Package ‘cellity’
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Title Quality Control for Single-Cell RNA-seq Data
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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
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Description

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

\section*{assess\_cell\_quality\_PCA}

\textit{ASSESS CELL QUALITY USING PCA AND OUTLIER DETECTION}

\section*{Usage}

\begin{verbatim}
assess_cell_quality_PCA(Features, file = "")
\end{verbatim}

\section*{Arguments}

\begin{verbatim}
features Input dataset containing features (cell x features)
file Output file where plot is saved
\end{verbatim}

\section*{Details}

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

\section*{Value}

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

\section*{Examples}

\begin{verbatim}
data(training_mES_features)
training_mES_features_all <- training_mES_features[[1]]
training_quality_PCA_allF <- assess_cell_quality_PCA(training_mES_features_all)
\end{verbatim}
assess_cell_quality_SVM

Assess quality of a cell - SVM version

Description
Assess quality of a cell - SVM version

Usage
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
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

```
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

```
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**

**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**

**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

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**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

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**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
Examples

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

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

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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

param_mES_common

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

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 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

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**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

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

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**training_mES_labels**

*Original training dataset containing annotation of cells*

**Description**

This dataframe 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

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uni.plot

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

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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
assess_cell_quality_PCA, 2
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