Package ‘demuxSNP’

January 26, 2024

Title scRNAseq demultiplexing using cell hashing and SNPs

Version 1.0.0

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/michaelplynch/demuxSNP

BugReports https://github.com/michaelplynch/demuxSNP/issues

License GPL-3

Encoding UTF-8

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RoxygenNote 7.2.3

Depends R (>= 4.3.0), SingleCellExperiment, VariantAnnotation, ensmbldb

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### Description

Add SNPs to SingleCellExperiment object

### Usage

```r
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

```r
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**


---

**common_genes**

Return a character vector of top n most frequent genes from a SingleCellExperiment 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

```r
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

```r
high_conf_calls(sce, assay = "HTO")
```

Arguments

- `sce`  
  Object of class `SingleCellExperiment` with HTO (or similar) altExp assay
- `assay`  
  Name of altExp for cell hashing counts to be retrieved from

Value

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

Examples

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

---

`multiplexed_scrnaseq_sce`  
*SingleCellExperiment object containing demultiplexed scRNAseq data from six biological samples*

---

Description

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

Usage

```r
data(multiplexed_scrnaseq_sce)
```
**reassign**

**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**

```r
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)

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 objec 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
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