Package 'DR.SC'

February 11, 2023

Type Package

Title Joint Dimension Reduction and Spatial Clustering

Version 3.1

Date 2023-02-11

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Description Joint dimension reduction and spatial clustering is conducted for Single-cell RNA sequencing and spatial transcriptomics data, and more details can be referred to Wei Liu, Xu Liao, Yi Yang, Huazhen Lin, Joe Yeong, Xiang Zhou, Xingjie Shi and Jin Liu. (2022) <doi:10.1093/nar/gkac219>. It is not only computationally efficient and scalable to the sample size increment, but also is capable of choosing the smoothness parameter and the number of clusters as well.

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Depends parallel, spatstat.geom, R (>= 4.0.0)

Imports CompQuadForm, irlba, cowplot, ggplot2, GiRaF, MASS, Matrix, mclust, methods, purrr, S4Vectors, RColorBrewer, Rcpp (>= 1.0.5), Seurat, stats

Suggests knitr, rmarkdown

LinkingTo Rcpp, RcppArmadillo

VignetteBuilder knitr

Encoding UTF-8

NeedsCompilation yes

RoxygenNote 7.1.1

URL https://github.com/feiyoung/DR.SC

BugReports https://github.com/feiyoung/DR.SC/issues

Repository CRAN

Date/Publication 2023-02-11 09:00:02 UTC

R topics documented:

`dlpfc151510` *A human dorsolateral prefrontal cortex data*

Description

A human dorsolateral prefrontal cortex dataset measured on the Visium platform, which invcludes 4634 spots and 500 genes, a subset of raw dataset at https://github.com/LieberInstitute/spatialLIBD.

Note

nothing

Author(s)

Wei Liu

References

None

Examples

```
data("dlpfc151510")
```

DR.SC *Joint dimension reduction and spatial clustering*

Description

Joint dimension reduction and spatial clustering for scRNA-seq and spatial transcriptomics data

Usage

```
## S3 method for class 'Seurat'
DR.SC(seu, K, q=15,  platform= c('Visium', "ST", "Other_SRT", "scRNAseq"),...)
```

Arguments

seu	an object of class "Seurat". The details of this object are given under 'Details'.
q	a positive integer, specify the number of latent features to be extracted, default as 15.
K	a positive integer or integer vector, specify the number of clusters. When K is a vector, it is automatically selected by MBIC criteria. Users can also use BIC and AIC to select K or refine model with MBIC by argument pen.const in the function selectModel.
platform	a string, specify the platform of the provided data, default as "Visium". There are more platforms to be chosen, including ("Visuim", "ST", "Other_SRT") and "scRNAseq", where the first group means there are spatial coordinates information in the metadata of seu, named "row" and "col" and a Hidden Markov random field is used to model the unobserved class label using spatial coordinates ("Other_SRT" represents the other SRT platforms except for 'Visium' and 'ST'), and the other group "scRNAseq" means there is no spatial information in object seu and a multinomial model is used to model the unobserved class labels. The platform helps to calculate the adjacency matrix.
...	Other arguments to pass into DR.SC_fit function.

Details

seu is an object named Seurat, thich can easily created by R package Seurat. DR-SC model can be applied to analyze both single cell RNA sequencing data and spatially resoved transcriptomics (SRT) data.

If the data are collected by the single cell RNA sequencing techonologies which means there is no spatial information in object seu then a multinomial model is used to model the unobserved class labels.

If the data is collected by the spatial transcriptomics technologies, then there are spatial coordinates information in the metadata of seu, named "row" and "col". DR-SC model uses a Hidden Markov random field to model the spatial coordinates. DR.SC supports different platforms of SRT data, such as 'Visium', 'ST' and any other platforms 'Other_SRT'.

For lattice grids in ST platform (ST), the interior spot has four neighbors (left, right, up and down),the boundary spot has three neighbors, and the spot in the corner has two neighbors. For hexagon grids, such as spatial coordinate in 10X Visium platform (Visium), the interior spot has six neighbors. For the irregular coordinates in other platforms (Other_SRT), Euclidean distance is adopted to decide whether a spot is an neighbor of another spot. For example, if the Euclidean distance between spot A and B is less than a radius, then A is taken as the neighbourhood of B. See function getAdj for more details.

Value

DR.SC returns a revised `Seurat` object. There are two revisions in the seu: 1. the metadata is added a new column named `spatial.drsc.cluster` that represents the clustering results from DR-SC model, and the `Idents(seu)` is assigned with `spatial.drsc.cluster`. 2. a DimReduc object named `dr-sc` is added in the slot `reductions`, which represents the features extracted by DR-SC model.

Note

nothing

Author(s)

Wei Liu

References

Wei Liu, Xu Liao, Yi Yang, Huazhen Lin, Joe Yeong, Xiang Zhou, Xingjie Shi & Jin Liu (2022). Joint dimension reduction and clustering analysis of single-cell RNA-seq and spatial transcriptomics data, Nucleic Acids Research, gkac219.

See Also

None

Examples

```
## we generate the spatial transcriptomics data with lattice neighborhood, i.e. ST platform.
seu <- gendata_RNAExp(height=10, width=10,p=50, K=4,platform="ST")
library(Seurat)
seu <- NormalizeData(seu, verbose=FALSE)
# choose 100 highly variable features
# seu <- FindVariableFeatures(seu, nfeatures = 100)
# maxIter = 2 is only used for illustration, and user can use default.
# seu1 <- DR.SC(seu, K=4, platform = 'ST', maxIter=2,verbose=FALSE)

# choose spatially variable features (SVGs)
seu <- FindSVGs(seu, nfeatures = 40, verbose=FALSE)
# use SVGs to fit DR.SC model
# maxIter = 2 is only used for illustration, and user can use default.
seu1 <- DR.SC(seu, K=4,platform = 'ST', maxIter=2, verbose=TRUE)
```

DR.SC_fit *Joint dimension reduction and spatial clustering*

Description

Joint dimension reduction and spatial clustering for scRNA-seq and spatial transcriptomics data

Usage

```
DR.SC_fit(X, K, Adj_sp=NULL, q=15,
          error.heter= TRUE, beta_grid=seq(0.5, 5, by=0.5),
          maxIter=25, epsLogLik=1e-5, verbose=FALSE, maxIter_ICM=6,
          wpca.int=FALSE, int.model="EEE", approxPCA=FALSE, coreNum = 5)
```

Arguments

X	a sparse matrix with class dgCMatrix or matrix, specify the log-normalization gene expression matrix used for DR-SC model.
K	a positive integer allowing scalar or vector, specify the number of clusters in model fitting.
Adj_sp	an optional sparse matrix with class dgCMatrix, specify the adjoint matrix used for DR-SC model. We provide this interface for those users who would like to define the adjacency matrix by their own.
q	a positive integer, specify the number of latent features to be extracted, default as 15. Usually, the choice of q is a trade-off between model complexity and fit to the data, and depends on the goals of the analysis and the structure of the data. A higher value will result in a more complex model with a higher number of parameters, which may lead to overfitting and poor generalization performance. On the other hand, a lower value will result in a simpler model with fewer parameters, but may also lead to underfitting and a poorer fit to the data.
error.heter	an optional logical value, whether use the heterogenous error for DR-SC model, default as TRUE. If error.heter=FALSE, then the homogenuous error is used for probabilistic PCA model in DR-SC.
beta_grid	an optional vector of positive value, the candidate set of the smoothing parameter to be searched by the grid-search optimization approach.
maxIter	an optional positive value, represents the maximum iterations of EM.
epsLogLik	an optional positive vlaue, tolerance vlaue of relative variation rate of the observed pseudo log-loglikelihood value, defualt as '1e-5'.
verbose	an optional logical value, whether output the information of the ICM-EM algorithm.
maxIter_ICM	an optional positive value, represents the maximum iterations of ICM.

wpca.int	an optional logical value, means whether use the weighted PCA to obtain the initial values of loadings and other paramters, default as FALSE which means the ordinary PCA is used.
int.model	an optional string, specify which Gaussian mixture model is used in evaluting the initial values for DR-SC, default as "EEE"; and see Mclust for more models' names.
approxPCA	an optional logical value, whether use approximated PCA to speed up the computation for initial values.
coreNum	an optional positive integer, means the number of thread used in parallel computating, default as 5. If the length of K is one, then coreNum will be set as 1 automatically.

Details

Nothing

Value

DR.SC_fit returns a list with class "drscObject" with the following three components:

Objdrsc	a list including the model fitting results, in which the number of elements is same as the length of K.
out_param	a numeric matrix used for model selection in MBIC.
K_set	a scalar or vector equal to input argument K.

In addition, each element of "Objdrsc" is a list with the following comoponents:

cluster	inferred class labels
hZ	extracted latent features.
beta	estimated smoothing parameter
Mu	mean vectors of mixtures components.
Sigma	covariance matrix of mixtures components.
W	estimated loading matrix
Lam_vec	estimated variance of errors in probabilistic PCA model
loglik	pseudo observed log-likelihood.

Note

nothing

Author(s)

Wei Liu

References

Wei Liu, Xu Liao, Yi Yang, Huazhen Lin, Joe Yeong, Xiang Zhou, Xingjie Shi & Jin Liu (2022). Joint dimension reduction and clustering analysis of single-cell RNA-seq and spatial transcriptomics data, Nucleic Acids Research, gkac219.

See Also

None

Examples

```
## we generate the spatial transcriptomics data with lattice neighborhood, i.e. ST platform.
seu <- gendata_RNAExp(height=10, width=10,p=50, K=4)
library(Seurat)
seu <- NormalizeData(seu, verbose=FALSE)
# choose 40 highly variable features using FindVariableFeatures in Seurat
# seu <- FindVariableFeatures(seu, nfeatures = 40)
# or choose 40 spatailly variable features using FindSVGs in DR.SC
seu <- FindSVGs(seu, nfeatures = 40, verbose=FALSE)
# users define the adjacency matrix
Adj_sp <- getAdj(seu, platform = 'ST')
var.features <- seu@assays$RNA@var.features
X <- Matrix::t(seu[["RNA"]]@data[var.features,])
# maxIter = 2 is only used for illustration, and user can use default.
drscList <- DR.SC_fit(X,Adj_sp=Adj_sp, K=4, maxIter=2, verbose=TRUE)
```

`drscPlot` *tNSE or UMAP plot visualization*

Description

Intuitive way of visualizing how cell types changes across the embeddings obatined by DR-SC.

Usage

```
drscPlot(seu, dims=1:5, visu.method='tSNE',...)
```

Arguments

`seu`	an object of class "Seurat" obtained by DR.SC.
`dims`	a positive integer to specify the number of latent features for visualiztion.
`visu.method`	a string including 'tSNE' or "UMAP".
`...`	Other arguments passing to DimPlot function.

Details

Nothing

Value

return a ggplot2 object.

Note

nothing

Author(s)

Wei Liu

References

None

See Also

None

Examples

```
## we generate the spatial transcriptomics data with lattice neighborhood, i.e. ST platform.
seu <- gendata_RNAExp(height=10, width=10,p=50, K=4)
library(Seurat)
seu <- NormalizeData(seu)
# choose spatially variable features
seu <- FindSVGs(seu)

# use SVGs to fit DR.SC model
# maxIter = 2 is only used for illustration, and user can use default.
seu1 <- DR.SC(seu, K=4,platform = 'ST', maxIter = 2,verbose=FALSE)
drscPlot(seu1)
```

`FindSVGs` *Find spatially variable genes*

Description

Identifies features that have spatially variation along spots using SPARK-X.

Usage

```
FindSVGs(seu, nfeatures=2000, covariates=NULL, num_core=1, verbose=TRUE)
```

Arguments

seu	an object of class "Seurat".
nfeatures	a positive integer, means how many spatially variable genes to be chosen. If there are less than 2000 features in seu, then all features are identified.
covariates	a covariate matrix named control variable matrix whose number of rows is equal to the number of columns of seu.
num_core	an optional positive integer, specify the cores used for identifying the SVGs in parallel.
verbose	an optional logical value, whether output the related information.

Details

Nothing

Value

return a revised Seurat object by adding three columns named "is.SVGs", "order.SVGs" and "adjusted.pval.SVGs" in the meta.features of default Assay.

Note

nothing

References

Zhu, J., Sun, S., Zhou, X.: Spark-x: non-parametric modeling enables scalable and robust detection of spatialexpression patterns for large spatial transcriptomic studies. Genome Biology 22(1), 1-25 (2021)

See Also

topSVGs

Examples

```
seu<-gendata_RNAExp(height=20, width=20,p=200, K=4)
seu<-FindSVGs(seu, nfeatures=100)
topSVGs(seu)
```

gendata_RNAExp *Generate simulated data*

Description

Generate simulated spatial transcriptomics data or scRNAseq data.

Usage

```
gendata_RNAExp(height=30, width=30, platform="ST", p =100, q=10, K=7,
                           G=4,sigma2=1, tau=8, seed=1, view=FALSE)
```

Arguments

height, width	Height and width of lattice grids for generating spatial coordinates. n=height * width cells for scRNAseq data
platform	set the platform for the simulated data, only support 'ST' and 'scRNAseq'.
p	number of genes to generate.
q	number of true latent features to generate gene expression
K	number of clusters (cell types).
seed	random seed for generate data
G	the number of neighbors. The latter must be one of G = 4 or G = 8, which respectively correspond to a first order and a second order dependency structure. By default, G = 4.
sigma2	Variance of error term in probabilitic PCA model.
tau	a positive factor of mixture mean values.
view	Logical value indicating whether the draw should be printed. Do not display the optional borders.

Details

Nothing

Value

return a "Seurat" object. If `platform="ST"`, then the metadata of this Seurat object will include two columns with names "row" and "col" which are the spatial coordinates; If `platform="scRNAseq"`, then the metadata of this Seurat object will not have them.

Note

nothing

Author(s)

Wei Liu

References

None

See Also

None

Examples

```
## we generate the spatial transcriptomics data with lattice neighborhood, i.e. ST platform.
seu <- gendata_RNAExp(height=20, width=20,p=200, K=4)
seu

## generate scRNAseq data
seu <- gendata_RNAExp(height=20, width=20, platform="scRNAseq", p=100, K=4)
seu
```

---

getAdj *Calculate the adjacency matrix given the spatial coordinates*

Description

Calculate the adjacency matrix for the spatial transcriptomics data measured on 10X Visium, ST or other platforms as a Seurat object.

Usage

```
  ## S3 method for class 'Seurat'
getAdj(obj, platform = c('Visium', "ST", "Other_SRT"), ...)
```

Arguments

obj	an object with class "Seurat", there are spatial coordinates information in the metadata of obj, named "row" and "col", where first column is x-axis coordinate, the second column is y-axis coordinate. getAdj_manual and getAdj_auto supports multi-dimensional spatial coordinates with a matrix as input.
platform	a string, specify the platform of the provided data, default as "Visium". There are more platforms to be chosen, including ("Visuim", "ST", "Other_SRT"), which means there are spatial coordinates information in the metadata of obj, named "row" and "col". The platform helps to calculate the adjacency matrix by defining the neighborhoods.
...	Other arguments to pass into getAdj_auto function.

Details

For lattice grids in ST platform (ST), the interior spot has four neighbors (left, right, up and down),the boundary spot has three neighbors, and the spot in the corner has two neighbors. For hexagon grids, such as spatial coordinate in 10X Visium platform (Visium), the interior spot has six neighbors. For the irregular coordinates in other platforms (Other_SRT), Euclidean distance is adopted to decide whether a spot is an neighbor of another spot. For example, if the Euclidean distance between spot A and B is less than a radius, then A is taken as the neighbourhood of B. See functions getAdj_auto and getAdj_manual for more details.

Value

Return a `dgCMatrix` object recording the information of neighborhoods about each spot.

Note

nothing

Author(s)

Wei Liu

References

Wei Liu, Xu Liao, Yi Yang, Huazhen Lin, Joe Yeong, Xiang Zhou, Xingjie Shi & Jin Liu (2022). Joint dimension reduction and clustering analysis of single-cell RNA-seq and spatial transcriptomics data, Nucleic Acids Research, gkac219.

See Also

getAdj_auto, getAdj_manual.

Examples

```
## S3 method for class "Seurat"
seu <- gendata_RNAExp(height=20, width=20,p=200, K=4)
Adj_sp <- getAdj(seu, platform = 'ST')
```

`getAdj_auto` *Calculate adjacency matrix by automatically choosing radius*

Description

an efficient function to find the radius by bi-section method , then find neighbors based on the matrix of position, which ensures that each spot has approximately lower.med~upper.med neighbors in the sense of median.

Usage

```
getAdj_auto(pos, lower.med=4, upper.med=6, radius.upper= NULL)
```

Arguments

pos	a n-by-2 matrix of position.
lower.med	an integer, the lower bound of median number of neighbors among all spots.
upper.med	an integer, the upper bound of median number of neighbors among all spots.
radius.upper	a real, the upper bound of radius, default as NULL. If radius.upper= NULL, the upper bound is automatically determined by algorithm.

Value

A sparse adjacency matrix containing the neighbourhood.

See Also

getAdj, getAdj_manual.

---

getAdj_manual *Calculate adjacency matrix by user-specified radius*

Description

an efficient function to find the neighbors based on the matrix of position and a pre-defined radius.

Usage

```
getAdj_manual(pos, radius)
```

Arguments

pos	is a n-by-d matrix of position, where n is the number of spots, and d is the dimension of coordinates.
radius	is a threashold of Euclidean distance to decide whether a spot is an neighborhood of another spot. For example, if the Euclidean distance between spot A and B is less than radius, then A is taken as the neighbourhood of B.

Value

A sparse matrix containing the neighbourhood

See Also

getAdj_auto, getAdj.

getneighborhood_fast *getneighborhood_fast*

Description

an efficient function to find the neighborhood based on the matrix of position and a pre-defined cutoff

Usage

```
getneighborhood_fast(x, radius)
```

Arguments

x	is a n-by-2 matrix of position.
radius	is a threashold of Euclidean distance to decide whether a spot is an neighborhood of another spot. For example, if the Euclidean distance between spot A and B is less than cutoff, then A is taken as the neighbourhood of B.

Value

A sparse matrix containing the neighbourhood

mbicPlot *MBIC plot visualization*

Description

Intuitive way of visualizing how modified BIC values changes across different number of clusters

Usage

```
mbicPlot(seu, criteria="MBIC")
```

Arguments

seu	an object of class Seurat revised by DR.SC with argument K=NULL.
criteria	a string specifying the information criteria such as AIC, BIC and MBIC to be plotted, default as MBIC.

Details

Nothing

Value

return a ggplot2 object.

Note

nothing

Author(s)

Wei Liu

References

None

See Also

None

Examples

```
## we generate the spatial transcriptomics data with lattice neighborhood, i.e. ST platform.
seu <- gendata_RNAExp(height=20, width=20,p=100, K=4)
library(Seurat)
seu <- NormalizeData(seu)
# choose spatially variable features
seu <- FindSVGs(seu)
## Just for illustrating the usage of mbicPlot
seu[["RNA"]]@misc[['icMat']] <- data.frame(K=2:5, MBIC=c(105, 101, 99, 108))
mbicPlot(seu)
```

---

read10XVisium *Read the spatial transcriptomics data measured on 10X Visium platform*

Description

Read the spatial transcriptomics data measured on 10X Visium platform as a Seurat object, where the spatial coordinates are saved in the metadata, named "row" and "col".

Usage

```
read10XVisium(dirname)
```

Arguments

dirname	A string, the dictory of Visium datasets

Details

Nothing

Value

return a Seurat object.

Note

nothing

Author(s)

Wei Liu

References

None

See Also

None

Examples

```
## Not run:
  ## set your file directory, then read it.
  data_name <- "D/HCC"
  HCC1 <- read10XVisium(data_name)

## End(Not run)
```

---

readscRNAseq *Read the scRNAseq data measured on scRNA sequencing platform*

Description

Read the single cell RNA sequencing data measured on scRNA sequencing platform as a Seurat object.

Usage

```
readscRNAseq(mtx, cells, features, ...)
```

Arguments

mtx	a string, ame or remote URL of the mtx file
cells	a string, Name or remote URL of the cells/barcodes file
features	a string, Name or remote URL of the features/genes file
...	the arguments passing to ReadMtx

Details

Nothing

Value

return a Seurat object including expression matrix.

Note

nothing

Author(s)

Wei Liu

References

None

See Also

None

Examples

```
## Not run:
  ### set the file directory, then read it.
  seu <- readscRNAseq(mtx="GSM3755564_16_Liver_Treg_matrix.mtx.gz",
                      features='GSM3755564_16_Liver_Treg_genes.tsv.gz',
                      cells='GSM3755564_16_Liver_Treg_barcodes.tsv.gz' )
  seu

## End(Not run)
```

RunWPCA *Run Weighted Principal Component Analysis*

Description

Run a weighted PCA dimensionality reduction

Usage

```
RunWPCA(object, q=15)
### S3 method for class "Seurat"
## RunWPCA(object, q=15)

### S3 method for class "matrix"
## RunWPCA(object, q=15)

### S3 method for class "dgCMatrix"
## RunWPCA(object, q=15)
```

Arguments

object	an object named "Seurat", "maxtrix" or "dgCMatrix". The object of class "Seurat" must include slot "scale.data".
q	an optional positive integer, specify the number of features to be extracted.

Details

Nothing

Value

For Seurat object, return a Seurat object. For objcet "matrix" and "dgCMatrix", return a object "matrix" with rownames same as the colnames of X, and colnames "WPCA1" to "WPCAq".

Note

nothing

Author(s)

Wei Liu

References

Bai, J. and Liao, Y. (2017). Inferences in panel data with interactive effects using large covariance matrices. Journal of Econometrics, 200(1):59–78.

See Also

None

Examples

```
## Not run:
  library(Seurat)
  seu <- gendata_RNAExp(height=20, width=20,p=100, K=4)
  ## log-normalization
  seu <- NormalizeData(seu)
  ##
  seu <- FindVariableFeatures(seu, nfeatures=80)
  ## Scale
  seu <- ScaleData(seu)
  ## Run WPCA
  seu <- RunWPCA(seu)
  seu
  ## Run tSNE based on wpca
  seu <- RunTSNE(seu, reduction='wpca')
  seu
  ## Find SVGs
  seu <- FindSVGs(seu, nfeatures=80)
  (genes <- topSVGs(seu, ntop=10))
 Idents(seu) <- factor(paste0("cluster", seu$true_clusters), levels=paste0("cluster",1:4))
  RidgePlot(seu, features = genes[1:2], ncol = 2)
  FeaturePlot(seu, features = genes[1:2], reduction = 'tsne' ,ncol=2)

## End(Not run)
```

`selectModel` *Select the number of clusters*

Description

Select the number of clusters by specified criteria.

Usage

```
  selectModel(obj, criteria = 'MBIC', pen.const=1)
  ## S3 method for class 'drscObject'
selectModel(obj, criteria = 'MBIC', pen.const=1)
  ## S3 method for class 'Seurat'
selectModel(obj, criteria = 'MBIC', pen.const=1)
```

Arguments

	S
	an object with class `Seurat` by DR.SC or class `drscObject` by DR.SC_fit.
`objteria`	a string, specify the criteria used for selecting the number of clusters, supporting "MBIC", "BIC" and "AIC".
`pen.const`	an optional positive value, the adjusted constant used in the MBIC criteria. It usually takes value between 0.1 to 1.

Value

For S3 method of `Seurat`, it return a revised "Seurat" object with updated `Idents(seu)`, `spatial.drsc.cluster` in the metadata and DimReduc object named `dr-sc` in the slot `reductions`. For S3 method of `drscObject`, it returns a list with the following components:

`bestK`	the selected number of clusters.
`cluster`	inferred class labels
`hZ`	extracted latent features.
`icMat`	a numeric matrix including the criteria value for each number of clusters K.

Note

nothing

Author(s)

Wei Liu

References

Wei Liu, Xu Liao, Yi Yang, Huazhen Lin, Joe Yeong, Xiang Zhou, Xingjie Shi & Jin Liu (2022). Joint dimension reduction and clustering analysis of single-cell RNA-seq and spatial transcriptomics data, Nucleic Acids Research, gkac219.

See Also

DR.SC, DR.SC_fit.

Examples

```
seu <- gendata_RNAExp(height=10, width=10,p=50, K=4)
library(Seurat)
seu <- NormalizeData(seu, verbose=FALSE)
# or choose 40 spatailly variable features using FindSVGs in DR.SC
seu <- FindSVGs(seu, nfeatures = 40, verbose=FALSE)
# users define the adjacency matrix
Adj_sp <- getAdj(seu, platform = 'ST')
var.features <- seu@assays$RNA@var.features
X <- Matrix::t(seu[["RNA"]]@data[var.features,])
```

```
# maxIter = 2 is only used for illustration, and user can use default.
drscList <- DR.SC_fit(X,Adj_sp=Adj_sp ,K=4, maxIter=2, verbose=TRUE)
drsc1 <- selectModel(drscList)
str(drsc1)
```

`spatialPlotClusters` *Spatial coordinates plot visualization*

Description

Intuitive way of visualizing how cell types changes across the spatial locations.

Usage

```
spatialPlotClusters(seu)
```

Arguments

`seu`	an object of class "Seurat" obtained by DR.SC.

Details

Nothing

Value

return a ggplot2 object.

Note

nothing

Author(s)

Wei Liu

References

None

See Also

None

Examples

```
## we generate the spatial transcriptomics data with lattice neighborhood, i.e. ST platform.
    seu <- gendata_RNAExp(height=10, width=10,p=50, K=4)
    library(Seurat)
    seu <- NormalizeData(seu)
    # choose spatially variable features using Seurat
    seu <- FindSVGs(seu)
    # use SVGs to fit DR.SC model
    # maxIter = 2 is only used for illustration, and user can use default.
    seu1 <- DR.SC(seu, K=4,platform = 'ST', maxIter=2,verbose=FALSE)
    spatialPlotClusters(seu1)
```

---

sp_means_Rcpp *Calculate column-wise or row-wise mean*

Description

Calculate column-wise or row-wise mean

Usage

```
sp_means_Rcpp(sp_data, rowMeans = FALSE)
```

Arguments

sp_data	A sparse matrix
rowMeans	A boolean value, whether to calculate row-wise mean

Value

A n x 1 or p x 1 matrix

---

sp_sums_Rcpp *Calculate column-wise or row-wise sum*

Description

Calculate column-wise or row-wise sum

Usage

```
sp_sums_Rcpp(sp_data, rowSums = FALSE)
```

Arguments

sp_data	A sparse matrix
rowSums	A boolean value, whether to calculate row-wise sum

Value

A n x 1 or p x 1 matrix

`topSVGs` *Return the top n SVGs*

Description

Return top n spatially variable genes given a Seurat object performed by FindSVGs.

Usage

```
topSVGs(seu, ntop=5)
```

Arguments

`seu`	an object of class "Seurat".
`ntop`	an optional positive integer, means how many spatially variable genes to access.

Details

Nothing

Value

return a character vector including the names of SVGs.

Note

nothing

Author(s)

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References

None

See Also

topSVGs

Examples

```
seu <- gendata_RNAExp(height=20, width=20,p=200, K=4)
seu <- FindSVGs(seu, nfeatures=100, verbose=FALSE)
(genes <- topSVGs(seu, ntop=10))
```

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