Package 'dandelionR'

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Title Single-cell Immune Repertoire Trajectory Analysis in R

Version 1.0.0

Description dandelionR is an R package for performing single-cell immune repertoire trajectory analysis, based on the original python implementation. It provides the necessary functions to interface with scRepertoire and a custom implementation of an absorbing Markov chain for pseudotime inference, inspired by the Palantir Python package.

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Author Jiawei Yu [aut] (ORCID: <https://orcid.org/0009-0005-9170-7881>),
Nicholas Borcherding [aut] (ORCID:
<https://orcid.org/0000-0003-1427-6342>),
Kelvin Tuong [aut, cre] (ORCID:
<https://orcid.org/0000-0002-6735-6808>)

Maintainer Kelvin Tuong <z.tuong@uq.edu.au>

Contents

`.addColData` *add the calculated probability to the colData*

Description

add the calculated probability to the colData

Usage

```
.addColData(probabilities_proj, terminal_state, milo, verbose)
```

Arguments

`probabilities_proj`	the probabilities need to be stored
`terminal_state`	Integer. The index of the terminal state in the Markov chain, passed from markovProbability
`milo`	the milo object provided by user
`verbose`	logical, print warnings.

Value

a Milo object with probabilties and pseudotime in its colData slot

.allowedChain *filtering cell without allowed chain status*

Description

filtering cell without allowed chain status

Usage

```
.allowedChain(sce, allowed_chain_status, verbose)
```

Arguments

sce	SingleCellExperiment object input
allowed_chain_status	the chain needs to be retain, passed from setupVdjPseudobulk
verbose	logical, print messages. Default is TRUE.

Value

SingleCellExperiment object with allowed chain status

.calDif *function help to reconstruct diffusion distance using Reduce*

Description

function help to reconstruct diffusion distance using Reduce

Usage

```
.calDif(dfm, i, j, eigenvector, lambda_t, K)
```

Arguments

dfm	an nrow(eigenvectors) x nrow(eigenvectors) matrix need to be filled with diffusion distance with iteration
i	integer the row selected in this iteration
j	integer the col selected in this iteration
eigenvector	numeric vector, the eigenvector from diffusion map
lambda_t	eigenvalues to the power of t(diffusion time)
K	The number of the eigenvectors to be used in calculation

Value

updated diffusion distance matrix after one iteration

.classCheck *.classCheck*

Description

check whether the input is with the correct class

Usage

```
.classCheck(input, must)
```

Arguments

input	the input need to be check
must	the type we need

Value

whether or not the input is the correct class

.collapse_nested_list *Collapse a nested list*

Description

Collapse a nested list

Usage

```
.collapse_nested_list(input_list)
```

Arguments

input_list	input nested list.

Value

collapsed list

.constructMarkovChain *.constructMarkovChain*

Description

Markov chain construction

Usage

```
.constructMarkovChain(wp_data, knn., pseudotime, waypoints, vb)
```

Arguments

wp_data	Multi scale data of the waypoints
knn.	Number of nearest neighbors for graph construction
pseudotime	pseudotime ordering of cells
waypoints	integer vector, index of selected waypoint used to
vb	whether to print messages

Value

transition matrix of the markov chain

.determExtractColN *determine the columns in the colData where the main VDJ information is stored*

Description

determine the columns in the colData where the main VDJ information is stored

Usage

```
.determExtractColN(extract_cols, mode_option, milo)
```

Arguments

extract_cols	names of columns in the colData where the main VDJ information stores, passed from vdjPseudobulk
mode_option	Specifies the mode for extracting V(D)J genes
milo	Milo or SingleCellExperiment object provided by user

Value

a character vector stores the names of columns in the colData where the main VDJ information stores

.determineMultiscaleSpace *.determineMultiscaleSpace*

Description

.determineMultiscaleSpace

Usage

```
.determineMultiscaleSpace(diffusionmap, n_eigs = NULL)
```

Arguments

diffusionmap	DiffusionMap object
n_eigs	integer, default is NULL. Number of eigen vectors to use. • If is not specified, the number of eigen vectors will be determined using the eigen gap.

Value

dataframe

.determTerminal *.determTerminal*

Description

function in Reduce to provide waypoints

Usage

```
.determTerminal(terminal_states, i, dm_boudaries, wp_data)
```

Arguments

terminal_states	integer vector to store the generated waypoint index
i	iteration index
dm_boudaries	index of the maxium or minium value of transition matrix per row
wp_data	Multi scale data of the waypoints

Value

integer vector store the index of waypoints serve as terminal state

.extractVdj *Specify the columns which store VDJ information, and extract the main chain from it*

Description

Specify the columns which store VDJ information, and extract the main chain from it

Usage

```
.extractVdj(sce, extract_cols, mode_option, verbose)
```

Arguments

sce	SingleCellExperiment object input
extract_cols	The setupVdjPseutobulk transfered parameter given by user to specify the VDJ information columns
mode_option	see document of setupVdjPseudobulk for detailed explanation
verbose	logical, print messages. Default is TRUE.

Value

SingleCellExperiment objects with column stores the information of the main VDJ information in colData slot

.featureSpaceConstruct *Construct VDJ feature space*

Description

Construct VDJ feature space

Usage

```
.featureSpaceConstruct(milo, extract_cols, pbs)
```

Arguments

milo	Milo or SingleCellExperiment object provided by user
extract_cols	columns of names where to extract the VDJ information
pbs	cell x pseudobulk adjacent matrix

Value

constructed feature space

`.filterCells` *.filterCells*

Description

Helper function that identifies filter_pattern hits in determined column of sce, and then either removes the offeending cells or masks the matched values with a uniform value of '(column's name)_missing'

Usage

```
.filterCells(
  sce,
  col_n,
  filter_pattern = ",|None|No_contig",
  remove_missing = TRUE
)
```

Arguments

`sce`	SingleCellExperiment object, adata in python data after combineTCR, contain both vdj and seq
`col_n`	mode for extraction the V(D)J genes.
`filter_pattern`	character string, optional ',|None|No_contig' by default
`remove_missing`	bool, True by default • If `TRUE`, will remove cells with contigs matching the filter from the object. • If `FALSE`, will mask them with a uniform value dependent on the column name.

Value

filtered SingleCellExperiment object according to the parameter.

`.filterProductivity` *filer out cell with unproductive chain*

Description

filer out cell with unproductive chain

Usage

```
.filterProductivity(
  sce,
  mode_option,
  productive_cols,
  productive_vj,
  productive_vdj,
  verbose
)
```

Arguments

sce	SingleCellExperiment input
mode_option	check setupVdjPseudobulk for detailed explanation
productive_vj	If TRUE, retains cells where the main VJ chain is productive.
productive_vdj	If TRUE, retains cells where the main VDJ chain is productive.
verbose	logical, print messages. Default is TRUE.

Value

SingleCellExperiment object after filtering on producive chain

---

.filterUnmapped *Filter out cell with unclear mapping in VDJ information*

Description

Filter out cell with unclear mapping in VDJ information

Usage

```
.filterUnmapped(
  sce,
  mode_option,
  check_vj_mapping,
  check_vdj_mapping,
  main_cols,
  check_extract_cols_mapping,
  remove_missing,
  verbose
)
```

Arguments

sce	SingleCellExperiment object input
mode_option	see document of setupVdjPseudobulk for explanation
check_vj_mapping	logical vector to set whether to check V and J gene in VJ chain, passed from setupVdjPseudobulk
check_vdj_mapping	logical vector to set whether to check V, D and J gene in VDJ chain, passed from setupVdjPseudobulk
main_cols	column names in colData in which The information of main chain stores
check_extract_cols_mapping	character vector,the names of columns that needs to be checked, passed from setupVdjPseudobulk
remove_missing	option for removing the unclear mappin or just mask it, passed from setupVdjPseudobulk
verbose	logical, print messages.

Value

filtered SingleCellExperiment object

.findNewWaypoints *function used in Reduce to find new waypoint in an iteration*

Description

function used in Reduce to find new waypoint in an iteration

Usage

```
.findNewWaypoints(iterdists, k, vecs, ind, datas)
```

Arguments

iterdists	a list containing both waypoints deteted in the former iterations and the distance matrix used to find waypoints
k	the iteration number
vecs	a numeric vector used to calculate distance of waypoints to each points
ind	colnames

Value

a list containing updated distance matrix and new waypoints

.generateExtractColumn *Check whether the columns with specified names exist, if not, create them with CTgene columns*

Description

Check whether the columns with specified names exist, if not, create them with CTgene columns

Usage

```
.generateExtractColumn(sce, extract_cols, verbose)
```

Arguments

sce	SingleCellExperiment object input
extract_cols	column names we aim to extract information from
verbose	logical, print messages. Default is TRUE.

Value

SingleCellExperiment with columns containing VDJ information in the names we've specified.

.generateExtractName *Generate the name of columns with given parameter*

Description

Generate the name of columns with given parameter

Usage

```
.generateExtractName(sce, mode_option, verbose)
```

Arguments

sce	SingleCellExperiment object input
mode_option	see document of setupVdjPseudobulk for explanation
verbose	logical, print messages. Default is TRUE.

Value

a vecotor of colnames we need to perform main chain extraction

`.getPbs` *.getPbs*

Description

Helper function to ensure we have cells by pseudobulks matrix which we can use for pseudobulking.

Usage

```
.getPbs(pbs, col_to_bulk, milo, verbose = TRUE)
```

Arguments

`pbs`	pbs parameter provided by vdjPseudobulk(), cells by pseudobulks matrix or NULL
`col_to_bulk`	col_to_bulk parameter provided by vdjPseudobulk(), column's name of colData from milo
`milo`	SingleCellExperiment object
`verbose`	logical, whether to print messages

Value

a cell x pseudobulk matrix

`.getPbsCol` *.getPbsCol*

Description

Helper function to create the new pseudobulk object's coldata.

Usage

```
.getPbsCol(pbs, col_to_take, milo)
```

Arguments

`pbs`	dgeMatrix, cell x pseudobulk binary matrix
`col_to_take`	character vector, names of colData of milo that need to be processed
`milo`	Milo or SingleCellExperiment object

Value

pbs_col, a DataFrame which will be passed to the new SingleCellExperiment object as colData of vdj x pseudobulk assays

.getPbsPerCol *.getPbsPerCol*

Description

function used in Reduce to get the PbsCol

Usage

```
.getPbsPerCol(pbs.col, anno_col, milo, pbs)
```

Arguments

pbs.col	DataFrame object used to store the result of each iteration
anno_col	colname where to generate the metadata from
milo	milo or SingleCellExperiment objects provided by user
pbs	dgeMatrix, cell x pseudobulk binary matrix

Value

DataFrame object, serve as part of metadata of the new milo object

.KNNind *Calculate the weight adjacent matricks of knn graph and its index*

Description

Calculate the weight adjacent matricks of knn graph and its index

Usage

```
.KNNind(wp_data, knn.)
```

Arguments

wp_data	Multi scale data of the waypoints
knn.	Number of nearest neighbors for graph construction

Value

a list containing the weight adjacent matrix and index

.maxMinSampling *.maxMinSampling*

Description

function for max min sampling of waypoints

Usage

```
.maxMinSampling(datas, num_waypoints, verbose = TRUE)
```

Arguments

datas	data matrix along which to sample the waypoints, usually diffusion components
num_waypoints	number of waypoints to sample
verbose	logical, print progress

Value

Series reprenting the sampled waypoints

.minMaxScale *minMaxScale*

Description

scale the value to range 0 to 1

Usage

```
.minMaxScale(data)
```

Arguments

data	dataframe need to be scale

Value

scaled value

`.normalizeFeatureSpace` *Normalize Feature Space*

Description

Make sure the sum of each V, D, and J gene within a pseudobulk equals to 1

Usage

```
.normalizeFeatureSpace(
  pseudo_vdj_feature,
  extract_cols,
  min_count,
  renormalize,
  milo
)
```

Arguments

`pseudo_vdj_feature`	constructed feature space
`extract_cols`	names of columns to extract the VDJ information
`min_count`	the minim count of a V/D/J gene
`renormalize`	Whether to renormalize the matrix
`milo`	Milo or SingleCellExperiment object provided by user

Value

normalized VDJ feature space

`.normalizePerVDJ` *function to normalize a specific kind of VDJ gene in feature space*

Description

function to normalize a specific kind of VDJ gene in feature space

Usage

```
.normalizePerVDJ(
  pseudo_vdj_feature,
  col_n,
  renormalize,
  define.mask,
  milo,
  min_count
)
```

Arguments

pseudo_vdj_feature	constructed feature space
col_n	name of column to extract the VDJ information
renormalize	Whether to renormalize the matrix
define.mask	logical vector determine whether the V/D/J gene should be masked when normalizing
milo	Milo or SingleCellExperiment object provided by user
min_count	the minim count of a V/D/J gene

Value

feature space normalized on specifed V/D/J gene

.packFeatureSpace *Pack the normalized feature space into new Milo object*

Description

The metadata will derived from the original milo

Usage

```
.packFeatureSpace(pbs, col_to_take, milo, pseudo_vdj_feature)
```

Arguments

pbs	cell x pseudobulk adjacent matrix
col_to_take	Optional character or vector of characters. Specifies names of colData of milo that need to identify the most common value for each pseudobulk
milo	Milo or SingleCellExperiment object provided by user
pseudo_vdj_feature	VDJ feature space

Value

Milo object with VDJ feature space stored in its assay

.removeEdge *function used in Reduce to remove KNN's backward edges except for edges that are within the computed standard deviation*

Description

function used in Reduce to remove KNN's backward edges except for edges that are within the computed standard deviation

Usage

```
.removeEdge(Knn, i, rem_edges)
```

Arguments

Knn	weight KNN adjacent matrix
i	the iteration number
rem_edges	the edges that need to be removes

Value

an updated matrix after one round of iteration

.subsetSce *Subset sce with given parameter*

Description

Subset sce with given parameter

Usage

```
.subsetSce(sce, subsetby, groups, verbose)
```

Arguments

sce	SingleCellExperiment object input
subsetby	subsetby Character. Name of a colData column for subsetting. given by setupVdjPsudobulk.
groups	Character vector. Specifies the subset condition for filtering. given by setupVdjPsudobulk.
verbose	logical, print messages. Default is TRUE.

Value

subsetted SingleCellExperiment object

`.terminalStateFromMarkovChain` *Determine terminal states using Markov chain if end states are not provided.*

Description

Determine terminal states using Markov chain if end states are not provided.

Usage

```
.terminalStateFromMarkovChain(
  Transmat,
  wp_data,
  pseudotime,
  waypoints,
  verbose
)
```

Arguments

`Transmat`	Transition matrix
`wp_data`	Multi scale data of the waypoints
`pseudotime`	numeric vector, pseudotime of each pseudobulk
`waypoints`	integer vector, waypoint selected to construct markov chain.
`verbose`	Boolean, whether to print messages/warnings.

Value

terminal_state

.typeCheck *.typeCheck*

Description

check whether the input has the correct type

Usage

```
.typeCheck(input, must)
```

Arguments

input	the input need to be check
must	the type we need

Value

whether or not the input is the correct type

.waypiontsPerCol *find the waypoints according to certain columns of data*

Description

find the waypoints according to certain columns of data

Usage

```
.waypiontsPerCol(waypoints, ind, datas, no.iterations)
```

Arguments

waypoints	integer vector used to store waypoints
ind	columns' colnames
datas	scaled diffusionmap

Value

a numeric vector containing waypoints' index

`chainAssign` *Assign the V(D)J gene to the right chain.*

Description

Assign the V(D)J gene to the right chain.

Usage

```
chainAssign(vec, num)
```

Arguments

`vec`	vector of V(D)J genes to assign to the right chain.
`num`	number of genes to return. should be 2(vj) or 3(vdj)

Value

list contain vector of VJ + VDJ of the cell input

`dandelionR` *dandelionR: Single-cell immune repertoire trajectory analysis*

Description

dandelionR is an R package for performing single-cell immune repertoire trajectory analysis, based on the original python implementation. It provides the necessary functions to interface with scRepertoire and a custom implementation of an absorbing Markov chain for pseudotime inference, inspired by the Palantir Python package.

Main functions

- `setupVdjPseudobulk`: Preprocess V(D)J Data for Pseudobulk Analysis.
- `vdjPseudobulk`: Generate Pseudobulk V(D)J Feature Space.
- `markovProbability`: Markov Chain Construction and Probability Calculation.
- `projectPseudotimeToCell`: Project Pseudotime and Branch Probabilities to Single Cells.

Vignettes

See the package vignettes for detailed workflows: `vignette('dandelionR')`

Installation

To install from Bioconductor, use:

```
if (!requireNamespace('BiocManager', quietly = TRUE))
    install.packages('BiocManager')
BiocManager::install('dandelionR')
```

Author(s)

Maintainer: Kelvin Tuong <z.tuong@uq.edu.au> (ORCID)

Authors:

- Jiawei Yu <jiawei.yu@uq.edu.au> (ORCID)
- Nicholas Borcherding <borcherding@wustl.edu> (ORCID)

See Also

Useful links:

- https://www.github.com/tuonglab/dandelionR/
- Report bugs at https://www.github.com/tuonglab/dandelionR/issues

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demo_airr *Example AIRR Dataset for V(D)J Analysis*

Description

The demo_airr object is a list of AIRR data frames from a down-sampled demo dataset derived from Suo et al., 2024, *Nature Biotechnology*.
This dataset is used in vignettes to demonstrate workflows for V(D)J analysis.
For details, see the original publication at https://www.nature.com/articles/s41587-023-01734-7.
The original files are available at https://github.com/zktuong/dandelion-demo-files.

Usage

```
data(demo_airr)
```

Format

A SingleCellExperiment object with the following slots:

`list` List of DataFrames containing the standardised AIRR data for each sample.
For information of AIRR rearrangements, see the AIRR Community standards at https://docs.airr-community.org/.

Source

Suo et al., 2024, *Nature Biotechnology*.
https://www.nature.com/articles/s41587-023-01734-7.

Examples

```
data(demo_airr)
```

---

demo_sce *Example SCE Dataset that does not contain V(D)J information*

Description

The demo_sce object is a down-sampled demo dataset derived from Suo et al., 2024, *Nature Biotechnology*.
This dataset is used in vignettes to demonstrate workflows for V(D)J analysis.
For details, see the original publication at https://www.nature.com/articles/s41587-023-01734-7.
The original Lymphoid cells data in h5ad format is available at https://developmental.cellatlas.io/fetal-immune.

Usage

```
data(demo_sce)
```

Format

A SingleCellExperiment object with the following slots:

colData A minimall DataFrame containing metadata about each sample, corresponding to obs in AnnData (Python). The following columns are relevant for vignette usage:

anno_lvl_2_final_clean Cell type annotations.

int_colData A DataFrame containing additional assay metadata important for further analysis. Includes:

- X_scvi: A dimensionality reduction matrix from the scVI model.
- UMAP: A UMAP reduction matrix.

Source

Suo et al., 2024, *Nature Biotechnology*.
https://www.nature.com/articles/s41587-023-01734-7.

Examples

```
data(demo_sce)
```

`differentiationProbabilities` *Compute Branch Probabilities Using Markov Chain*

Description

This function calculates branch probabilities for differentiation trajectories based on a Markov chain constructed from waypoint data and pseudotime ordering.

Usage

```
differentiationProbabilities(
  wp_data,
  terminal_states = NULL,
  knn = 30L,
  pseudotime,
  waypoints,
  verbose = TRUE
)
```

Arguments

`wp_data`	A multi-scale data matrix or data frame representing the waypoints.
`terminal_states`	Integer vector. Indices of the terminal states. Default is `NULL`.
`knn`	Integer. Number of nearest neighbors for graph construction. Default is `30L`.
`pseudotime`	Numeric vector. Pseudotime ordering of cells.
`waypoints`	Integer vector. Indices of selected waypoints used to construct the Markov chain.
`verbose`	Boolean, whether to print messages/warnings.

Value

A numeric matrix or data frame containing branch probabilities for each waypoint.

`formatVdj` *Change the format of splitCTgene output.*

Description

Change the format of splitCTgene output.

Usage

```
formatVdj(gene_list)
```

Arguments

gene_list	list containing the output from splitCTgene.

Value

list contain vector of VJ + VDJ information of the cell input

---

markovProbability *Markov Chain Construction and Probability Calculation*

Description

This function preprocesses data, constructs a Markov chain, and calculates transition probabilities based on pseudotime information.

Usage

```
markovProbability(
  milo,
  diffusionmap,
  terminal_state = NULL,
  root_cell,
  knn = 30L,
  diffusiontime = NULL,
  pseudotime_key = "pseudotime",
  scale_components = TRUE,
  num_waypoints = 500,
  n_eigs = NULL,
  verbose = TRUE
)
```

Arguments

milo	A Milo or SingleCellExperiment object. This object should have pseudotime stored in colData, which will be used to calculate probabilities. If pseudotime is available in milo, it takes precedence over the value provided through the diffusiontime parameter.
diffusionmap	A DiffusionMap object corresponding to the milo object. Used for Markov chain construction.
terminal_state	Integer. The index of the terminal state in the Markov chain.
root_cell	Integer. The index of the root state in the Markov chain.
knn	Integer. The number of nearest neighbors for graph construction. Default is 30L.
diffusiontime	Numeric vector. If pseudotime is not stored in milo, this parameter can be used to provide pseudotime values to the function.

pseudotime_key Character. The name of the column in colData that contains the inferred pseudotime.

scale_components
Logical. If TRUE, the components will be scaled before constructing the Markov chain. Default is FALSE.

num_waypoints Integer. The number of waypoints to sample when constructing the Markov chain. Default is 500L.

n_eigs integer, default is NULL. Number of eigen vectors to use.

- If is not specified, the number of eigen vectors will be determined using the eigen gap.

verbose Logical. If TRUE, print progress. Default is TRUE.

Value

milo or SinglCellExperiment object with pseudotime, probabilities in its colData

Examples

```
data(sce_vdj)
# downsample to first 2000 cells
sce_vdj <- sce_vdj[, 1:2000]
sce_vdj <- setupVdjPseudobulk(sce_vdj,
    already.productive = FALSE,
    allowed_chain_status = c("Single pair", "Extra pair")
)
# Build Milo Object
set.seed(100)
milo_object <- miloR::Milo(sce_vdj)
milo_object <- miloR::buildGraph(milo_object,
    k = 50, d = 20,
    reduced.dim = "X_scvi"
)
milo_object <- miloR::makeNhoods(milo_object,
    reduced_dims = "X_scvi",
    d = 20
)

# Construct Pseudobulked VDJ Feature Space
pb.milo <- vdjPseudobulk(milo_object, col_to_take = "anno_lvl_2_final_clean")
pb.milo <- scater::runPCA(pb.milo, assay.type = "Feature_space")

# Define root and branch tips
pca <- t(as.matrix(SingleCellExperiment::reducedDim(pb.milo, type = "PCA")))
branch.tips <- c(which.min(pca[, 2]), which.max(pca[, 2]))
names(branch.tips) <- c("CD8+T", "CD4+T")
root <- which.min(pca[, 1])

# Construct Diffusion Map
dm <- destiny::DiffusionMap(t(pca), n_pcs = 10, n_eigs = 5)
dif.pse <- destiny::DPT(dm, tips = c(root, branch.tips), w_width = 0.1)
```

```
# Markov Chain Construction
pb.milo <- markovProbability(
    milo = pb.milo,
    diffusionmap = dm,
    diffusiontime = dif.pse[[paste0("DPT", root)]],
    terminal_state = branch.tips,
    root_cell = root,
    pseudotime_key = "pseudotime"
)
```

`miloUmap` *Perform UMAP on the Adjacency Matrix of a Milo Object*

Description

This function uses `uwot::umap` to perform UMAP dimensionality reduction on the adjacency matrix of the KNN graph in a Milo object.

Usage

```
miloUmap(
  milo,
  slot_name = "UMAP_knngraph",
  n_neighbors = 50L,
  metric = "euclidean",
  min_dist = 0.3,
  ...
)
```

Arguments

`milo`	the milo object with knn graph that needed to conduct umap on.
`slot_name`	character, with default 'UMAP_knngraph'. • The slot name in reduceDim where the result store
`n_neighbors`	integer, with default 50L. • the size of local neighborhood (in terms of number of neighboring sample points) used for manifold approximation. • Here, the goal is to create large enough neighborhoods to capture the local manifold structure to allow for hypersampling.
`metric`	character, with default 'euclidean' • the choice of metric used to measure distance to find nearest neighbors. Default is 'euclidean'.
`min_dist`	numeric, with default 0.3 • the minimum distance between points in the low dimensional space
`...`	other parameters passed to uwot::umap

Value

milo object with umap reduction

Examples

```
data(sce_vdj)
# downsample to just 1000 cells
sce_vdj <- sce_vdj[, 1:1000]
sce_vdj <- setupVdjPseudobulk(sce_vdj,
    already.productive = FALSE,
    allowed_chain_status = c("Single pair", "Extra pair")
)
# Build Milo Object
milo_object <- miloR::Milo(sce_vdj)
milo_object <- miloR::buildGraph(milo_object,
    k = 50, d = 20,
    reduced.dim = "X_scvi"
)
milo_object <- miloR::makeNhoods(milo_object,
    reduced_dims = "X_scvi", d = 20
)

# Construct UMAP on Milo Neighbor Graph
milo_object <- miloUmap(milo_object)
```

---

projectProbability *Project Probabilities from Markov Chain to Pseudobulks*

Description

This function projects probabilities calculated from a Markov chain onto each pseudobulk based on a diffusion distance matrix.

Usage

```
projectProbability(
  diffusionmap,
  waypoints,
  probabilities,
  t = 1,
  verbose = TRUE
)
```

Arguments

diffusionmap	diffusion map, used to reconstruct diffustion distance matrix
waypoints	Integer vector. Indices of the waypoints used in the Markov chain.

probabilities	Numeric vector. Probabilities associated with the waypoints, calculated from the Markov chain.
t	Numeric. The diffusion time to be used in the projection.
verbose	Boolean, whether to print messages/warnings.

Value

each pseudobulk's probabilites

`projectPseudotimeToCell` *Project Pseudotime and Branch Probabilities to Single Cells*

Description

This function projects pseudotime and branch probabilities from pseudobulk data to single-cell resolution (`milo`). The results are stored in the `colData` of the `milo` object.

Usage

```
projectPseudotimeToCell(
  milo,
  pb_milo,
  term_states = NULL,
  pseudotime_key = "pseudotime",
  suffix = "",
  verbose = TRUE
)
```

Arguments

milo	A `SingleCellExperiment` or `Milo` object. Represents single-cell data where pseudotime and branch probabilities will be projected.
pb_milo	A pseudobulk `Milo` object. Contains aggregated branch probabilities and pseudotime information to be transferred to single cells.
term_states	Named vector of terminal states, with branch probabilities to be transferred. The names should correspond to branches of interest.
pseudotime_key	Character. The column name in `colData` of `pb_milo` that contains the pseudotime information which was used in the `markovProbability` function. Default is `"pseudotime"`.
suffix	Character. A suffix to be added to the new column names in `colData`. Default is an empty string (`''`).
verbose	Boolean, whether to print messages/warnings.

Value

subset of milo or SingleCellExperiment object where cell that do not belong to any neighbourhood are removed and projected pseudotime information stored colData

Examples

```
data(sce_vdj)
# downsample to first 2000 cells
sce_vdj <- sce_vdj[, 1:2000]
sce_vdj <- setupVdjPseudobulk(sce_vdj,
    already.productive = FALSE,
    allowed_chain_status = c("Single pair", "Extra pair")
)
# Build Milo Object
set.seed(100)
milo_object <- miloR::Milo(sce_vdj)
milo_object <- miloR::buildGraph(milo_object,
    k = 50, d = 20,
    reduced.dim = "X_scvi"
)
milo_object <- miloR::makeNhoods(milo_object,
    reduced_dims = "X_scvi",
    d = 20
)

# Construct Pseudobulked VDJ Feature Space
pb.milo <- vdjPseudobulk(milo_object, col_to_take = "anno_lvl_2_final_clean")
pb.milo <- scater::runPCA(pb.milo, assay.type = "Feature_space")

# Define root and branch tips
pca <- t(as.matrix(SingleCellExperiment::reducedDim(pb.milo, type = "PCA")))
branch.tips <- c(which.min(pca[, 2]), which.max(pca[, 2]))
names(branch.tips) <- c("CD8+T", "CD4+T")
root <- which.min(pca[, 1])

# Construct Diffusion Map
dm <- destiny::DiffusionMap(t(pca), n_pcs = 10, n_eigs = 5)
dif.pse <- destiny::DPT(dm, tips = c(root, branch.tips), w_width = 0.1)

# Markov Chain Construction
pb.milo <- markovProbability(
    milo = pb.milo,
    diffusionmap = dm,
    diffusiontime = dif.pse[[paste0("DPT", root)]],
    terminal_state = branch.tips,
    root_cell = root,
    pseudotime_key = "pseudotime"
)
# Project Pseudobulk Data
projected_milo <- projectPseudotimeToCell(
    milo_object,
    pb.milo,
```

```
    branch.tips,
    pseudotime_key = "pseudotime"
)
```

---

sce_vdj *Example Dataset for V(D)J Analysis*

Description

The sce_vdj object is a down-sampled demo dataset derived from Suo et al., 2024, *Nature Biotechnology*.
This dataset is used in vignettes to demonstrate workflows for V(D)J analysis.
For details, see the original publication at https://www.nature.com/articles/s41587-023-01734-7.

Usage

```
data(sce_vdj)
```

Format

A SingleCellExperiment object with the following slots:

colData A DataFrame containing metadata about each sample, corresponding to obs in AnnData (Python). The following columns are relevant for vignette usage:

productive_(mode)_VDJ, productive_(mode)_VJ Factors indicating whether the heavy or light chain is productive. mode refers to the extraction mode for V(D)J genes and can be one of:

- 'abT': TCR alpha-beta
- 'gdT': TCR gamma-delta
- 'B': BCR

Gene segment fields Gene segment annotations with column names in the format (v/d/j)_call_(mode)_(VDJ/VJ). Examples include:

- v_call_abT_VDJ: V gene for TCR alpha-beta VDJ recombination
- d_call_abT_VJ: D gene for TCR alpha-beta VJ recombination

chain_status A factor describing the receptor chain's status.

anno_lvl_2_final_clean Cell type annotations.

int_colData A DataFrame containing additional assay metadata important for further analysis. Includes:

- X_scvi: A dimensionality reduction matrix from the scVI model.
- UMAP: A UMAP reduction matrix.

Source

Suo et al., 2024, *Nature Biotechnology*.
https://www.nature.com/articles/s41587-023-01734-7.

Examples

```
data(sce_vdj)
```

`setupVdjPseudobulk` *Preprocess V(D)J Data for Pseudobulk Analysis*

Description

This function preprocesses single-cell V(D)J sequencing data for pseudobulk analysis. It filters data based on productivity and chain status, subsets data, extracts main V(D)J genes, and removes unmapped entries.

Usage

```
setupVdjPseudobulk(
  sce,
  mode_option = c("abT", "gdT", "B"),
  already.productive = TRUE,
  productive_cols = NULL,
  productive_vj = TRUE,
  productive_vdj = TRUE,
  allowed_chain_status = NULL,
  subsetby = NULL,
  groups = NULL,
  extract_cols = NULL,
  filter_unmapped = TRUE,
  check_vj_mapping = c(TRUE, TRUE),
  check_vdj_mapping = c(TRUE, FALSE, TRUE),
  check_extract_cols_mapping = NULL,
  remove_missing = TRUE,
  verbose = TRUE
)
```

Arguments

`sce`	A `SingleCellExperiment` object. V(D)J data should be contained in `colData` for filtering.
`mode_option`	Optional character. Specifies the mode for extracting V(D)J genes. If `NULL`, `extract_cols` must be specified. Default is `NULL`.
`already.productive`	Logical. Whether the data has already been filtered for productivity. If `TRUE`, skips productivity filtering. Default is `FALSE`.
`productive_cols`	Character vector. Names of `colData` columns used for productivity filtering. Default is `NULL`.

productive_vj Logical. If TRUE, retains cells where the main VJ chain is productive. Default is TRUE.

productive_vdj Logical. If TRUE, retains cells where the main VDJ chain is productive. Default is TRUE.

allowed_chain_status
Character vector. Specifies chain statuses to retain. Valid options include`c('single pair', 'Extra pair', 'Extra pair-exception','Orphan VDJ', 'Orphan VDJ-exception')`. Default is NULL.

subsetby Character. Name of a colData column for subsetting. Default is NULL.

groups Character vector. Specifies the subset condition for filtering. Default is NULL.

extract_cols Character vector. Names of colData columns where V(D)J information is stored, used instead of the standard columns. Default is NULL.

filter_unmapped
Logic. Whether to filter unmapped data. Default is TRUE.

check_vj_mapping
Logic vector. Whether to check for VJ mapping. Default is c(TRUE, TRUE).

- If the first element is TRUE, function will filter the unmapped data in V gene of the VJ chain
- If the second element is TRUE, function will filter the unmapped data in J gene of the VJ chain

check_vdj_mapping
Logic vector. Specifies columns to check for VDJ mapping. Default is c(TRUE, FALSE, 'TRUE).

- If the first element is TRUE, function will filter the unmapped data in V gene of the VDJ chain
- If the second element is TRUE, function will filter the unmapped data in D gene of the VDJ chain
- If the third element is TRUE, function will filter the unmapped data in J gene of the VDJ chain

check_extract_cols_mapping
Character vector. Specifies columns related to extract_cols for mapping checks. Default is NULL.

remove_missing Logical. If TRUE, removes cells with contigs matching the filter. If FALSE, masks them with uniform values. Default is TRUE.

verbose Logical. Whether to print messages. Default is TRUE.

Details

The function performs the following preprocessing steps:

- **Productivity Filtering**:
  - Skipped if already.productive = TRUE.
  - Filters cells based on productivity using productive_cols or standard colData columns named productive_{mode_option}_{type} (where type is 'VDJ' or 'VJ').
  - *mode_option*

    - function will check colData(s) named `productive_{mode_option}_{type}`, where type should be 'VDJ' or 'VJ' or both, depending on values of productive_vj and productive_vdj.
    - If set as `NULl`, the function needs the option 'extract_cols' to be specified
  - *productive_cols*
    - must be be specified when productivity filtering is need to conduct and mode_option is NULL.
    - where VDJ/VJ information is stored so that this will be used instead of the standard columns.
  - *productive_vj, productive_vdj*
    - If `TRUE`, cell will only be kept if the main V(D)J chain is productive
- **Chain Status Filtering**:
  - Retains cells with chain statuses specified by `allowed_chain_status`.
- **Subsetting**:
  - Conducted only if both `subsetby` and `groups` are provided.
  - Retains cells matching the `groups` condition in the `subsetby` column.
- **Main V(D)J Extraction**:
  - Uses `extract_cols` to specify custom columns for extracting V(D)J information.
- **Unmapped Data Filtering**:
  - decided to removes or masks cells based on `filter_unmapped`.
  - Checks specific columns for unclear mappings using `check_vj_mapping`, `check_vdj_mapping`, or `check_extract_cols_mapping`.
  - *filter_unmapped*
    - pattern to be filtered from object.
    - If is set to be `NULL`, the filtering process will not start
  - *check_vj_mapping, check_vdj_mapping*
    - only `colData` specified by these arguments (`check_vj_mapping` and `check_vdj_mapping`) will be checked for unclear mappings
  - *check_extract_cols_mapping, related to extract_cols*
    - Only `colData` specified by the argument will be checked for unclear mapping, the colData should first specified by extract_cols
  - remove_missing
    - If `TRUE`, will remove cells with contigs matching the filter from the object.
    - If `FALSE`, will mask them with a uniform value dependent on the column name.

Value

filtered SingleCellExperiment object

Examples

```
# load data
data(sce_vdj)
# check the dimension
```

```
dim(sce_vdj)
# filtered the data
sce_vdj <- setupVdjPseudobulk(
    sce = sce_vdj,
    mode_option = "abT", # set the mode to alpha-beta TCR
    allowed_chain_status = c("Single pair", "Extra pair"),
    already.productive = FALSE
) # need to filter the unproductive cells
# check the remaining dim
dim(sce_vdj)
```

---

splitCTgene *Split the V(D)J genes from* CTgene *column and store them separately.*

Description

Split the V(D)J genes from CTgene column and store them separately.

Usage

```
splitCTgene(sce)
```

Arguments

sce	SingleCellExperiment object after conducting scRepertoire::combineTCR()

Value

list contain vector of VJ & VDJ genes from each cell

---

vdjPseudobulk *Generate Pseudobulk V(D)J Feature Space*

Description

This function creates a pseudobulk V(D)J feature space from single-cell data, aggregating V(D)J information into pseudobulk groups. It supports input as either a Milo object or a SingleCellExperiment object.

Usage

```
vdjPseudobulk(
  milo,
  pbs = NULL,
  col_to_bulk = NULL,
 extract_cols = c("v_call_abT_VDJ_main", "j_call_abT_VDJ_main", "v_call_abT_VJ_main",
    "j_call_abT_VJ_main"),
  mode_option = c("abT", "gdT", "B"),
  col_to_take = NULL,
  normalise = TRUE,
  renormalize = FALSE,
  min_count = 1L,
  verbose = TRUE
)
```

Arguments

milo	A Milo or SingleCellExperiment object containing V(D)J data.
pbs	Optional. A binary matrix with cells as rows and pseudobulk groups as columns. • If milo is a Milo object, this parameter is not required. • If milo is a SingleCellExperiment object, either pbs or col_to_bulk must be provided.
col_to_bulk	Optional character or character vector. Specifies colData column(s) to generate pbs. If multiple columns are provided, they will be combined. Default is NULL. • If milo is a Milo object, this parameter is not required. • If milo is a SingleCellExperiment object, either pbs or col_to_bulk must be provided.
extract_cols	Character vector. Specifies column names where V(D)J information is stored. Default is c('v_call_abT_VDJ_main', 'j_call_abT_VDJ_main', ' 'v_call_abT_VJ_main', 'j_ca
mode_option	Character. Specifies the mode for extracting V(D)J genes. Must be one of c('B', 'abT', 'gdT'). Default is 'abT'. • Note: This parameter is considered only when extract_cols = NULL. • If NULL, uses column names such as v_call_VDJ instead of v_call_abT_VDJ.
col_to_take	Optional character or vector of characters. Specifies names of colData of milo that need to identify the most common value for each pseudobulk Default is NULL.
normalise	Logical. If TRUE, scales the counts of each V(D)J gene group to 1 for each pseudobulk. Default is TRUE.
renormalize	Logical. If TRUE, rescales the counts of each V(D)J gene group to 1 for each pseudobulk after removing 'missing' calls. Useful when setupVdjPseudobulk() was run with remove_missing = FALSE. Default is FALSE.
min_count	Integer. Sets pseudobulk counts in V(D)J gene groups with fewer than this many non-missing calls to 0. Default is 1.
verbose	Logical. If TRUE, prints messages and warnings. Default is TRUE.

Details

This function aggregates V(D)J data into pseudobulk groups based on the following logic:

- **Input Requirements**:
- If `milo` is a `Milo` object, neither `pbs` nor `col_to_bulk` is required.
- If `milo` is a `SingleCellExperiment` object, the user must provide either `pbs` or `col_to_bulk`.
- **Normalization**:
- When `normalise = TRUE`, scales V(D)J counts to 1 for each pseudobulk group.
- When `renormalize = TRUE`, rescales the counts after removing 'missing' calls.
- **Mode Selection**:
- If `extract_cols = NULL`, the function relies on `mode_option` to determine which V(D)J columns to extract.
- **Filtering**:
- Uses `min_count` to filter pseudobulks with insufficient counts for V(D)J groups.

Value

SingleCellExperiment object

Examples

```
data(sce_vdj)
sce_vdj <- setupVdjPseudobulk(sce_vdj,
    already.productive = FALSE,
    allowed_chain_status = c("Single pair", "Extra pair")
)
# Build Milo Object
milo_object <- miloR::Milo(sce_vdj)
milo_object <- miloR::buildGraph(milo_object,
    k = 50, d = 20,
    reduced.dim = "X_scvi"
)
milo_object <- miloR::makeNhoods(milo_object,
    reduced_dims = "X_scvi",
    d = 20
)

# Construct pseudobulked VDJ feature space
pb.milo <- vdjPseudobulk(milo_object, col_to_take = "anno_lvl_2_final_clean")
```

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