

Package ‘Mestimate’

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Type Package

Title Estimate M of fish using boosting trees

Version 0.1.0

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Description

This package is used for estimating M of fish based on life history parameters, using the tree-based ensemble methods.

Use four spaces when indenting paragraphs within the Description.

Imports caret, gbm, ggplot2, reshape2, cowplot

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Encoding UTF-8

LazyData true

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Mestimate	<i>Estimate M of fish using boosting trees</i>
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Description

Tree-based ensemble learnig methods can significantly improve the prediction performance of fish mortality. This package provides three optimal boosting trees models according to the life history parameters used for M estimate. People are not always able to get all the fish life history parameters. We recommend using the BRT1 model when only the parameter tmax is available, and BRT2 model when only the parameters K and Linf are available. When all life parameters are available, we recommend using the BRT3 model, which performs best in M estimation. An example data with 3 Chanondrichthyes fish and 3 Osteichthyes fish is given in the package. See also "Examples" to use this package. class=1, represents Chondrichthyes fish, and class=0 represents Osteichthyes fish.

Usage

```
Mestimate(mydata,method)
```

Arguments

mydata	Dataframe containing the life history parameters
method	BRT1,BRT2 or BRT3

Author(s)

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Examples

```
library(Mestimate)
data(mydata)
K=mydata$K
Linf=mydata$Linf
tmax=mydata$tmax
Class=as.factor(mydata$class)
mydata1=data.frame(tmax,Class)
mydata2=data.frame(K,Linf,Class)
mydata3=data.frame(K,Linf,tmax,Class)
predictedM1=Mestimate(mydata1,method="BRT1")
predictedM2=Mestimate(mydata2,method="BRT2")
predictedM3=Mestimate(mydata3,method="BRT3")
```

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