Package ‘BayesSpace’

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Description Tools for clustering and enhancing the resolution of spatial gene expression experiments. BayesSpace clusters a low-dimensional representation of the gene expression matrix, incorporating a spatial prior to encourage neighboring spots to cluster together. The method can enhance the resolution of the low-dimensional representation into ‘`sub-spots``

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.adjust_hex_centers

Adjust hex spot positions so hexagons are adjacent to each other in plot

Description
Spots are regular hexagons with one unit of horizontal distance between centers

Usage
.adjust_hex_centers(spot_positions)

Value
Shifted spot centers

.bsData
Access BayesSpace metadata

Description
Access BayesSpace metadata

Usage
.bsData(sce, name, default = NULL, warn = FALSE)

Arguments
sce SingleCellExperiment
name Metadata name

Value
Requested metadata
.clean_chain

Tidy C++ outputs before writing to disk.

Description

1) Convert each parameter to matrix (n_iterations x n_indices) 2) Add appropriate colnames 3) Thin evenly (for enhance)

Usage

.clean_chain(out, method = c("cluster", "enhance"), thin = 100)

Arguments

out List returned by cluster() or deconvolve().
method Whether the output came from clustering or enhancement. (Different params are included in each.)
thin Thinning rate. Some enhanced parameters are thinned within C++ loop, others (mu and Ychange) need to be thinned afterwards.

Value

List with standardized parameters

.compute_interspot_distances

Estimate the distance between two neighboring spots

Description

Fit linear models between each image pixel coordinate and its corresponding array coordinate to estimate the pixel distance between two spots along each axis. Add these distances to estimate the L1 distance between two spots, then add a small buffer.

Usage

.compute_interspot_distances(sce, scale.factor = 1.02)

Arguments

sce SingleCellExperiment (must include row, col, imagerow, imagecol in colData)
scale.factor Scale estimated L1 difference up by this amount.

Value

doubles xdist, ydist, radius
`.find_neighbors`  
*Find neighboring spots based on array coordinates*

**Description**

Find neighboring spots based on array coordinates

**Usage**

```r
.find_neighbors(sce, platform)
```

**Arguments**

- `sce` SingleCellExperiment
- `platform` If "Visium", select six neighboring spots around center; if "ST", select four adjacent spots.

**Value**

`df_j` a list of neighbor indices (zero-indexed) for each spot

---

`.flatten_matrix_list`  
*Convert a list of matrices to a single matrix, where each row is a flattened matrix from the original list*

**Description**

Convert a list of matrices to a single matrix, where each row is a flattened matrix from the original list

**Usage**

```r
.flatten_matrix_list(xs, ...)
```

**Arguments**

- `xs` List of matrices

**Value**

Matrix
.infer_param_dims

Infer original dimensions of parameter (per iteration) from colnames

Description

Used to avoid writing colnames directly to HDF5 as attribute, which fails for large parameters (e.g. Y)

Usage

.infer_param dims(cnames)

Arguments

cnames List of column names

Value

Numeric vector (nrow, ncol)

.init_cluster

Initialize cluster assignments

Description

Initialize cluster assignments

Usage

.init_cluster(Y, q, init = NULL, init.method = c("mclust", "kmeans"))

Arguments

q Number of clusters
init Vector of initial cluster assignments
init.method Initialization clustering algorithm
sce SingleCellExperiment
inputs Results from .prepare_inputs()

Value

Vector of cluster assignments.
**.make_hex_spots**  
*Make vertices for each hex spot*

**Description**
Make vertices for each hex spot

**Usage**
```
.make_hex_spots(cdata, fill)
```

**Value**
Table of (x.pos, y.pos, spot, fill); where spot groups the vertices outlining the spot’s border

---

**.make_index_names**  
*Make colnames for parameter indices.*

**Description**
Scalar parameters are named "name". Vector parameters are named "name[i]". Matrix parameters are named "name[i,j]".

**Usage**
```
.make_index_names(name, m = NULL, n = NULL, dim = 1)
```

**Arguments**
- `name`: Parameter name
- `m, n`: Dimensions of parameter (m=nrow, n=ncol)
- `dim`: Dimensionality of parameter (0=scalar, 1=vector, 2=matrix)

**Value**
List of names for parameter values
.make_square_spots

--

.make_square_spots  Make vertices for each square spot

Description

Squares are simple, just make a unit square at each array coordinate

Usage

.make_square_spots(cdata, fill = "spatial.cluster", scale.factor = 1)

Value

Table of (x.pos, y.pos, spot, fill); where spot groups the vertices outlining the spot’s border

--

.make_spot_vertices  Compute vertex coordinates for each spot in frame of plot

Description

Compute vertex coordinates for each spot in frame of plot

Usage

.make_spot_vertices(spot_positions, vertex_offsets)

Arguments

spot_positions  Center for hex, top left for square
vertex_offsets  Data frame of (x, y) offsets wrt spot position for each vertex of spot

Value

Cartesian product of positions and offsets, with coordinates computed as (pos + offset)
.make_subspot_coldata

Description

Subspots are stored as (1.1, 2.1, 3.1, ..., 1.2, 2.2, 3.2, ...)

Usage

.make_subspot_coldata(positions, sce, n_subspots_per)

Arguments

sce Original sce (to obtain number of spots and original row/col)
n_subspots_per Number of subspots per spot
cdata Table of colData (imagerow and imagecol; from deconv$positions)

Value

Data frame with added subspot names, parent spot indices, and offset row/column coordinates

.make_subspot_offsets

Description

Hex spots are divided into 6 triangular subspots, square spots are divided into 9 squares. Offsets are relative to the spot center.

Usage

.make_subspot_offsets(n_subspots_per)

Arguments

n_subspots_per Number of subspots per spot

Value

Matrix of x and y offsets, one row per subspot
.make_triangle_subspots

Make vertices for each triangle subspot of a hex

Description

Make vertices for each triangle subspot of a hex

Usage

.make_triangle_subspots(cdata, fill = "spatial.cluster")

Value

Table of (x.pos, y.pos, spot, fill); where spot groups the vertices outlining the spot’s border

.make_vertices

Make vertices outlining spots/subspots for geom_polygon()

Description

Make vertices outlining spots/subspots for geom_polygon()

Usage

.make_vertices(sce, fill, platform, is.enhanced)

Arguments

sce SingleCellExperiment with row/col in colData
fill Name of a column in colData(sce) or a vector of values to use as fill for each spot
platform "Visium" or "ST", used to determine spot layout
is.enhanced If true, sce contains enhanced subspot data instead of spot-level expression. Used to determine spot layout.

Value

Table of (x.pos, y.pos, spot, fill); where spot groups the vertices outlining the spot’s border
### prepare_inputs

**Prepare cluster/deconvolve inputs from SingleCellExperiment object**

**Description**

Prepare cluster/deconvolve inputs from SingleCellExperiment object

**Usage**

```r
.prepare_inputs(
  sce,
  use.dimred = "PCA",
  d = 15,
  positions = NULL,
  position.cols = c("imagecol", "imagerow"),
  radius = NULL,
  xdist = NULL,
  ydist = NULL
)
```

**Value**

List of PCs, names of columns with x/y positions, and inter-spot distances

### read_chain

**Load saved chain from disk.**

**Description**

Load saved chain from disk.

**Usage**

```r
.read_chain(h5.fname, params = NULL, is.enhanced = FALSE)
```

**Arguments**

- `h5.fname` Path to hdf5 file containing chain
- `params` List of parameters to read from file (will read all by default)

**Value**

MCMC chain, represented as a coda::mcmc object
.select_spot_positions

Helper to extract x, y, fill ID from colData

Description
Helper to extract x, y, fill ID from colData

Usage
.select_spot_positions(cdata, x = "col", y = "row", fill = "spatial.cluster")

Value
Dataframe of (x.pos, y.pos, fill) for each spot

.select_subspot_positions

Helper to pull out subspot position columns Probably redundant with select_spot_positions above, but we need subspot.idx

Description
Helper to pull out subspot position columns Probably redundant with select_spot_positions above, but we need subspot.idx

Usage
.select_subspot_positions(
cdata,
x = "spot.col",
y = "spot.row",
fill = "spatial.cluster"
)

Value
Dataframe of (x.pos, y.pos, fill) for each spot
BayesSpace: A package for processing spatial transcriptomes

Description

Tools for clustering and enhancing the resolution of spatial gene expression experiments. BayesSpace clusters a low-dimensional representation of the gene expression matrix, incorporating a spatial prior to encourage neighboring spots to cluster together. The method can enhance the resolution of the low-dimensional representation into "sub-spots", for which features such as gene expression or cell type composition can be imputed.

Details

For an overview of the functionality provided by the package, please see the vignette: `vignette("BayesSpace", package="BayesSpace")`

cluster

Wrapper around C++ iterate_*() functions

Usage

```r
cluster(
  Y,
  q,
  df_j,
  init = rep(1, nrow(Y)),
  model = c("t", "normal"),
  precision = c("equal", "variable"),
  mu0 = colMeans(Y),
  lambda0 = diag(0.01, nrow = ncol(Y)),
  gamma = 3,
  alpha = 1,
  beta = 0.01,
  nrep = 1000
)
```

Value

List of clustering parameter values at each iteration
clusterPlot

Plot spatial cluster assignments.

Description

Plot spatial cluster assignments.

Usage

clusterPlot(
  sce,
  label = "spatial.cluster",
  palette = NULL,
  color = NULL,
  platform = NULL,
  is.enhanced = NULL,
  ...
)

Arguments

sce  SingleCellExperiment. If fill is specified and is a string, it must exist as a column in colData(sce).
label  Labels used to color each spot. May be the name of a column in colData(sce), or a vector of discrete values.
palette  Optional vector of hex codes to use for discrete spot values.
color  Optional hex code to set color of borders around spots. Set to NA to remove borders.
platform  Spatial sequencing platform. If "Visium", the hex spot layout will be used, otherwise square spots will be plotted.
NOTE: specifying this argument is only necessary if sce was not created by spatialCluster() or spatialEnhance().
is.enhanced  True if sce contains subspot-level data instead of spots. Spatial sequencing platform. If true, the respective subspot lattice for each platform will be plotted.
NOTE: specifying this argument is only necessary if sce was not created by spatialCluster() or spatialEnhance().
...  Additional arguments for geom_polygon(). size, to specify the linewidth of these borders, is likely the most useful.

Value

Returns a ggplot object.

See Also

Other spatial plotting functions: featurePlot()
Examples

```r
sce <- exampleSCE()
clusterPlot(sce)
```

Description

Wrapper around C++ iterate_deconv() function

Usage

```r
deconvolve(
  Y,
  positions,
  xdist,
  ydist,
  q,
  init,
  nrep = 1000,
  model = "normal",
  platform = c("Visium", "ST"),
  verbose = TRUE,
  jitter_scale = 5,
  jitter_prior = 0.01,
  mu0 = colMeans(Y),
  gamma = 2,
  lambda0 = diag(0.01, nrow = ncol(Y)),
  alpha = 1,
  beta = 0.01
)
```

Value

List of enhancement parameter values at each iteration
enhanceFeatures  

Predict feature vectors from enhanced PCs.

Description

Predict feature vectors from enhanced PCs.

Usage

```r
enhanceFeatures(
  sce.enhanced,
  sce.ref,
  feature_names = NULL,
  model = c("xgboost", "dirichlet", "lm"),
  use.dimred = "PCA",
  assay.type = "logcounts",
  altExp.type = NULL,
  feature.matrix = NULL,
  nrounds = 0,
  train.n = round(ncol(sce.ref) * 2/3)
)
```

Arguments

- `sce.enhanced`: SingleCellExperiment object with enhanced PCs.
- `sce.ref`: SingleCellExperiment object with original PCs and expression.
- `feature_names`: List of genes/features to predict expression/values for.
- `model`: Model used to predict enhanced values.
- `use.dimred`: Name of dimension reduction to use.
- `assay.type`: Expression matrix in `assays(sce.ref)` to predict.
- `altExp.type`: Expression matrix in `altExps(sce.ref)` to predict. Overrides `assay.type` if specified.
- `feature.matrix`: Expression/feature matrix to predict, if not directly attached to `sce.ref`. Must have columns corresponding to the spots in `sce.ref`. Overrides `assay.type` and `altExp.type` if specified.
- `nrounds`: Nonnegative integer to set the `nrounds` parameter (max number of boosting iterations) for xgboost. `nrounds = 100` works reasonably well in most cases. If `nrounds` is set to 0, the parameter will be tuned using a train-test split. We recommend tuning `nrounds` for improved feature prediction, but note this will increase runtime.
- `train.n`: Number of spots to use in the training dataset for tuning `nrounds`. By default, 2/3 the total number of spots are used.
**Details**

Enhanced features are computed by fitting a predictive model to a low-dimensional representation of the original expression vectors. By default, a linear model is fit for each gene using the top 15 principal components from each spot, i.e. $\text{lm}(\text{gene} \sim \text{PCs})$, and the fitted model is used to predict the enhanced expression for each gene from the subspots’ principal components.

Diagnostic measures, such as RMSE for `xgboost` or `R.squared` for linear regression, are added to the ‘rowData’ of the enhanced experiment if the features are an assay of the original experiment. Otherwise they are stored as an attribute of the returned matrix/altExp.

Note that feature matrices will be returned and are expected to be input as $p \times n$ matrices of $p$-dimensional feature vectors over the $n$ spots.

**Value**

If `assay.type` or `altExp.type` are specified, the enhanced features are stored in the corresponding slot of `sce.enhanced` and the modified SingleCellExperiment object is returned.

If `feature.matrix` is specified, or if a subset of features are requested, the enhanced features are returned directly as a matrix.

**Examples**

```r
set.seed(149)
sce <- exampleSCE()
sce <- spatialCluster(sce, 7, nrep=100, burn.in=10)
enhanced <- spatialEnhance(sce, 7, init=sce$spatial.cluster, nrep=100, burn.in=10)
enhanced <- enhanceFeatures(enhanced, sce, feature_names=c("gene_1", "gene_2"))
```

---

**exampleSCE**

Create minimal SingleCellExperiment for documentation examples.

**Description**

Create minimal SingleCellExperiment for documentation examples.

**Usage**

`exampleSCE(nrow = 8, ncol = 12, n_genes = 100, n_PCs = 10)`

**Arguments**

- `nrow` Number of rows of spots
- `ncol` Number of columns of spots
- `n_genes` Number of genes to simulate
- `n_PCs` Number of principal components to include
Details

Inspired by scuttle’s mockSCE().

Value

A SingleCellExperiment object with simulated counts, corresponding logcounts and PCs, and positional data in colData. Spots are distributed over an (nrow x ncol) rectangle.

Examples

set.seed(149)
sce <- exampleSCE()

---

**featurePlot**  
Plot spatial gene expression.

Description

Plot spatial gene expression.

Usage

```r
featurePlot(
  sce,
  feature,
  assay.type = "logcounts",
  diverging = FALSE,
  low = NULL,
  high = NULL,
  mid = NULL,
  color = NULL,
  platform = NULL,
  is.enhanced = NULL,
  ...
)
```

Arguments

- **sce**: SingleCellExperiment. If feature is specified and is a string, it must exist as a row in the specified assay of sce.
- **feature**: Feature vector used to color each spot. May be the name of a gene/row in an assay of sce, or a vector of continuous values.
- **assay.type**: String indicating which assay in sce the expression vector should be taken from.
- **diverging**: If true, use a diverging color gradient in featurePlot() (e.g. when plotting a fold change) instead of a sequential gradient (e.g. when plotting expression).
find_neighbors

- low, mid, high: Optional hex codes for low, mid, and high values of the color gradient used for continuous spot values.
- color: Optional hex code to set color of borders around spots. Set to NA to remove borders.
- platform: Spatial sequencing platform. If "Visium", the hex spot layout will be used, otherwise square spots will be plotted.
- is.enhanced: True if sce contains subspot-level data instead of spots. Spatial sequencing platform. If true, the respective subspot lattice for each platform will be plotted.
- ...: Additional arguments for geom_polygon(). size, to specify the linewidth of these borders, is likely the most useful.

Value

Returns a ggplot object.

See Also

Other spatial plotting functions: clusterPlot()

Examples

```r
sce <- exampleSCE()
featurePlot(sce, "gene_2")
```

find_neighbors

Compute pairwise distances between all spots and return list of neighbors for each spot.

Description

Compute pairwise distances between all spots and return list of neighbors for each spot.

Usage

```r
find_neighbors(positions, radius, method = c("manhattan", "euclidean"))
```

Arguments

- positions: (n x 2) matrix of spot coordinates.
- radius: The maximum distance for two spots to be considered neighbors.
- method: Distance metric to use.
mcmcChain

Value

List df_j, where df_j[[i]] is a vector of zero-indexed neighbors of i.

getRDS

*Download a processed sample from our S3 bucket*

Description

Datasets are cached locally using BiocFileCache. The first time using this function, you may need to consent to creating a BiocFileCache directory if one does not already exist.

Usage

getRDS(dataset, sample, cache = TRUE)

Arguments

dataset
  Dataset identifier

sample
  Sample identifier

cache
  If true, cache the dataset locally with BiocFileCache. Otherwise, download directly from our S3 bucket. Caching saves time on subsequent loads, but consumes disk space.

Value

see A SingleCellExperiment with positional information in colData and PCs based on the top 2000 HVGs

Examples

sce <- getRDS("2018_thrane_melanoma", "ST_mel1_rep2", cache=FALSE)

mcmcChain

*Read MCMC chain associated with a BayesSpace clustering or enhancement*

Description

BayesSpace stores the MCMC chain associated with a clustering or enhancement on disk in an HDF5 file. The mcmcChain() function reads any parameters specified by the user into a coda::mcmc object compatible with TidyBayes.
Usage

mcmcChain(sce, params = NULL)
removeChain(sce)

Arguments

sce SingleCellExperiment with a file path stored in its metadata.
params List of model parameters to read

Details

To interact with the HDF5 file directly, obtain the filename from the SingleCellExperiment’s metadata: metadata(sce)$chain.h5. Each parameter is stored as a separate dataset in the file, and is represented as a matrix of size (n_iterations x n_parameter_indices). Parameter choices for the spot-level clustering include:

- \( z \) (cluster assignments)
- \( \text{weights} (w_i) \)
- \( \mu \) (mean vectors)
- \( \lambda \) (precision matrix)
- \( \text{plogLik} \) (pseudo-log-likelihood)

Parameter choices for the subspot-level enhanced clustering include:

- \( z \) (cluster assignments)
- \( \text{weights} (w_i) \)
- \( Y \) (enhanced PCs)
- \( \mu \) (mean vectors)
- \( \lambda \) (precision matrix)
- \( Y\text{change} \) (acceptance rate for the jittering of PCs)

Value

Returns an mcmc object containing the values of the requested parameters over the constructed chain.

Examples

```r
set.seed(149)
sce <- exampleSCE()
sce <- spatialCluster(sce, 7, nrep=100, burn.in=10, save.chain=TRUE)
chain <- mcmcChain(sce)
removeChain(sce)
```
Mode

**Find the mode**

**Description**

Used for finding the most frequent cluster for each z.

**Usage**

```r
Mode(x)
```

**Arguments**

- `x`: Numeric vector

**Value**

- `mode`: Numeric scalar, most frequent element in x

---

**qTune**

**Tuning the choice of q (number of clusters) before running spatialCluster**

**Description**

Before running `spatialCluster()`, we recommend tuning the choice of q by choosing the q that maximizes the model's negative log likelihood over early iterations. `qTune()` computes the average negative log likelihood for a range of q values over iterations 100:1000, and `qPlot()` displays the results.

**Usage**

```r
qPlot(sce, qs = seq(3, 7), force.retune = FALSE, ...)
qTune(sce, qs = seq(3, 7), burn.in = 100, nrep = 1000, ...)
```

**Arguments**

- `sce`: A `SingleCellExperiment` object containing the spatial data.
- `qs`: The values of q to evaluate.
- `force.retune`: If specified, existing tuning values in `sce` will be overwritten.
- `burn.in, nrep`: Integers specifying the range of repetitions to compute.
Details

qTune() takes the same parameters as spatialCluster() and will run the MCMC clustering algorithm up to nrep iterations for each value of q. The first burn.in iterations are discarded as burn-in and the log likelihood is averaged over the remaining iterations.

qPlot() plots the computed negative log likelihoods as a function of q. If qTune() was run previously, i.e. there exists an attribute of sce named "q.logliks", the pre-computed results are displayed. Otherwise, or if force.retune is specified, qplot() will automatically run qTune() before plotting (and can take the same parameters as spatialCluster()).

Value

qTune() returns a modified sce with tuning log likelihoods stored as an attribute named "q.logliks". 
qPlot() returns a ggplot object.

Examples

set.seed(149)
sce <- exampleSCE()
sce <- qTune(sce, seq(3, 7), burn.in=10, nrep=100)
qPlot(sce)

Description

Load a Visium spatial dataset as a SingleCellExperiment.

Usage

readVisium(dirname)

Arguments

dirname  Path to spaceranger output directory (e.g. "sampleID/outs/"). This directory must contain the counts matrix and feature/barcode TSVs in filtered_feature_bc_matrix/ and the spot positions at spatial/tissue_positions_list.csv. (These are default locations for spaceranger outputs.)

Details

We store two variables associated with downstream BayesSpace functions in a list called BayesSpace.data in the SingleCellExperiment’s metadata.

• platform is set to "Visium", and is used to determine spot layout and neighborhood structure.
• is.enhanced is set to FALSE to denote the object contains spot-level data.
spatialCluster

Value

SingleCellExperiment containing the counts matrix in counts and spatial data in colData. Array coordinates for each spot are stored in columns row and col, while image coordinates are stored in columns imagerow and imagecol.

Examples

```r
## Not run:
sce <- readVisium("path/to/outs/")
## End(Not run)
```

spatialCluster Spatial clustering

Description

Cluster a spatial expression dataset.

Usage

```r
spatialCluster(
  sce,
  q,
  use.dimred = "PCA",
  d = 15,
  platform = c("Visium", "ST"),
  init = NULL,
  init.method = c("mclust", "kmeans"),
  model = c("t", "normal"),
  precision = c("equal", "variable"),
  nrep = 50000,
  burn.in = 1000,
  gamma = NULL,
  mu0 = NULL,
  lambda0 = NULL,
  alpha = 1,
  beta = 0.01,
  save.chain = FALSE,
  chain.fname = NULL
)
```

Arguments

- `sce`: A SingleCellExperiment object containing the spatial data.
- `q`: The number of clusters.
spatialCluster

use.dimred  Name of a reduced dimensionality result in reducedDims(sce). If provided, cluster on these features directly.

d  Number of top principal components to use when clustering.

platform  Spatial transcriptomic platform. Specify 'Visium' for hex lattice geometry or 'ST' for square lattice geometry. Specifying this parameter is optional when analyzing SingleCellExperiments processed using readVisium or spatialPreprocess, as this information is included in their metadata.

init  Initial cluster assignments for spots.

init.method  If init is not provided, cluster the top d PCs with this method to obtain initial cluster assignments.

model  Error model. ('normal' or 't')

precision  Covariance structure. ('equal' or 'variable' for EEE and VVV covariance models, respectively.)

nrep  The number of MCMC iterations.

burn.in  The number of MCMC iterations to exclude as burn-in period.

gamma  Smoothing parameter. Defaults to 2 for platform="ST" and 3 for platform="Visium". (Values in range of 1-3 seem to work well.)

mu0  Prior mean hyperparameter for mu. If not provided, mu0 is set to the mean of PCs over all spots.

lambda0  Prior precision hyperparam for mu. If not provided, lambda0 is set to a diagonal matrix 0.01I.

alpha  Hyperparameter for Wishart distributed precision lambda.

beta  Hyperparameter for Wishart distributed precision lambda.

save.chain  If true, save the MCMC chain to an HDF5 file.

chain.fname  File path for saved chain. Tempfile used if not provided.

Details

The input SCE must have row and col columns in its colData, corresponding to the array row and column coordinates of each spot. These are automatically parsed by readVisium or can be added manually when creating the SCE.

Cluster labels are stored in the spatial.cluster column of the SCE, and the cluster initialization is stored in cluster.init.

Value

Returns a modified sce with cluster assignments stored in colData under the name spatial.cluster.

See Also

spatialPreprocess for preparing the SCE for clustering, spatialEnhance for enhancing the clustering resolution, clusterPlot for visualizing the cluster assignments, featurePlot for visualizing expression levels in spatial context, and mcmcChain for examining the full MCMC chain associated with the clustering.
Examples

```r
set.seed(149)
sce <- exampleSCE()
sce <- spatialCluster(sce, 7, nrep=100, burn.in=10)
```

spatialEnhance

```
spatialEnhance(sce, q, platform = c("Visium", "ST"),
               use.dimred = "PCA",
               d = 15,
               init = NULL,
               init.method = c("spatialCluster", "mclust", "kmeans"),
               model = c("t", "normal"),
               nrep = 2e+05,
               gamma = NULL,
               mu0 = NULL,
               lambda0 = NULL,
               alpha = 1,
               beta = 0.01,
               save.chain = FALSE,
               chain.fname = NULL,
               burn.in = 10000,
               jitter_scale = 5,
               jitter_prior = 0.3,
               verbose = FALSE)
```

Arguments

- **sce**: A SingleCellExperiment object containing the spatial data.
- **q**: The number of clusters.
- **platform**: Spatial transcriptomic platform. Specify 'Visium' for hex lattice geometry or 'ST' for square lattice geometry. Specifying this parameter is optional when analyzing SingleCellExperiments processed using `readVisium`, `spatialPreprocess`, or `spatialCluster`, as this information is included in their metadata.

Description

Enhanced clustering of a spatial expression dataset to subspot resolution.

Usage

Enhance spot resolution
use.dimred Name of a reduced dimensionality result in reducedDims(sce). If provided, cluster on these features directly.

d Number of top principal components to use when clustering.

init Initial cluster assignments for spots.

init.method If init is not provided, cluster the top d PCs with this method to obtain initial cluster assignments.

model Error model. (’normal’ or ’t’)

nrep The number of MCMC iterations.

gamma Smoothing parameter. (Values in range of 1-3 seem to work well.)

mu0 Prior mean hyperparameter for mu. If not provided, mu0 is set to the mean of PCs over all spots.

lambda0 Prior precision hyperparam for mu. If not provided, lambda0 is set to a diagonal matrix 0.01I.

alpha Hyperparameter for Wishart distributed precision lambda.

beta Hyperparameter for Wishart distributed precision lambda.

save.chain If true, save the MCMC chain to an HDF5 file.

chain.fname File path for saved chain. Tempfile used if not provided.

burn.in Number of iterations to exclude as burn-in period. The MCMC iterations are currently thinned to every 100; accordingly burn.in is rounded down to the nearest multiple of 100.

jitter_scale Controls the amount of jittering. Small amounts of jittering are more likely to be accepted but result in exploring the space more slowly. We suggest tuning jitter_scale so that Ychange is on average around 25%-40%.

jitter_prior Scale factor for the prior variance, parameterized as the proportion (default = 0.3) of the mean variance of the PCs. We suggest making jitter_prior smaller if the jittered values are not expected to vary much from the overall mean of the spot.

verbose Log progress to stderr.

Details

The enhanced SingleCellExperiment has most of the properties of the input SCE - rowData, colData, reducedDims - but does not include expression data in counts or logcounts. To impute enhanced expression vectors, please use [enhanceFeatures()] after running spatialEnhance.

The colData of the enhanced SingleCellExperiment includes the following columns to permit referencing the subspots in spatial context and linking back to the original spots:

- **spot.idx**: Index of the spot this subspot belongs to (with respect to the input SCE).
- **subspot.idx**: Index of the subspot within its parent spot.
- **spot.row**: Array row of the subspot’s parent spot.
- **spot.col**: Array col of the subspot’s parent spot.
- **row**: Array row of the subspot. This is the parent spot’s row plus an offset based on the subspot’s position within the spot.
spatialPlot

- **color**: Array col of the subspot. This is the parent spot’s col plus an offset based on the subspot’s position within the spot.
- **imagerow**: Pixel row of the subspot. This is the parent spot’s row plus an offset based on the subspot’s position within the spot.
- **imagecol**: Pixel col of the subspot. This is the parent spot’s col plus an offset based on the subspot’s position within the spot.

**Value**

Returns a new SingleCellExperiment object. By default, the assays of this object are empty, and the enhanced resolution PCs are stored as a reduced dimensionality result accessible with reducedDim(sce, 'PCA').

**See Also**

- `spatialCluster` for clustering at the spot level before enhancing, `clusterPlot` for visualizing the cluster assignments, `enhanceFeatures` for imputing enhanced expression, and `mcmcChain` for examining the full MCMC chain associated with the enhanced clustering.

**Examples**

```r
set.seed(149)
sce <- exampleSCE()
sce <- spatialCluster(sce, 7, nrep=100, burn.in=10)
enhanced <- spatialEnhance(sce, 7, nrep=100, burn.in=10)
```

---

**spatialPlot**  
*Spatial plotting functions*

### Description

Spatial plotting functions

### Arguments

- **color**: Optional hex code to set color of borders around spots. Set to NA to remove borders.
- **...**: Additional arguments for geom_polygon(). size, to specify the linewidth of these borders, is likely the most useful.
- **platform**: Spatial sequencing platform. If "Visium", the hex spot layout will be used, otherwise square spots will be plotted.  
  NOTE: specifying this argument is only necessary if sce was not created by `spatialCluster()` or `spatialEnhance()`.
- **is.enhanced**: True if sce contains subspot-level data instead of spots. Spatial sequencing platform. If true, the respective subspot lattice for each platform will be plotted.  
  NOTE: specifying this argument is only necessary if sce was not created by `spatialCluster()` or `spatialEnhance()`.
spatialPreprocess

Preprocess a spatial dataset for BayesSpace

Description

Adds metadata required for downstream analyses, and (optionally) performs PCA on log-normalized expression of top HVGs.

Usage

```r
spatialPreprocess(
  sce,
  platform = c("Visium", "ST"),
  n.PCs = 15,
  n.HVGs = 2000,
  skip.PCA = FALSE,
  log.normalize = TRUE,
  assay.type = "logcounts",
  BSPARAM = ExactParam()
)
```

Arguments

- **sce**: SingleCellExperiment to preprocess
- **platform**: Spatial sequencing platform. Used to determine spot layout and neighborhood structure (Visium = hex, ST = square).
- **n.PCs**: Number of principal components to compute. We suggest using the top 15 PCs in most cases.
- **n.HVGs**: Number of highly variable genes to run PCA upon.
- **skip.PCA**: Skip PCA (if dimensionality reduction was previously computed.)
- **log.normalize**: Whether to log-normalize the input data with scater. May be omitted if log-normalization previously computed.
- **assay.type**: Name of assay in sce containing normalized counts. Leave as "logcounts" unless you explicitly pre-computed a different normalization and added it to sce under another assay. Note that we do not recommend running BayesSpace on PCs computed from raw counts.
- **BSPARAM**: A BiocSingularParam object specifying which algorithm should be used to perform the PCA. By default, an exact PCA is performed, as current spatial datasets are generally small (<10,000 spots). To perform a faster approximate PCA, please specify FastAutoParam() and set a random seed to ensure reproducibility.

Value

SingleCellExperiment with PCA and BayesSpace metadata
Examples

sce <- exampleSCE()
sce <- spatialPreprocess(sce)
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