Package ‘cellity’

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Title Quality Control for Single-Cell RNA-seq Data

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License GPL (>= 2)

Depends R (>= 3.3)

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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

```
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

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