Package ‘CytoMethIC’

May 2, 2024

Type Package
Title DNA methylation-based classification and regression
Description This package provides DNA methylation-based prediction of cancer type, molecular signature and clinical outcomes. It provides convenience functions for missing value imputation, probe ID conversion, model interpretation and visualization. The package links to our models on ExperimentHub. The package currently supports HM450, EPIC and EPICv2.
Version 1.0.0
License Artistic-2.0
Depends R (>= 4.4.0), ExperimentHub
Imports tibble, utils, stats, tools, sesame, methods, sesameData, BiocParallel, BiocManager
VignetteBuilder knitr
Suggests BiocStyle, randomForest, testthat, knitr, rmarkdown, e1071, xgboost, keras, tensorflow
URL https://github.com/zhou-lab/CytoMethIC
BugReports https://github.com/zhou-lab/CytoMethIC/issues
biocViews ExperimentData, MicroarrayData, Genome, ExperimentHub, MethylationArrayData, CancerData, PackageTypeData
NeedsCompilation no
RoxygenNote 7.3.1
Encoding UTF-8
git_url https://git.bioconductor.org/packages/CytoMethIC
git_branch RELEASE_3_19
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Description

print package version of cytometric and depended packages to help troubleshoot installation issues.

Usage

```r
cki_checkVersion()
```

Value

print the versions of cytometric and dependencies

Examples

```r
cmi_checkVersion()
```

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**cmi_models**

Master data frame for all model objects

Description

This is an internal object which will be updated on every new release

Value

master sheet of CytoMethIC model objects

Examples

```r
print(cmi_models[,c("EHID","Title")])
```
The `cmi_predict` function takes in a model and a sample, and uses the model to predict it. This function supports `randomForest`, `e1071::svm`, `xgboost`, and `keras/tensorflow` models. For `xgboost` and `keras` models, the features used in classification as well as a label mapping must be provided for output.

**Description**

The `cmi_predict` function takes in a model and a sample, and uses the model to predict it. This function supports `randomForest`, `e1071::svm`, `xgboost`, and `keras/tensorflow` models. For `xgboost` and `keras` models, the features used in classification as well as a label mapping must be provided for output.

**Usage**

```r
cmi_predict(
  betas,  
  cmi_model,  
  source_platform = NULL,  
  lift_over = FALSE,  
  verbose = FALSE,  
  BPPARAM = SerialParam()
)
```

**Arguments**

- `betas` DNA methylation beta
- `cmi_model` Cytomethic model downloaded from ExperimentHub
- `source_platform` source platform If not given, will infer from probe ID.
- `lift_over` whether to allow mLiftOver to convert probe IDs
- `verbose` be verbose with warning
- `BPPARAM` use MulticoreParam(n) for parallel processing

**Value**

predicted cancer type label

**Examples**

```r
library(sesame)
library(ExperimentHub)
library(CytoMethIC)

## Cancer Type
```
model = ExperimentHub()['EH8395']
cmi_predict(openSesame(sesameDataGet('EPICv2.8.SigDF')[1]), model, lift_over=TRUE)

cmi_predict(openSesame(sesameDataGet('EPIC.1.SigDF')), model, lift_over=TRUE)

cmi_predict(sesameDataGet('HM450.1.TCGA.PAAD')$betas, model, lift_over=TRUE)
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