Package ‘CytoMethIC’

August 15, 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

**git_last_commit**  b0e6b16

**git_last_commit_date**  2024-04-30

**Repository**  Bioconductor 3.19

**Date/Publication**  2024-08-15
**cmi_checkVersion**

**Description**

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

**Usage**

```r
cmi_checkVersion()
```

**Value**

print the versions of cytomethic and dependencies

**Examples**

```r
cmi_checkVersion()
```

---

**cmi_models**

**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.

**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)
Index

cmi_checkVersion, 2
cmi_models, 2
cmi_predict, 3