

# Package ‘EpiSemble’

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**Type** Package

**Title** Ensemble Based Machine Learning Approach for Predicting Methylation States

**Version** 0.1.1

**Author** Dipro Sinha [aut, cre],  
Sunil Archak [aut],  
Dwijesh Chandra Mishra [aut],  
Tanwy Dasmandal [aut],  
Md Yeasin [aut]

**Maintainer** Dipro Sinha <diprosinha@gmail.com>

**Description** DNA methylation (6mA) is a major epigenetic process by which alteration in gene expression took place without changing the DNA sequence. Predicting these sites in-vitro is laborious, time consuming as well as costly. This 'EpiSemble' package is an in-silico pipeline for predicting DNA sequences containing the 6mA sites. It uses an ensemble-based machine learning approach by combining Support Vector Machine (SVM), Random Forest (RF) and Gradient Boosting approach to predict the sequences with 6mA sites in it. This package has been developed by using the concept of Chen et al. (2019) <[doi:10.1093/bioinformatics/btz015](https://doi.org/10.1093/bioinformatics/btz015)>.

**License** GPL-3

**Encoding** UTF-8

**RoxygenNote** 7.2.0

**Imports** stats, devtools, tidyverse, seqinr, Biostrings,  
splitstackshape, entropy, party, stringr, tibble, doParallel,  
parallel, e1071, caret, randomForest, gbm, foreach, ftrCOOL,  
iterators

**NeedsCompilation** no

**Repository** CRAN

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epiPred	<i>Epigenetic Modification Prediction</i>
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**Description**

Predicting sequences with 6mA sites.

**Usage**

```
epiPred(FastaData, Species)
```

**Arguments**

FastaData	Sequence file (.fasta format)
Species	Model organism

**Value**

MethStatus: Sequences with their methylation state (methylated or non-methylated)

**References**

Chen, W., Lv, H., Nie, F., & Lin, H. (2019). i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. *Bioinformatics*, 35(16), 2796-2800.

**Examples**

```
library(EpiSemble)
data<-system.file("exdata/test.fasta", package = "EpiSemble")
pred<-epiPred(FastaData=data, Species="Rice")
```

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ImpFeatures	<i>Important Features</i>
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**Description**

Find out the most suitable features for predicting sequences with 6mA sites.

**Usage**

```
ImpFeatures(Fastafilename, Species)
```

**Arguments**

Fastafilename	Sequence file in .fasta format
Species	Model organism

**Value**

test\_data\_input: A matrix containing important features for prediction

**References**

Chen, W., Lv, H., Nie, F., & Lin, H. (2019). i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. *Bioinformatics*, 35(16), 2796-2800.

**Examples**

```
library(EpiSemble)
data<-system.file("exdata/test.fasta", package = "EpiSemble")
imp<-ImpFeatures(Fastafilename=data, Species="Rice")
```

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