# 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

**License** GPL (>= 2.0)

**Encoding** UTF-8

**LazyData** true

## R topics documented:

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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.

### 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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