# Package 'MSML'

## December 13, 2023

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Title Model Selection Based on Machine Learning (ML)
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<b>Description</b> Models evaluation based on a modified version of the recursive feature elimination algorithm. This package is designed to determine the optimal model(s) by leveraging all available features. (Olkin and Finn, 1995) <doi:10.1037 0033-2909.118.1.155="">, (De-Long et al., 1998) <doi:10.2307 2531595="">, (Guyon et al., 2002) <doi:10.1023 a:1012487302797=""> and (Momin et al., 2002) <doi:10.1023 a:1012487302797=""></doi:10.1023></doi:10.1023></doi:10.2307></doi:10.1037>
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## Description

data\_test

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A dataset containing 7 sets of PRSs for test dataset and target phenotype

7 sets of PRSs for test dataset and target phenotype

2 data\_train

## Usage

```
data_test
```

#### **Format**

A data frame for test dataset:

V1 PRS1, for bin1

V2 PRS2, for bin1

V3 PRS3, for bin1

V4 PRS4, for bin1

V5 PRS5, for bin1

V6 PRS6, for bin1

V7 PRS7, for bin1

phenotype Target Phenotype, value

data\_train

7 sets of PRSs for training data set and target phenotype

## Description

A dataset containing 7 sets of PRSs for training data set and target phenotype

## Usage

```
data_train
```

#### **Format**

A data frame for training dataset:

V1 PRS1, for bin1

V2 PRS2, for bin1

V3 PRS3, for bin1

V4 PRS4, for bin1

V5 PRS5, for bin1

V6 PRS6, for bin1

V7 PRS7, for bin1

phenotype Target Phenotype, value

data\_valid 3

data\_valid

7 sets of PRSs for validation dataset and target phenotype

#### **Description**

A dataset containing 7 sets of PRSs for validation dataset and target phenotype

#### Usage

```
data_valid
```

#### **Format**

A data frame for validation dataset:

V1 PRS1, for bin1

V2 PRS2, for bin1

V3 PRS3, for bin1

V4 PRS4, for bin1

V5 PRS5, for bin1

V6 PRS6, for bin1

V7 PRS7, for bin1

phenotype Target Phenotype, value

model\_configuration

 $model\_configuration\ function$ 

## Description

This function will generate features (e.g. PRSs) based on all possible combinations of model. The total number of models required to explore the combinations of these 'n' features can be calculated by summing the combinations for each possible number of features, ranging from 1 to 'n' (C(n,i)). where C(n,k) represents the binomial coefficient or "n choose k," with n denoting the total number of features and k indicating the number of features to include in each model.

#### Usage

```
model_configuration(data_train, data_valid, mv)
```

## **Arguments**

data\_train This is the matrix for the training dataset
data\_valid This is the matrix for the validation dataset

mv The total number of columns in data\_train/data\_valid

4 model\_evaluation

#### Value

This function will generate all possible model outcomes for validation and test dataset

#### **Examples**

```
## Not run:
data_train <- data_train
data_valid <- data_valid
mv=8
out=model_configuration(data_train,data_valid,mv)
#This process will produce predicted values for the validation datasets,
#corresponding to each model configuration trained on the training dataset.
#The outcome of this function will yield variables named 'predict_validation'
#and 'total_model_configurations.
#To print the outcomes run out$predict_validation and out$total_model_configurations.
#For details (see https://github.com/mommy003/MSML).
## End(Not run)</pre>
```

## Description

model\_evaluation

This function will identify the best model in the validation and test dataset.

model\_evaluation function

## Usage

```
model_evaluation(dat, mv, tn, prev, pthreshold = 0.05, method = "R2ROC")
```

### Arguments

mv This is the matrix for all the combinations of the model
to The total number of columns in data\_train/data\_valid
to The total no of best models to be identified

prev The prevalence of disease in the data

pthreshold The P value threshold for the significance level method The methods to be used to evaluate models

## Value

This function will generate all possible model outcomes for validation and test dataset

## **Examples**

```
## Not run:
dat <- predict_validation
mv=8
tn=15
prev=0.047
model_evaluation(dat,mv,tn,prev)</pre>
```

```
#This process will generate three distinct output files in the working directory
#named evaluation1.out, evaluation2.out and evaluation3.out.
#For details (see https://github.com/mommy003/MSML).
## End(Not run)
```

predict\_validation target phenotype and 127 sets of model configurations based on validation dataset

#### **Description**

A dataset containing target phenotype and 127 sets of model configurations based on validation dataset

#### Usage

```
predict_validation
```

#### **Format**

A data frame for models test:

- V1 target, phenotype
- V2 model1, based on configurations
- V3 model2, based on configurations
- V4 model3, based on configurations
- V5 model4, based on configurations
- V6 model5, based on configurations
- V7 model6, based on configurations
- V8 model7, based on configurations
- **V9** model8, based on configurations
- V10 model9, based on configurations
- V11 model10, based on configurations
- V12 model11, based on configurations
- V13 model12, based on configurations
- V14 model13, based on configurations
- V15 model14, based on configurations
- V16 model15, based on configurations
- V17 model16, based on configurations
- V18 model17, based on configurations
- V19 model18, based on configurations
- **V20** model19, based on configurations
- V21 model10, based on configurationsV22 model21, based on configurations

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- V26 model25, based on configurations
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- V28 model27, based on configurations
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