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 1.1.0

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

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Contents

`cmi_checkVersion` *Check CytoMethIC versions*

Description

print package verison of cytomethic and depended packages to help troubleshoot installation issues.

Usage

```
cmi_checkVersion()
```

Value

print the versions of cytomethic and dependencies

Examples

```
cmi_checkVersion()
```

`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

```
print(cmi_models[,c("EHID","Title")])
```

cmi_predict *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

```
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

```
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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