Package ‘cellity’

January 31, 2017

Type Package

Title Quality Control for Single-Cell RNA-seq Data

Version 1.3.0

Date 2016-02-22

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Description A support vector machine approach to identifying and filtering low quality cells from single-cell RNA-seq datasets.

License GPL (>= 2)

Depends R (>= 3.3)

Imports AnnotationDbi, e1071, ggplot2, graphics, grDevices, grid, mvoutlier, org.Hs.eg.db, org.Mm.eg.db, robustbase, stats, topGO, utils

Suggests BiocStyle, caret, knitr, testthat, rmarkdown

VignetteBuilder knitr

LazyData true

biocViews RNASeq, QualityControl, Preprocessing, Normalization, Visualization, DimensionReduction, Transcriptomics, GeneExpression, Sequencing, Software, SupportVectorMachine

RoxygenNote 5.0.1

NeedsCompilation no

R topics documented:

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cellity-package Quality Control for Single-Cell RNA-seq Data

Description

cellity provides a support vector machine and PCA approaches to identifying and filtering low quality cells from single-cell RNA-seq datasets.

assess_cell_quality_PCA

ASSESS CELL QUALITY USING PCA AND OUTLIER DETECTION

Description

ASSESS CELL QUALITY USING PCA AND OUTLIER DETECTION

Usage

assess_cell_quality_PCA(features, file = "")

Arguments

features Input dataset containing features (cell x features)
file Output_file where plot is saved

Details

This function applies PCA on features and uses outlier detection to determine which cells are low and which are high quality

Value

Returns a dataframe indicating which cell is low or high quality (0 or 1 respectively)

Examples

data(training_mES_features)
training_mES_features_all <- training_mES_features[[1]]
training_quality_PCA_allF <- assess_cell_quality_PCA(training_mES_features_all)
assess_cell_quality_SVM

Assess quality of a cell - SVM version

**Description**

Assess quality of a cell - SVM version

**Usage**

```r
assess_cell_quality_SVM(training_set_features, training_set_labels, 
ensemble_param, test_set_features)
```

**Arguments**

- `training_set_features`: A training set containing features (cells x features) for prediction
- `training_set_labels`: Annotation of each individual cell if high or low quality (1 or 0 respectively)
- `ensemble_param`: Dataframe of parameters for SVM
- `test_set_features`: Dataset to predict containing features (cells x features)

**Details**

This function takes a training set + annotation to predict a test set. It requires that hyper-parameters have been optimised.

**Value**

Returns a dataframe indicating which cell is low or high quality (0 or 1 respectively)

data.frame with decision on quality of cells

**Examples**

```r
data(param_mES_all)
data(training_mES_features)
data(training_mES_labels)
data(mES1_features)
data(mES1_labels)
mES1_features_all <- mES1_features[[1]]
training_mES_features_all <- training_mES_features[[1]]
mES1_quality_SVM <- assess_cell_quality_SVM( training_mES_features_all, 
training_mES_labels[,2], param_mES_all, mES1_features_all)
```
**extract_features**  
*Extracts biological and technical features for given dataset*

**Description**

Extracts biological and technical features for given dataset

**Usage**

```r
extract_features(counts_nm, read_metrics, prefix = "", output_dir = "",  
common_features = NULL, GO_terms = NULL, extra_genes = NULL,  
organism = "mouse")
```

**Arguments**

- `counts_nm`: Gene expression counts dataframe (genes x cells). Either normalised by library size or TPM values
- `read_metrics`: Dataframe with mapping statistics produced by python pipeline
- `prefix`: Prefix of output files
- `output_dir`: Output directory of files
- `common_features`: Subset of features that are applicable within one species, but across cell types
- `GO_terms`: DataFrame with gene ontology term IDs, that will be used in feature extraction
- `extra_genes`: Additional genes used for feature extraction
- `organism`: The target organism to generate the features for

**Details**

This function takes a combination of gene counts and mapping statistics to extract biological and technical features, which than can be used for quality data analysis

**Value**

a list with two elements, one providing all features, and one providing common features.

**Examples**

```r
data(sample_counts)  
data(sample_stats)  
sample_counts_nm <- normalise_by_factor(sample_counts, colSums(sample_counts))  
sample_features <- extract_features(sample_counts_nm, sample_stats)
```
**extra_human_genes**  
*Additional human genes that are used in feature extraction*

**Description**  
This list contains human genes that are used for feature extraction of biological features

**Usage**  
extra_human_genes

**Format**  
a list containing vectors of genes. Name indicates which GO category.

**Value**  
NULL, but makes available a list with metadata

**Author(s)**  
Tomislav Ilicic & Davis McCarthy, 2015-03-05

**Source**  
Wellcome Trust Sanger Institute

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**extra_mouse_genes**  
*Additional mouse genes that are used in feature extraction*

**Description**  
This list contains mouse genes that are used for feature extraction of biological features

**Usage**  
extra_mouse_genes

**Format**  
a list containing vectors of genes. Name indicates which GO category.

**Value**  
NULL, but makes available a list with metadata

**Author(s)**  
Tomislav Ilicic & Davis McCarthy, 2015-03-05

**Source**  
Wellcome Trust Sanger Institute
feature_generation  

**Helper Function to create all features**

**Description**

Helper Function to create all features

**Usage**

```r
feature_generation(counts_nm, read_metrics, GO_terms, extra_genes, organism)
```

**Arguments**

- `counts_nm`: Gene expression counts dataframe (genes x cells). Either normalised by library size or TPM values
- `read_metrics`: Dataframe with mapping statistics produced by python pipeline
- `GO_terms`: DataFrame with gene ontology term IDs, that will be used in feature extraction
- `extra_genes`: Additional genes used for feature extraction
- `organism`: The target organism to generate the features for

**Value**

Returns the entire set of features in a data.frame

feature_info  

**Information which genes and GO categories should be included as features. Also defines which features are cell-type independent (common features)**

**Description**

This list contains metadata information that is used to extract features from in the function extract_features

**Usage**

```r
feature_info
```

**Format**

- a list with 2 elements (GO_terms, common_features).

**Value**

NULL, but makes available a list with metadata

**Author(s)**

Tomislav Ilicic & Davis McCarthy, 2015-03-05
**mES1_features**

**Source**
Wellcome Trust Sanger Institute

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**mES1_features**  
*Real test dataset containing all and common features from the paper (mES1)*

**Description**
This list contains 2 dataframes where each contains features per cell (cell X features) that can be used for classification.

**Usage**
mES1_features

**Format**
a list with 2 elements (all_features, common_features).

**Value**
NULL, but makes available a list with 2 dataframes

**Author(s)**
Tomislav Ilicic & Davis McCarthy, 2015-03-05

**Source**
Wellcome Trust Sanger Institute

---

**mES1_labels**  
*Real test dataset containing annotation of cells*

**Description**
This data frame has 2 columns: First showing cell names, the second indicating if cell is of low (0) or high (1) quality.

**Usage**
mES1_labels

**Format**
a dataframe with 2 columns (cell_names, label).

**Value**
NULL, but makes available a dataframe with cell annotations
Author(s)
Tomislav Ilicic & Davis McCarthy, 2015-03-05

Source
Wellcome Trust Sanger Institute

multiplot
Internal multiplot function to combine plots onto a grid

Description
Internal multiplot function to combine plots onto a grid

Usage
multiplot(..., plotlist = NULL, file, cols = 6, layout = NULL)

Arguments
...
individual plots to combine into a single plot
plotlist
a vector with names of plots to use in the plot
file
string giving filename to which pdf of plots is to be saved
cols
integer giving number of columns for the plot
layout
matrix defining the layout for the plots

Value
a plot object

normalise_by_factor
Internal function to normalize by library size

Description
Internal function to normalize by library size

Usage
normalise_by_factor(counts, norm_factor)

Arguments
counts
matrix of counts
norm_factor
vector of normalisation factors

Value
a matrix with normalized gene counts
param_mES_all

Examples

```r
data(sample_counts)
data(sample_stats)
sample_counts_nm <- normalise_by_factor(sample_counts, colSums(sample_counts))
```

---

**param_mES_all**  
*Parameters used for SVM classification*

**Description**

This data frame has 3 columns: gamma, cost, class.weights and is optimised for all features and our training data.

**Usage**

```r
param_mES_all
```

**Format**

A dataframe with 3 columns (gamma, cost, class.weights).

**Value**

NULL, but makes available a dataframe with parameters.

**Author(s)**

Tomislav Ilicic & Davis McCarthy, 2015-03-05

**Source**

Wellcome Trust Sanger Institute

---

**param_mES_common**  
*Parameters used for SVM classification*

**Description**

This data frame has 3 columns: gamma, cost, class.weights and is optimised for common features and our training data.

**Usage**

```r
param_mES_common
```

**Format**

A dataframe with 3 columns (gamma, cost, class.weights).
plot_pca

Value

NULL, but makes available a dataframe with parameters

Author(s)

Tomislav Ilicic & Davis McCarthy, 2015-03-05

Source

Wellcome Trust Sanger Institute

plot_pca

Plots PCA of all features. Colors high and low quality cells based on outlier detection.

Description

Plots PCA of all features. Colors high and low quality cells based on outlier detection.

Usage

plot_pca(features, annot, pca, col, output_file)

Arguments

features Input dataset containing features (cell x features)
annot Matrix annotation of each cell
pca PCA of features
col color code indicating what color high and what low quality cells
output_file where plot is stored

Details

This function plots PCA of all features + most informative features

Value

Plots of PCA
**sample_counts**

| sample_counts | Sample gene expression data containing 40 cells |

**Description**
This data frame contains genes (rows) and cells (columns) showing raw read counts

**Usage**
sample_counts

**Format**
a dataframe with genes x cells

**Value**
NULL, but makes available a dataframe with raw read counts

**Author(s)**
Tomislav Ilicic & Davis McCarthy, 2015-03-05

**Source**
Wellcome Trust Sanger Institute

---

**sample_stats**

| sample_stats | Sample read statistics data containing 40 cells |

**Description**
This data frame contains read metrics (columns) and cells (rows)

**Usage**
sample_stats

**Format**
a dataframe with cells x metrics

**Value**
NULL, but makes available a dataframe with read statistics

**Author(s)**
Tomislav Ilicic & Davis McCarthy, 2015-03-05

**Source**
Wellcome Trust Sanger Institute
simple_cap  
*Converts all first letters to capital letters*

**Description**

Converts all first letters to capital letters

**Usage**

`simple_cap(x)`

**Arguments**

- `x`  
  string

**Value**

a character vector in title case

---

sum_prop  
*Sums up normalised values of genes to groups.*

**Description**

Supports TPM and proportion of mapped reads.

**Usage**

`sum_prop(counts, genes_interest)`

**Arguments**

- `counts`  
  Normalised gene expression count matrix

- `genes_interest`  
  dataframe of genes of interest to merge

**Value**

a vector of sums per group
training_mES_features Original training dataset containing all and common features from the paper (training mES)

Description
This list contains 2 dataframes where each contains features per cell (cell X features) that can be used for classification.

Usage
training_mES_features

Format
a list with 2 elements (all_features, common_features).

Value
NULL, but makes available a list with 2 dataframes

Author(s)
Tomislav Ilicic & Davis McCarthy, 2015-03-05

Source
Wellcome Trust Sanger Institute

training_mES_labels Original training dataset containing annotation of cells

Description
This data frame has 2 columns: First showing cell names, the second indicating if cell is of low (0) or high (1) quality

Usage
training_mES_labels

Format
a dataframe with 2 columns (cell_names, label).

Value
NULL, but makes available a dataframe with cell annotations
uni.plot

Author(s)
Tomislav Ilicic & Davis McCarthy, 2015-03-05

Source
Wellcome Trust Sanger Institute

---

## Description

Internal function to detect outliers from the mvoutlier package Modified slightly so that plots are not printed

## Usage

```
uni.plot(x, symb = FALSE, quan = 1/2, alpha = 0.025)
```

## Arguments

- `x`: A matrix containing counts
- `symb`: Symbols
- `quan`: quan
- `alpha`: alpha

## Value

a list of outlier indicators
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