

Package ‘demuxSNP’

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Title scRNAseq demultiplexing using cell hashing and SNPs

Version 1.3.0

Description

This package assists in demultiplexing scRNAseq data using both cell hashing and SNPs data. The SNP profile of each group is learned using high confidence assignments from the cell hashing data.

Cells which cannot be assigned with high confidence from the cell hashing data are assigned to their most similar group based on their SNPs.

We also provide some helper function to optimise SNP selection, create training data and merge SNP data into the SingleCellExperiment framework.

URL <https://github.com/michaelplynych/demuxSNP>

BugReports <https://github.com/michaelplynych/demuxSNP/issues>

License GPL-3

Encoding UTF-8

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Contents

| | |
|-------------------------------------------|---|
| add_snps | 2 |
| commonvariants_1kgenomes_subset | 3 |
| common_genes | 3 |
| high_conf_calls | 4 |
| multiplexed_scrnaseq_sce | 5 |
| reassign | 5 |
| reassign_balanced | 6 |
| reassign_jaccard | 7 |
| subset_vcf | 8 |
| vartrix_consensus_snps | 9 |

| | |
|--------------|-----------|
| Index | 10 |
|--------------|-----------|

| | |
|----------|------------------------------------------------|
| add_snps | <i>Add SNPs to SingleCellExperiment object</i> |
|----------|------------------------------------------------|

Description

Add SNPs to SingleCellExperiment object

Usage

```
add_snps(sce, mat, thresh = 0.8)
```

Arguments

| | |
|--------|---------------------------------------------------------------------------|
| sce | object of class SingleCellExperiment |
| mat | object of class matrix, output from VarTrix in 'consensus' mode (default) |
| thresh | threshold presence of SNP, defaults to 0.8 |

Value

Updated SingleCellExperiment object with snps in altExp slot

Examples

```
data(multiplexed_scrnaseq_sce, vartrix_consensus_snps)
multiplexed_scrnaseq_sce <- add_snps(sce = multiplexed_scrnaseq_sce,
mat = vartrix_consensus_snps,
thresh = 0.8)
```

```
commonvariants_1kgenomes_subset
      Sample vcf file
```

Description

VCF file containing SNPs from a subset of the 1k Genomes common variants HG38 genome build.

Usage

```
data(commonvariants_1kgenomes_subset)
```

Format

An object of class CollapsedVCF with 2609 rows and 0 columns.

Value

```
commonvariants_1kgenomes_subset:
An object of class CollapsedVcf
```

Source

https://cellsnp-lite.readthedocs.io/en/latest/snp_list.html

```
common_genes      Return a character vector of top n most frequent genes from a Single-
CellExperiment object.
```

Description

Returns a character vector of the top n most frequently expressed genes from the counts of the SingleCellExperiment object. Expression is based on having a count > 0 in a given cell.

Usage

```
common_genes(sce, n = 100)
```

Arguments

sce a SingleCellExperiment object
n number of genes to be returned. Defaults to n=100.

Value

character vector of n most frequently expressed genes.

Examples

```
data(multiplexed_scrnaseq_sce)  
multiplexed_scrnaseq_sce <- common_genes(multiplexed_scrnaseq_sce)
```

high_conf_calls *Run demuxmix to determine high-confidence calls*

Description

Run demuxmix to determine high-confidence calls

Usage

```
high_conf_calls(sce, assay = "HTO", pacpt = 0.95)
```

Arguments

sce Object of class SingleCellExperiment with HTO (or similar) altExp assay
assay Name of altExp for cell hashing counts to be retrieved from
pacpt acceptance probability for demuxmix model

Value

Updated SingleCellExperiment object with logical vector indicating training data, data to be classified (all cells) and assigned labels for all cells.

Examples

```
data(multiplexed_scrnaseq_sce)  
multiplexed_scrnaseq_sce <- high_conf_calls(multiplexed_scrnaseq_sce)
```

multiplexed_scrnaseq_sce

SingleCellExperiment object containing multiplexed RNA and HTO data from six biological smamples

Description

Example SingleCellExperiment object containing demultiplexed scRNAseq data from six donors, used throughout and built upon in demuxSNP workflow.

Usage

```
data(multiplexed_scrnaseq_sce)
```

Format

An object of class SingleCellExperiment with 259 rows and 2000 columns.

Value

multiplexed_scrnaseq_sce:
An object of class SingleCellExperiment

reassign

Reassign cells using knn

Description

k-nearest neighbour classification of cells. Training data is intended to be labels of cells confidently called using cell hashing based methods and their corresponding SNPs. Prediction data can be remaining cells but can also include the training data. Doublets are simulated by randomly combining 'd' SNP profiles from each grouping combination.

Usage

```
reassign(
  sce,
  k = 10,
  d = 10,
  train_cells = sce$train,
  predict_cells = sce$predict
)
```

Arguments

sce object of class SingleCellExperiment
k number of neighbours used in knn, defaults to 10
d number of doublets per group combination to simulate, defaults to 10
train_cells logical vector specifying which cells to use to train classifier
predict_cells logical vector specifying which cells to classify

Value

A SingleCellExperiment with updated group assignments called 'knn'

Examples

```
data(multiplexed_scrnaseq_sce, vartrix_consensus_snps)
multiplexed_scrnaseq_sce <- high_conf_calls(multiplexed_scrnaseq_sce)
multiplexed_scrnaseq_sce <- add_snps(sce = multiplexed_scrnaseq_sce,
mat = vartrix_consensus_snps,
thresh = 0.8)
multiplexed_scrnaseq_sce <- reassign(sce = multiplexed_scrnaseq_sce, k = 10)
```

reassign_balanced *Reassign cells using balanced knn with jaccard distance*

Description

k-nearest neighbour classification of cells. Training data is intended to be labels of cells confidently called using cell hashing based methods and their corresponding SNPs. Prediction data can be remaining cells but can also include the training data. Doublets are simulated by randomly combining 'd' SNP profiles from each grouping combination.

Usage

```
reassign_balanced(
  sce,
  k = 10,
  d = 10,
  train_cells = sce$train,
  predict_cells = sce$predict,
  n = NULL,
  nmin = 50
)
```

Arguments

| | |
|---------------|----------------------------------------------------------------------|
| sce | object of class SingleCellExperiment |
| k | number of neighbours used in knn, defaults to 10 |
| d | number of doublets per group combination to simulate, defaults to 10 |
| train_cells | logical vector specifying which cells to use to train classifier |
| predict_cells | logical vector specifying which cells to classify |
| n | number of cells per group (otherwise will be calculated from data) |
| nmin | min n per class (where available) |

Value

A SingleCellExperiment with updated group assignments called 'knn'

Examples

```
data(multiplexed_scrnaseq_sce, vartrix_consensus_snps)
multiplexed_scrnaseq_sce <- high_conf_calls(multiplexed_scrnaseq_sce)
multiplexed_scrnaseq_sce <- add_snps(sce = multiplexed_scrnaseq_sce,
mat = vartrix_consensus_snps,
thresh = 0.8)
multiplexed_scrnaseq_sce <- reassign_balanced(sce = multiplexed_scrnaseq_sce, k = 10)
```

reassign_jaccard *Reassign cells using knn with jaccard distance*

Description

k-nearest neighbour classification of cells. Training data is intended to be labels of cells confidently called using cell hashing based methods and their corresponding SNPs. Prediction data can be remaining cells but can also include the training data. Doublets are simulated by randomly combining 'd' SNP profiles from each grouping combination.

Usage

```
reassign_jaccard(
  sce,
  k = 10,
  d = 10,
  train_cells = sce$train,
  predict_cells = sce$predict
)
```

Arguments

| | |
|---------------|----------------------------------------------------------------------|
| sce | object of class SingleCellExperiment |
| k | number of neighbours used in knn, defaults to 10 |
| d | number of doublets per group combination to simulate, defaults to 10 |
| train_cells | logical vector specifying which cells to use to train classifier |
| predict_cells | logical vector specifying which cells to classify |

Value

A SingleCellExperiment with updated group assignments called 'knn'

Examples

```
data(multiplexed_scrnaseq_sce, vartrix_consensus_snps)
multiplexed_scrnaseq_sce <- high_conf_calls(multiplexed_scrnaseq_sce)
multiplexed_scrnaseq_sce <- add_snps(sce = multiplexed_scrnaseq_sce,
mat = vartrix_consensus_snps,
thresh = 0.8)
multiplexed_scrnaseq_sce <- reassign(sce = multiplexed_scrnaseq_sce, k = 10)
```

subset_vcf

Subset common variants vcf file to only SNPs seen in 'top_genes'

Description

Subset common variants vcf file to only SNPs seen in 'top_genes'

Usage

```
subset_vcf(vcf, top_genes, ensdb)
```

Arguments

| | |
|-----------|---------------------------------------------------------------------------------------------------|
| vcf | object of class CollapsedVCF |
| top_genes | output from 'common_genes' function, alternatively character vector containing custom gene names. |
| ensdb | object of class EnsDb corresponding to organism, genome of data |

Value

object of class CollapsedVCF containing subset of SNPs from supplied vcf seen in commonly expressed genes

Examples

```
data(multiplexed_scrnaseq_sce, commonvariants_1kgenomes_subset)
top_genes <- common_genes(multiplexed_scrnaseq_sce)
ensdb <- EnsDb.Hsapiens.v86::EnsDb.Hsapiens.v86
small_vcf <- subset_vcf(commonvariants_1kgenomes_subset, top_genes, ensdb)
```

vartrix_consensus_snps

Sample VarTrix output

Description

A sample output from VarTrix corresponding to the sce SingleCellExperiment object for a subset of SNPs located in well observed genes.

Usage

```
data(vartrix_consensus_snps)
```

Format

An object of class `matrix` (inherits from `array`) with 2542 rows and 2000 columns.

Value

`vartrix_consensus_snps`:
An object of class `matrix`

Index

* datasets

- commonvariants_1kgenomes_subset, [3](#)
- multiplexed_scrnaseq_sce, [5](#)
- vartrix_consensus_snps, [9](#)

add_snps, [2](#)

common_genes, [3](#)

commonvariants_1kgenomes_subset, [3](#)

high_conf_calls, [4](#)

multiplexed_scrnaseq_sce, [5](#)

reassign, [5](#)

reassign_balanced, [6](#)

reassign_jaccard, [7](#)

subset_vcf, [8](#)

vartrix_consensus_snps, [9](#)