

# Package ‘OpEnCAMEO’

July 30, 2026

**Type** Package

**Title** Optimized Ensemble Predictor for 'C' and 'A' Methylation in Organism

**Version** 0.1.1

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**Description** DNA methylation is an important epigenetic process that regulates gene activity through chemical modifications of DNA without changing its sequence. 'OpEnCAMEO' is a organism based ensemble model for prediction of 4mC, 6mA and No methylation sites directly from DNA sequences. It combines multiple machine learning algorithms trained on Bacteria (Escherichia coli), Fungi (Saccharomyces cerevisiae) and Nematode (Caenorhabditis elegans) as reference models to deliver accurate predictions. This methodology is being inspired by the ensemble algorithm for methylation prediction developed by Sinha et al. (2025) <[doi:10.1101/2025.11.10.687509](https://doi.org/10.1101/2025.11.10.687509)>.

**Imports** Biostrings, seqinr, stringr, tibble, entropy, ftrCOOL, stats, elmNNRcpp

**Suggests** caret, kernlab, ranger, xgboost, gbm

**Encoding** UTF-8

**License** GPL-3

**Config/roxygen2/version** 8.0.0

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2026-07-30 17:40:22 UTC

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| Bacteria_MethPred | <i>DNA Methylation Prediction in Bacteria</i> |
|-------------------|-----------------------------------------------|

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**Description**

Predicting sequences with DNA methylation sites like 4mC or 6mA based on Escherichia coli as reference model.

**Usage**

```
Bacteria_MethPred(fasta_file_path, Reference = "E.Coli")
```

**Arguments**

- fasta\_file\_path

Sequence file (.fasta format)
- Reference

Escherichia coli as Reference Model for Bacteria

**Value**

Methylation Status: Sequences with their probable DNA methylation state such as 4mC, 6mA or Non Methhylated.

**References**

Ly, H., Dao, F. Y., Zhang, D., Guan, Z. X., Yang, H., Su, W., ... & Lin, H. (2020). iDNA-MS: an integrated computational tool for detecting DNA modification sites in multiple genomes. Iscience, 23(4).

**Examples**

```
library(OpEnCAME0)
data<-system.file("exdata/test.fasta", package = "OpEnCAME0")
pred<-Bacteria_MethPred(fasta_file_path=data, Reference="E.Coli")
```

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Fungi\_MethPred*DNA Methylation Prediction in Fungi*

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**Description**

Predicting sequences with DNA methylation sites like 4mC or 6mA based on *Saccharomyces cerevisiae* as reference model.

**Usage**

```
Fungi_MethPred(fasta_file_path, Reference = "S.cerevisiae")
```

**Arguments**

fasta\_file\_path

Sequence file (.fasta format)

Reference

*Saccharomyces cerevisiae* as Reference Model for Fungi

**Value**

Methylation Status: Sequences with their probable DNA methylation state such as 4mC, 6mA or Non Methhyllated.

**References**

Lv, H., Dao, F. Y., Zhang, D., Guan, Z. X., Yang, H., Su, W., ... & Lin, H. (2020). iDNA-MS: an integrated computational tool for detecting DNA modification sites in multiple genomes. *Iscience*, 23(4).

**Examples**

```
library(OpEnCAME0)
data<-system.file("exdata/test.fasta", package = "OpEnCAME0")
pred<-Fungi_MethPred(fasta_file_path=data, Reference="S.cerevisiae")
```

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Nematode\_MethPred*DNA Methylation Prediction in Nematode*

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**Description**

Predicting sequences with DNA methylation sites like 4mC or 6mA based on *Caenorhabditis elegans* as reference model.

**Usage**

```
Nematode_MethPred(fasta_file_path, Reference = "C.elegans")
```

**Arguments**

|                 |                                                         |
|-----------------|---------------------------------------------------------|
| fasta_file_path | Sequence file (.fasta format)                           |
| Reference       | Caenorhabditis elegans as Reference Model for Nematodes |

**Value**

Methylation Status: Sequences with their probable DNA methylation state such as 4mC, 6mA or Non Methhylyated.

**References**

Lv, H., Dao, F. Y., Zhang, D., Guan, Z. X., Yang, H., Su, W., ... & Lin, H. (2020). iDNA-MS: an integrated computational tool for detecting DNA modification sites in multiple genomes. *Iscience*, 23(4).

**Examples**

```
library(OpEnCAME0)
data<-system.file("exdata/test.fasta", package = "OpEnCAME0")
pred<-Nematode_MethPred(fasta_file_path=data, Reference="C.elegans")
```

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