specified value will be changed to the applicable equivalent. For example, if the geometry is point but "linetype" is specified, then "shaped" will be used instead.

divergent
Logical, whether a divergent palette should be used.

diverge_center
If divergent = TRUE, the center from which the palette should diverge. If NULL, then not centering.
annot_divergent

Just as divergent, but for the annotGeometry in case it's different.

annot_diverge_center

Just as diverge_center, but for the annotGeometry in case it's different.

size

Fixed size of points. For points defaults to 0.5. Ignored if size_by is specified.

shape

Fixed shape of points, ignored if shape_by is specified and applicable.

linewidth

Width of lines, including outlines of polygons. For polygons, this defaults to 0, meaning no outlines.

linetype

Fixed line type, ignored if linetype_by is specified and applicable.

alpha

Transparency.

color

Fixed color for colGeometry if color_by is not specified or not applicable, or for annotGeometry if annot_color_by is not specified or not applicable.

fill

Similar to color, but for fill.

scattermore

Logical, whether to use the scattermore package to greatly speed up plotting numerous points. Only used for POINT colGeometries. If the geometry is not POINT, then the centroids are used. Recommended for plotting hundreds of thousands or more cells where the cell polygons can't be seen when plotted due to the large number of cells and small plot size such as when plotting multiple panels for multiple features.

pointsize

Radius of rasterized point in scattermore. Default to 0 for single pixels (fastest).

bins

If binning the colGeometry in space due to large number of cells or spots, the number of bins, passed to geom_bin2d or geom_hex. If NULL (default), then the colGeometry is plotted without binning. If binning, a point geometry is recommended. If the geometry is not point, then the centroids will be used.

summary_fun

Function to summarize the feature value when the colGeometry is binned.

hex

Logical, whether to use geom_hex. Note that geom_hex is broken in ggplot2 version 3.4.0. Please update ggplot2 if you are getting horizontal stripes when hex = TRUE.

dark

Logical, whether to use dark theme. When using dark theme, the palette will have lighter color represent higher values as if glowing in the dark. This is intended for plotting gene expression on top of fluorescent images.

...

Other arguments passed to wrap_plots.

Value

Same as in plotSpatialFeature. A ggplot2 object if plotting one component. A patchwork object if plotting multiple components.

See Also

scater::plotReducedDim
Examples

```r
library(SFEData)
library(scater)
sfe <- McKellarMuscleData("small")
sfe <- logNormCounts(sfe)
sfe <- runPCA(sfe, ncomponents = 2)
spatialReducedDim(sfe, "PCA", ncomponents = 2, "spotPoly",
    annotGeometryName = "tissueBoundary",
    divergent = TRUE, diverge_center = 0
)
# Basically PC1 separates spots not on tissue from those on tissue.
```

---

variogram-internal  Compute variograms

Description

Wrapper of `automap::autofitVariogram` to facilitate computing variograms for multiple genes in SFE objects as an EDA tool. These functions are written to conform to a uniform format for univariate methods to be called internally. These functions are not exported, but the documentation is written to show users the extra arguments to use when alling `calculateUnivariate` or `runUnivariate`.

Usage

```r
.variogram(x, coords_df, formula = x ~ 1, scale = TRUE, ...)
.variogram_bv(x, y, coords_df, scale = TRUE, map = FALSE, ...)
.cross_variogram(x, y, coords_df, scale = TRUE, ...)
.cross_variogram_map(x, y, coords_df, width, cutoff, scale = TRUE, ...)
.variogram_map(x, coords_df, formula = x ~ 1, width, cutoff, scale = TRUE, ...)
```

Arguments

- **x**: A numeric vector whose variogram is computed.
- **coords_df**: A sf data frame with the geometry and regressors for variogram modeling.
- **formula**: A formula defining the response vector and (possible) regressors, in case of absence of regressors, use `x ~ 1`.
- **scale**: Logical, whether to scale `x`. Defaults to `TRUE` so the variogram is easier to interpret and is more comparable between features with different magnitudes when the length scale of spatial autocorrelation is of interest.
... Other arguments passed to automap::autofitVariogram such as model and variogram such as alpha for anisotropy. Note that gstat does not fit anisotropic models and you will get a warning if you specify alpha. Nevertheless, plotting the empirical anisotropic variograms and comparing them to the variogram fitted to the entire dataset can be a useful EDA tool.

y For bivariate, another numeric vector whose variogram is computed.

map logical; if TRUE, and cutoff and width are given, a variogram map is returned. This requires package sp. Alternatively, a map can be passed, of class SpatialDataFrameGrid (see sp docs)

width the width of subsequent distance intervals into which data point pairs are grouped for semivariance estimates

cutoff spatial separation distance up to which point pairs are included in semivariance estimates; as a default, the length of the diagonal of the box spanning the data is divided by three.

Value

An autofitVariogram object.
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