Package 'demuxSNP'

April 15, 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 os 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

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

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

Imports MatrixGenerics, BiocGenerics, class, GenomeInfoDb, IRanges, Matrix, SummarizedExperiment, demuxmix, methods, combinat

Suggests knitr, rmarkdown, Seurat, ComplexHeatmap, viridisLite, ggpubr, dittoSeq, EnsDb.Hsapiens.v86, BiocStyle, RefManageR, testthat (>= 3.0.0)

biocViews Classification, SingleCell

VignetteBuilder knitr

LazyData false

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/demuxSNP

git_branch RELEASE_3_18

git_last_commit 1af04e3

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-04-15

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R topics documented:

`add_snps` *Add SNPs to SingleCellExperiment object*

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 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 multiplexed RNA and HTO data from six biological smamples

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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)
```

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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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