Package ‘CytoMethIC’

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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, 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
git_last_commit  b0e6b16
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cmi_models

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  cmi_checkVersion   Check CytoMethIC versions

Description

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

Usage

  cmi_checkVersion()

Value

  print the versions of cytomethic and dependencies

Examples

  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

  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.

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)
#
```
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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