# Package 'cellity'

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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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# Contents

cellity-package . . . 2
assess_cell_quality_PCA . . . 2
assess_cell_quality_SVM . . . 3
extract_features . . . 4
extra_human_genes . . . 5
extra_mouse_genes . . . 6
feature_generation . . . 6
feature_info . . . 7
mES1_features . . . 7
mES1_labels . . . 8
multiplot . . . 9
normalise_by_factor . . . 9
param_mES_all . . . 10
param_mES_common . . . 10
plot_pca . . . 11
sample_counts . . . 12
sample_stats . . . 12
simple_cap . . . 13
sum_prop . . . 13
training_mES_features . . . 14
training_mES_labels . . . 14
uni.plot . . . 15

**Index** **16**

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

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## Description

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

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`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

```
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 traning 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 outputfiles |
| 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 *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

## 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

```
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

```
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

### Source

Wellcome Trust Sanger Institute

---

`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

## 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

---

`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

## 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

## Author(s)

Tomislav Ilicic & Davis McCarthy, 2015-03-05

## Source

Wellcome Trust Sanger Institute

---

`uni.plot` *Internal function to detect outliers from the mvoultier pacakge Modified slightly so that plots are not printed*

---

## Description

Internal function to detect outliers from the mvoultier pacakge 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

# Index

assess_cell_quality_PCA, 2
assess_cell_quality_SVM, 3

cellity-package, 2

extra_human_genes, 5
extra_mouse_genes, 6
extract_features, 4

feature_generation, 6
feature_info, 7

mES1_features, 7
mES1_labels, 8
multiplot, 9

normalise_by_factor, 9

param_mES_all, 10
param_mES_common, 10
plot_pca, 11

sample_counts, 12
sample_stats, 12
simple_cap, 13
sum_prop, 13

training_mES_features, 14
training_mES_labels, 14

uni.plot, 15