Package: EpiSemble (via r-universe)

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Type Package

Title Ensemble Based Machine Learning Approach for Predicting Methylation States

Version 0.1.1

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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>.

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

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Repository https://diprosinha.r-universe.dev

RemoteUrl https://github.com/cran/EpiSemble

RemoteRef HEAD

RemoteSha 66778bf71277d0ae03b5f447e0ba1566ffc4d14e

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epiPred   *Epigenetic Modification Prediction*

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")
```

ImpFeatures   *Important Features*

Description

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

Usage

```
ImpFeatures(Fastafile,Species)
```

Arguments

Fastafile   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(Fastafile=data, Species="Rice")
```

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