

# Package ‘CytoMethIC’

June 25, 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

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**Repository** Bioconductor 3.19

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|                  |                                  |
|------------------|----------------------------------|
| cmi_checkVersion | <i>Check CytoMethIC versions</i> |
|------------------|----------------------------------|

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### 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 | <i>Master data frame for all model objects</i> |
|------------|--|

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### 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 | <i>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.</i> |
|-------------|---|

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### 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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