Package 'OpEnHiMR'

July 21, 2025

Type Package

Title Optimization Based Ensemble Model for Prediction of Histone
Modifications in Rice

Version 0.1.1

Description The comprehensive knowledge of epigenetic modifications in plants, encompassing histone modifications in regulating gene expression, is not completely ingrained. It is noteworthy that histone deacetylation and histone H3 lysine 27 trimethylation (H3K27me3) play a role in repressing transcription in eukaryotes. In contrast, histone acetylation (H3K9ac) and H3K4me3 have been inevitably linked to the stimulation of gene expression, which significantly influences plant development and plays a role in plant responses to biotic and abiotic stresses. To our knowledge this the first multiclass classifier for predicting histone modification in plants. <doi:10.1186/s12864-019-5489-4>.

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Encoding UTF-8

Imports Biostrings, devtools, tidyverse, seqinr, splitstackshape,
entropy, party, e1071, caret, randomForest, gbm, stats,
stringr, ftrCOOL, dplyr, RCurl

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

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pred_hmc *Prediction of Histone Modification for Multiclass Data*

Description

Prediction of H3K27me3, H3K9ac and H3K4me3 modification in rice.

Usage

```
pred_hmc(fasta_file_path)
```

Arguments

fasta_file_path

Sequence file path (.fasta format)

Value

Modications: sequences with their modifications (H3K27me3, H3K9ac and H3K4me3) or no modification.

References

Yin, Q., Wu, M., Liu, Q. et al. DeepHistone: a deep learning approach to predicting histone modifications. BMC Genomics 20 (Suppl 2), 193 (2019).

Examples

```
example_path <- system.file("exdata/test.fasta", package = "OpEnHiMR")
pred <- pred_hmc(fasta_file_path = example_path)
```

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