Package ‘demuxSNP’

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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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**add_snps**

Add SNPs to SingleCellExperiment object

**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

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")

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

data(multiplexed_scrnaseq_sce)
multiplexed_scrnaseq_sce <- high_conf_calls(multiplexed_scrnaseq_sce)

multiplexed_scrnaseq_sce

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_scnnaseq_sce;`

An object of class `SingleCellExperiment`

---

```r
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**

```r
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**

```r
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**

```r
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)
```
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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