

# Package: GB5mcPred (via r-universe)

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**Type** Package

**Title** Gradient Boosting Algorithm for Predicting Methylation States

**Version** 0.1.0

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**Description** DNA methylation of 5-methylcytosine (5mC) is the result of a multi-step, enzyme-dependent process. Predicting these sites in-vitro is laborious, time consuming as well as costly. This 'Gb5mC-Pred' package is an in-silico pipeline for predicting DNA sequences containing the 5mC sites. It uses a machine learning approach which uses Stochastic Gradient Boosting approach for prediction of the sequences with 5mC sites. This package has been developed by using the concept of Navarez and Roxas (2022) <[doi:10.1109/TCBB.2021.3082184](https://doi.org/10.1109/TCBB.2021.3082184)>.

**License** GPL-3

**Encoding** UTF-8

**RoxygenNote** 7.2.1

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

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**NeedsCompilation** no

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**Repository** <https://diprosinha.r-universe.dev>

**RemoteUrl** <https://github.com/cran/GB5mcPred>

**RemoteRef** HEAD

**RemoteSha** 0cf9b9499e07b091b61cdee2230d9acfb2bb1ec0

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### Description

Prediction of sequences with 5mc sites.

### Usage

```
Pred5mc(Fastafile)
```

### Arguments

Fastafile      Sequence file (.fasta format)

### 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(GB5mcPred)
data<-system.file("exdata/test.fasta", package = "GB5mcPred")
pred<-Pred5mc(Fastafile=data)
```

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