Package 'Voyager'

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Type Package

Title From geospatial to spatial omics

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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.

Depends R (>= 4.2.0), SpatialFeatureExperiment (>= 1.7.3)

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'geom_spi.R' 'gstat.R' 'listSFEMethods.R' 'multivariate.R'
'plot-non-spatial.R' 'plot-transcripts.R'
'plot-univar-downstream.R' 'plot.R' 'plotLocalResult.R'
'plotSpatialReducedDim.R' 'spatial-misc.R'
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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

```
## 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,
  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,
  zero.policy = NULL,
  p.adjust.method = "BH",
  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 func-

tions 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 attr(listw, "zero.policy") as set when listw was created, if attribute not set, 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.

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

```
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],]
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

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

tions 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 attr(listw, "zero.policy") as set when listw was created, if attribute not set, 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 sotred 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.

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

Dray, S., Said, S. and Debias, F. (2008) Spatial ordination of vegetation data using a generalization of Wartenberg's multivariate spatial correlation. Journal of vegetation science, 19, 45-56.

Anselin, L. (2019), A Local Indicator of Multivariate Spatial Association: Extending Geary's c. Geogr Anal, 51: 133-150. doi:10.1111/gean.12164

Examples

```
# example code
library(SFEData)
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 stiatistics*

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

```
## S4 method for signature 'ANY,SFEMethod'
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 '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"
)

## 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,
  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(),
  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 attr(listw, "zero.policy") as set when listw was created, if attribute not set, 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.

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

Cliff, A. D., Ord, J. K. 1981 Spatial processes, Pion, p. 17.

Anselin, L. (1995), Local Indicators of Spatial Association-LISA. Geographical Analysis, 27: 93-115. doi:10.1111/j.1538-4632.1995.tb00338.x

Ord, J. K., & Getis, A. 2012. Local spatial heteroscedasticity (LOSH), The Annals of Regional Science, 48 (2), 529-539.

Ord, J. K. and Getis, A. 1995 Local spatial autocorrelation statistics: distributional issues and an application. Geographical Analysis, 27, 286-306

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.
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(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)
)
```

---

clusterMoranPlot *Find clusters on the Moran plot*

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

```
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.

Usage

```
clusterVariograms(
  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]
genes <- 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)
```

---

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

```
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

```
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.

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)
getDivergeRange(v, diverge_center = 0)
```

`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")
```

---

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 $(I - \mathbb{1}\mathbb{1}^T/n)C(I - \mathbb{1}\mathbb{1}^T/n)$, where $\mathbb{1}$ is a vector of all 1's. This implementation follows the implementation in `adespatial` 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 the 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

de Jong, P., Sprenger, C., & van Veen, F. (1984). On extreme values of Moran's I and Geary's C. Geographical Analysis, 16(1), 17-24.

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.

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.

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.

binwidth — Width of bins, passed to geom_bin2d or geom_hex.

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.

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

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

name	Name under which the Moran plot results are stored. By default "moran.plot".
...	Other arguments to pass to geom_density2d.

Value

A ggplot object.

Examples

```
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

```
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 nega 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

Dray, S., Said, S. and Debias, F. (2008) Spatial ordination of vegetation data using a generalization of Wartenberg's multivariate spatial correlation. Journal of vegetation science, 19, 45-56.

Examples

```
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)
```

---

plotBivariate *Plot expression of two genes or features with bivariate palette*

Description

This function uses the 'biscale' package to plot two features simultaneously using a bivariate palette. The features can come from the assays or colData.

Usage

```
plotBivariate(
  sfe,
  feature1,
  feature2,
  colGeometryName = 1L,
  sample_id = "all",
  bbox = NULL,
  palette = "BlueGold",
  size = 0.5,
  dim = 4,
  style = "fisher",
  exprs_values = "logcounts",
  swap_rownames = NULL,
```

```
  show_axes = FALSE,
  ncol = NULL
)
```

Arguments

sfe	A SpatialFeatureExperiment object.
feature1	First feature to plot
feature2	Second feature to plot
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.
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.
palette	Name of bivariate palette; see bi_pal for complete list of built-in palettes in the 'biscale' package.
size	Fixed size of points. For points defaults to 0.5. Ignored if size_by is specified.
dim	The dimensions of the palette. To use the built-in palettes, this value must be either 2, 3, or 4. A value of 3, for example, would be used to create a three-by-three bivariate map with a total of 9 classes. If you are using a custom palette, this value may be larger (though these maps can be very hard to interpret). If you are using pre-made factors, both factors must have the same number of levels as this value.
style	A string identifying the style used to calculate breaks. Currently supported styles are "quantile", "equal", "fisher", and "jenks". If both x and y are factors, this argument can be omitted. Note that older versions of biscale used "quantile" as the default for this argument. Now that bi_class accepts factors, this argument no longer as a default and older code will error.
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.
show_axes	Logical, whether to show axes.

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.

Note

Legend must be plotted separated as another 'ggplot' object. See bi_legend.

---

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

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

```
library(SFEData)
sfe <- HeNSCLCData()
plotCellBin2D(sfe)
```

`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

```
plotColDataFreqpoly(
  sce,
  feature,
  color_by = NULL,
  subset = NULL,
  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 or rowData 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 takes x after scale transformation as input and returns a single numeric value. 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	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The position argument accepts the following: • The result of calling a position function, such as position_jitter(). This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the position_ prefix. For example, to use position_jitter(), give the position as "jitter". • For more information and other ways to specify the position, see the layer position documentation.

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` or `rowData` to plot. When multiple features are specified, they will be plotted in separate facets.
`fill_by`	Name of a categorical column in `colData` or `rowData` to fill the histogram.
`facet_by`	Column in `colData` or `rowData` 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 takes x after scale transformation as input and returns a single numeric value. 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` A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The `position` argument accepts the following:

- The result of calling a position function, such as `position_jitter()`. This method allows for passing extra arguments to the position.
- A string naming the position adjustment. To give the position as a string, strip the function name of the `position_` prefix. For example, to use `position_jitter()`, give the position as `"jitter"`.
- For more information and other ways to specify the position, see the layer position documentation.

`...` Other arguments passed on to `layer()`'s `params` argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the `position` argument, or aesthetics that are required can *not* be passed through `...`. Unknown arguments that are not part of the 4 categories below are ignored.

- Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, `colour = "red"` or `linewidth = 3`. The geom's documentation has an **Aesthetics** section that lists the available options. The 'required' aesthetics cannot be passed on to the `params`. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data.
- When constructing a layer using a `stat_*()` function, the `...` argument can be used to pass on parameters to the `geom` part of the layer. An example of this is `stat_density(geom = "area", outline.type = "both")`. The geom's documentation lists which parameters it can accept.
- Inversely, when constructing a layer using a `geom_*()` function, the `...` argument can be used to pass on parameters to the `stat` part of the layer. An example of this is `geom_area(stat = "density", adjust = 0.5)`. The stat's documentation lists which parameters it can accept.
- The `key_glyph` argument of `layer()` may also be passed on through `...`. This can be one of the functions described as key glyphs, to change the display of the layer in the legend.

Value

A ggplot object

See Also

plotColDataFreqpoly

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 *Plot spatial graphs*

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.
geometry_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"
    )
plotAnnotGraph(sfe,
    annotGraphName = "myofibers",
    annotGeometryName = "myofiber_simplified",
    weights = TRUE
)
```

`plotCorrelogram` *Plot correlogram*

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.
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
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.
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.
plot_signif	Logical, whether to plot significance symbols: $p < 0.001$: ***, $p < 0.01$: **, $p < 0.05$ *, $p < 0.1$: ., 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.
p_adj_method	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.
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.

Examples

```
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")
```

---

plotCrossVariogram *Plot cross variogram*

Description

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

Usage

```
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.

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

```
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)
```

---

plotDimLoadings *Plot top PC loadings of genes*

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

```
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. When multiple geometries are plotted at the same time, they will be differentiated by color, by default using the dittoSeq palette, but this can be overridden with scale_color_* functions. Transcript spots of different genes are differentiated by point shape if plotted, so the number of genes plotted shouldn't exceed about 6 or a warning will be issued.

Usage

```
plotGeometry(
  sfe,
  type = lifecycle::deprecated(),
  MARGIN = lifecycle::deprecated(),
  colGeometryName = NULL,
  annotGeometryName = NULL,
  rowGeometryName = NULL,
  gene = "all",
  sample_id = "all",
  fill = TRUE,
  ncol = NULL,
  bbox = NULL,
  tx_alpha = 1,
```

```
  tx_size = 1,
  tx_file = NULL,
  image_id = NULL,
  channel = NULL,
  maxcell = 5e+05,
  show_axes = FALSE,
  dark = FALSE,
  palette = colorRampPalette(c("black", "white"))(255),
  normalize_channels = FALSE
)
```

Arguments

sfe	A SpatialFeatureExperiment object.
type	Name of the geometry associated with the MARGIN of interest for which to compute the graph.
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
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.
rowGeometryName	Name of a rowGeometry of the SFE object to plot.
gene	Character vector of names of genes to plot. If "all" then transcript spots of all genes are plotted.
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.
fill	Logical, whether to fill polygons.
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.
tx_alpha	Transparency for transcript spots, helpful when the transcript spots are overplotting.

tx_size — Point size for transcript spots.

tx_file — File path to GeoParquet file of the transcript spots if you don't wish to load all transcript spots into the SFE object. See formatTxSpots on generating such a GeoParquet file.

image_id — ID of the image to plot behind the geometries. If NULL, then not plotting images. Use imgData to see image IDs present. To plot multiple grayscale images as different RGB channels, use a named vector here, whose names are channel names (r, g, b), and values are image_ids of the corresponding images. The RGB colorization may not be colorblind friendly. When plotting multiple samples, it is assumed that the same image_id is used for each channel across different samples.

channel — Numeric vector indicating which channels in a multi-channel image to plot. If NULL, grayscale is plotted if there is 1 channel and RGB for the first 3 channels. The numeric vector can be named (r, g, b) to indicate which channel maps to which color. The RGB colorization may not be colorblind friendly. This argument cannot be specified while image_id is a named vector to plot different grayscale images as different channels.

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.

show_axes — Logical, whether to show axes.

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.

palette — Vector of colors to use to color grayscale images.

normalize_channels — Logical, whether to normalize each channel of the image individually. Should be FALSE for bright field color images such as H&E but should set to TRUE for fluorescent images.

Value

A ggplot object.

Examples

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

plotImage *Show image without plotting geometries*

Description

This function plots the images in SFE objects without plotting geometries. When showing axes, the numbers are coordinates within the image itself and have the same units as the spatial extent, but are not the actual spatial extent when plotting multiple samples to avoid excessive empty space.

Usage

```
plotImage(
  sfe,
  sample_id = "all",
  image_id = NULL,
  channel = NULL,
  ncol = NULL,
  bbox = NULL,
  maxcell = 5e+05,
  show_axes = FALSE,
  dark = FALSE,
  palette = colorRampPalette(c("black", "white"))(255),
  normalize_channels = FALSE
)
```

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.
image_id	ID of the image(s) to plot. If NULL, then the first image present is plotted. Can be a vector of IDs to use different grayscale images for different channels. The vector can be named ('r', 'g', 'b'), to assign channels to images. The vector must be named if it's length 2.
channel	Numeric vector indicating which channels in a multi-channel image to plot. If NULL, grayscale is plotted if there is 1 channel and RGB for the first 3 channels. The numeric vector can be named (r, g, b) to indicate which channel maps to which color. The RGB colorization may not be colorblind friendly. This argument cannot be specified while image_id is a named vector to plot different grayscale images as different channels.
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.

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.

show_axes — Logical, whether to show axes.

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.

palette — Vector of colors to use to color grayscale images.

normalize_channels — Logical, whether to normalize each channel of the image individually. Should be FALSE for bright field color images such as H&E but should set to TRUE for fluorescent images.

Value

A ggplot object.

Examples

```
library(SFEData)
library(SpatialFeatureExperiment)
fn <- XeniumOutput("v2", file_path = "xenium_example")
# Weird RBioFormats null pointer error the first time it's run
try(sfe <- readXenium(fn))
sfe <- readXenium(fn)
# Plot one channel
plotImage(sfe, image_id = "morphology_focus", channel = 1L)
plotImage(sfe, image_id = "morphology_focus", channel = 1L, show_axes = TRUE, dark = TRUE)
# Colorize based on different channels
plotImage(sfe, image_id = "morphology_focus", channel = c(2,4,1), show_axes = TRUE, dark = TRUE)
unlink("xenium_example", recursive = TRUE)
```

---

plotLocalResult *Plot local results*

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,
  rowGeometryName = NULL,
  rowGeometryFeatures = NULL,
  ncol = NULL,
  ncol_sample = NULL,
  annot_aes = list(),
  annot_fixed = list(),
  tx_fixed = list(),
  bbox = NULL,
  tx_file = NULL,
  image_id = NULL,
  channel = 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,
  show_axes = FALSE,
  dark = FALSE,
  palette = colorRampPalette(c("black", "white"))(255),
  normalize_channels = 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.
rowGeometryName	Name of a rowGeometry of the SFE object to plot.
rowGeometryFeatures	Which features from rowGeometry to plot. Can only be a small number to avoid overplotting. Different features are distinguished by point shape. By default (NULL), when rowGeometryName is specified, this will be whichever items in features that are also in the row names of the SFE object. If features specified for this argument are not the same as or a subset of those in argument features, then the spots of all features specified here will be plotted, differentiated by point shape.
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 facetted 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.
tx_fixed	Similar to annot_fixed, but to specify fixed aesthetic for transcript spots.

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.

tx_file — File path to GeoParquet file of the transcript spots if you don't wish to load all transcript spots into the SFE object. See formatTxSpots on generating such a GeoParquet file.

image_id — ID of the image to plot behind the geometries. If NULL, then not plotting images. Use imgData to see image IDs present. To plot multiple grayscale images as different RGB channels, use a named vector here, whose names are channel names (r, g, b), and values are image_ids of the corresponding images. The RGB colorization may not be colorblind friendly. When plotting multiple samples, it is assumed that the same image_id is used for each channel across different samples.

channel — Numeric vector indicating which channels in a multi-channel image to plot. If NULL, grayscale is plotted if there is 1 channel and RGB for the first 3 channels. The numeric vector can be named (r, g, b) to indicate which channel maps to which color. The RGB colorization may not be colorblind friendly. This argument cannot be specified while image_id is a named vector to plot different grayscale images as different channels.

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.
show_axes	Logical, whether to show axes.
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.
palette	Vector of colors to use to color grayscale images.
normalize_channels	Logical, whether to normalize each channel of the image individually. Should be FALSE for bright field color images such as H&E but should set to TRUE for 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 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

```
plotMoranMC(
  sfe,
  features,
  sample_id = "all",
  facet_by = c("sample_id", "features"),
  ncol = NULL,
  colGeometryName = NULL,
  annotGeometryName = NULL,
  reducedDimName = NULL,
  ptype = c("density", "histogram", "freqpoly"),
  swap_rownames = NULL,
  name = "moran.mc",
  ...
)
```

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)
sfe <- McKellarMuscleData("small")
colGraph(sfe, "visium") <- findVisiumGraph(sfe)
sfe <- colDataUnivariate(sfe, type = "moran.mc", "nCounts", nsim = 100)
plotMoranMC(sfe, "nCounts")
```

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,
  rowGeometryName = NULL,
  rowGeometryFeatures = NULL,
  annot_aes = list(),
  annot_fixed = list(),
  tx_fixed = list(),
  exprs_values = "logcounts",
  bbox = NULL,
  tx_file = NULL,
  image_id = NULL,
  channel = 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,
  show_axes = FALSE,
```

```
  dark = FALSE,
  palette = colorRampPalette(c("black", "white"))(255),
  normalize_channels = 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 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 facetted by samples.
annotGeometryName	Name of a annotGeometry of the SFE object, to annotate the gene expression plot.
rowGeometryName	Name of a rowGeometry of the SFE object to plot.
rowGeometryFeatures	Which features from rowGeometry to plot. Can only be a small number to avoid overplotting. Different features are distinguished by point shape. By default (NULL), when rowGeometryName is specified, this will be whichever items in features that are also in the row names of the SFE object. If features specified for this argument are not the same as or a subset of those in argument features, then the spots of all features specified here will be plotted, differentiated by point shape.
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.
tx_fixed	Similar to annot_fixed, but to specify fixed aesthetic for transcript spots.
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.

tx_file — File path to GeoParquet file of the transcript spots if you don't wish to load all transcript spots into the SFE object. See formatTxSpots on generating such a GeoParquet file.

image_id — ID of the image to plot behind the geometries. If NULL, then not plotting images. Use imgData to see image IDs present. To plot multiple grayscale images as different RGB channels, use a named vector here, whose names are channel names (r, g, b), and values are image_ids of the corresponding images. The RGB colorization may not be colorblind friendly. When plotting multiple samples, it is assumed that the same image_id is used for each channel across different samples.

channel — Numeric vector indicating which channels in a multi-channel image to plot. If NULL, grayscale is plotted if there is 1 channel and RGB for the first 3 channels. The numeric vector can be named (r, g, b) to indicate which channel maps to which color. The RGB colorization may not be colorblind friendly. This argument cannot be specified while image_id is a named vector to plot different grayscale images as different channels.

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.
show_axes	Logical, whether to show axes.
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.
palette	Vector of colors to use to color grayscale images.
normalize_channels	Logical, whether to normalize each channel of the image individually. Should be FALSE for bright field color images such as H&E but should set to TRUE for 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 overriden 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(SFEData)
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
plotSpatialFeature(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))
```

plotTxBin2D *Plot transcript spot density as 2D histogram*

Description

Plot transcript spot density as 2D histogram

Usage

```
plotTxBin2D(
  sfe = NULL,
  data_dir = NULL,
  tech = c("Vizgen", "Xenium", "CosMX"),
  file = NULL,
  sample_id = "all",
  bins = 200,
  binwidth = NULL,
  hex = FALSE,
  ncol = NULL,
  bbox = NULL,
  gene = "all",
  spatialCoordsNames = c("X", "Y"),
  gene_col = "gene",
  rowGeometryName = "txSpots",
  flip = FALSE,
  tx_file = NULL
)
```

Arguments

sfe	A SpatialFeatureExperiment object.
data_dir	Top level directory of the output files. This can be specified in place of sfe to directly read the transcript spot coordinates from the file. When reading from file, transcripts from this file are plotted and argument sample_id is ignored.
tech	Name of the commercial technology, must be one of Vizgen, Xenium, and CosMX.
file	File (not GeoParquet) with numeric columns for xy coordinates of the transcript spots. Ignored if data_dir is specified.
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.

gene — Character vector of names of genes to plot. If "all" then transcript spots of all genes are plotted.

spatialCoordsNames — Column names for the x, y, and optionally z coordinates of the spots. The defaults are for Vizgen.

gene_col — Column name for genes.

rowGeometryName — Name of a rowGeometry of the SFE object to plot.

flip — Logical, whether to flip the y axis when plotting data from file.

tx_file — File path to GeoParquet file of the transcript spots if you don't wish to load all transcript spots into the SFE object. See formatTxSpots on generating such a GeoParquet file.

Value

A ggplot object, facetting by sample.

---

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

```
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.
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

```
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

```
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.
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

```
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

```
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 dimentions 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

```
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.

Usage

```
spatialReducedDim(
  sfe,
  dimred,
  ncomponents = NULL,
  components = ncomponents,
  colGeometryName = 1L,
  sample_id = "all",
  ncol = NULL,
  ncol_sample = NULL,
  annotGeometryName = NULL,
  rowGeometryName = NULL,
  rowGeometryFeatures = NULL,
  annot_aes = list(),
  annot_fixed = list(),
  tx_fixed = list(),
  exprs_values = "logcounts",
  bbox = NULL,
  tx_file = NULL,
  image_id = NULL,
  channel = 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,
  show_axes = FALSE,
  dark = FALSE,
  palette = colorRampPalette(c("black", "white"))(255),
  normalize_channels = FALSE,
  ...
)
```

Arguments

sfe	A SpatialFeatureExperiment object.
dimred	A string or integer scalar indicating the reduced dimension result in reducedDims(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 facetted by samples.
annotGeometryName	Name of a annotGeometry of the SFE object, to annotate the gene expression plot.
rowGeometryName	Name of a rowGeometry of the SFE object to plot.

rowGeometryFeatures
: Which features from rowGeometry to plot. Can only be a small number to avoid overplotting. Different features are distinguished by point shape. By default (NULL), when rowGeometryName is specified, this will be whichever items in features that are also in the row names of the SFE object. If features specified for this argument are not the same as or a subset of those in argument features, then the spots of all features specified here will be plotted, differentiated by point shape.

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.

tx_fixed
: Similar to annot_fixed, but to specify fixed aesthetic for transcript spots.

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.

tx_file
: File path to GeoParquet file of the transcript spots if you don't wish to load all transcript spots into the SFE object. See formatTxSpots on generating such a GeoParquet file.

image_id
: ID of the image to plot behind the geometries. If NULL, then not plotting images. Use imgData to see image IDs present. To plot multiple grayscale images as different RGB channels, use a named vector here, whose names are channel names (r, g, b), and values are image_ids of the corresponding images. The RGB colorization may not be colorblind friendly. When plotting multiple samples, it is assumed that the same image_id is used for each channel across different samples.

channel
: Numeric vector indicating which channels in a multi-channel image to plot. If NULL, grayscale is plotted if there is 1 channel and RGB for the first 3 channels. The numeric vector can be named (r, g, b) to indicate which channel maps to which color. The RGB colorization may not be colorblind friendly. This argument cannot be specified while image_id is a named vector to plot different grayscale images as different channels.

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`.

`show_axes` Logical, whether to show axes.

`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.

`palette` Vector of colors to use to color grayscale images.

`normalize_channels`
Logical, whether to normalize each channel of the image individually. Should be `FALSE` for bright field color images such as H&E but should set to `TRUE` for 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

```
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

```
.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 ansotropic 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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