

# Package ‘cellity’

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**Type** Package

**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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cellity-package	<i>Quality Control for Single-Cell RNA-seq Data</i>
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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	<i>ASSESS CELL QUALITY USING PCA AND OUTLIER DETECTION</i>
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### 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 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)
```

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extract_features	<i>Extracts biological and technical features for given dataset</i>
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### 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	<i>Helper Function to create all features</i>
--------------------	---

---

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

---

**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

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mES1_features	<i>Real test dataset containing all and common features from the paper (mES1)</i>
---------------	---

---

**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	<i>Real test dataset containing annotation of cells</i>
-------------	---

---

**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

---

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

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plot_pca	<i>Plots PCA of all features. Colors high and low quality cells based on outlier detection.</i>
----------	---

---

**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	<i>Sample gene expression data containing 40 cells</i>
---------------	--

---

**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	<i>Sample read statistics data containing 40 cells</i>
--------------	--

---

**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

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simple_cap	<i>Converts all first letters to capital letters</i>
------------	--

---

**Description**

Converts all first letters to capital letters

**Usage**

```
simple_cap(x)
```

**Arguments**

x                      string

**Value**

a character vector in title case

---

sum_prop	<i>Sums up normalised values of genes to groups.</i>
----------	--

---

**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 mvoutlier package Modified slightly so that plots are not printed*

---

**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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