

Package ‘MBMethPred’

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Type Package

Title Medulloblastoma Subgroups Prediction

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Description Utilizing a combination of machine learning models (Random Forest, Naive Bayes, K-Nearest Neighbor, Support Vector Machines, Extreme Gradient Boosting, and Linear Discriminant Analysis) and a deep Artificial Neural Network model, 'MBMethPred' can predict medulloblastoma subgroups, including wingless (WNT), sonic hedgehog (SHH), Group 3, and Group 4 from DNA methylation beta values. See Sharif Rahmani E, Lawarde A, Lingasamy P, Moreno SV, Salumets A and Modhukur V (2023), MBMethPred: a computational framework for the accurate classification of childhood medulloblastoma subgroups using data integration and AI-based approaches. Front. Genet. 14:1233657. <[doi:10.3389/fgene.2023.1233657](https://doi.org/10.3389/fgene.2023.1233657)> for more details.

URL <https://github.com/sharifrahmanie/MBMethPred>

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BugReports <https://github.com/sharifrahmanie/MBMethPred/issues>

License GPL

Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.2.3

Imports stringr, ggplot2, parallel, caTools, caret, keras, MASS, Rtsne, SNFtool, class, dplyr, e1071, pROC, randomForest, readr, reshape2, reticulate, rgl, tensorflow, xgboost

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Contents

BoxPlot	2
ConfusionMatrix	3
Data1	4
Data2	4
Data3	5
KNearestNeighborModel	5
LinearDiscriminantAnalysisModel	6
ModelMetrics	7
NaiveBayesModel	7
NeuralNetworkModel	8
NewDataPredictionResult	9
RandomForestModel	9
ReadMethylFile	10
ReadSNFData	11
RLabels	11
SimilarityNetworkFusion	12
SupportVectorMachineModel	13
TSNEPlot	14
XGBoostModel	14
Index	16

BoxPlot	<i>Box plot</i>
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Description

A function to draw a box plot for the DNA methylation dataset.

Usage

BoxPlot(File, Projname = NULL)

Arguments

File The output of ReadMethylFile function.
 Projname A name used to name the plot. The default is null.

Value

A ggplot2 object

Examples

```
data <- Data2[1:10,]
data <- cbind(rownames(data), data)
colnames(data)[1] <- "ID"
BoxPlot(File = data)
```

ConfusionMatrix	<i>Confusion matrix</i>
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Description

A function to calculate the confusion matrix of the machine and deep learning models. It outputs Accuracy, Precision, Sensitivity, F1-Score, Specificity, and AUC_average.

Usage

```
ConfusionMatrix(y_true, y_pred)
```

Arguments

y_true True labels
 y_pred Predicted labels

Value

A data frame

Examples

```
set.seed(1234)
data <- Data1[1:10,]
data$subgroup <- factor(data$subgroup)
fac <- ncol(data)
split <- caTools::sample.split(data[, fac], SplitRatio = 0.8)
training_set <- subset(data, split == TRUE)
test_set <- subset(data, split == FALSE)
rf <- randomForest::randomForest(x = training_set[-fac],
                                  y = training_set[, fac],
                                  ntree = 10)
```

```
y_pred <- predict(rf, newdata = test_set[-fac])
ConfusionMatrix(y_true = test_set[, fac],
                 y_pred = y_pred)
```

Data1

*Training data***Description**

Data1 is a medulloblastoma DNA methylation beta values from a GEO series (GSE85212) and focuses on 399 as the most important probes. This dataset is used to train and test the machine and deep learning models.

Value

A data frame

Source

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE85212>

Examples

```
data(Data1)
```

Data2

*Data2***Description**

Data2 is a medulloblastoma DNA methylation beta values (GSE85212, 50 samples) including 10000 most variable probes used for similarity network fusion.

Value

A data frame

Source

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE85212>

References

Cavalli FMG, Remke M, Rampasek L, Peacock J et al. Intertumoral Heterogeneity within Medulloblastoma Subgroups. Cancer Cell 2017 Jun 12;31(6):737-754.e6. PMID: 28609654

Examples

```
data(Data2)
```

Data3

Data3

Description

Data3 is an gene expression dataset from primary medulloblastoma samples (GSE85217, 50 samples) used for similarity network fusion.

Value

A data frame

Source

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE85217>

References

Cavalli FMG, Remke M, Rampasek L, Peacock J et al. Intertumoral Heterogeneity within Medulloblastoma Subgroups. Cancer Cell 2017 Jun 12;31(6):737-754.e6. PMID: 28609654

Examples

```
data(Data3)
```

KNearestNeighborModel *K nearest neighbor model*

Description

A function to train a K nearest neighbor model to classify medulloblastoma subgroups using DNA methylation beta values (Illumina Infinium HumanMethylation450). Prediction is followed by training if new data is provided.

Arguments

SplitRatio	Train and test split ratio. A value greater or equal to zero and less than one.
CV	The number of folds for cross-validation. It should be greater than one.
K	The number of nearest neighbors.
NCores	The number of cores for parallel computing.
NewData	A methylation beta values input from the ReadMethylFile function.

Value

A list

```
set.seed(111)
knn <- KNearestNeighborModel(SplitRatio = 0.8,
                             CV = 3,
                             K = 3,
                             NCores = 1,
                             NewData = NULL)
```

Linear discriminant analysis model

A function to train a linear discriminant analysis model to classify medulloblastoma subgroups using the DNA methylation beta values (Illumina Infinium HumanMethylation450). Prediction is followed by training if new data is provided.

SplitRatio	Train and test split ratio. A value greater or equal than zero and less than one.
CV	The number of folds for cross validation. It should be greater than one.
NCores	The number of cores for parallel computing.
NewData	A methylation beta values input from the ReadMethylFile function.

A list

```
set.seed(123)
lda <- LinearDiscriminantAnalysisModel(SplitRatio = 0.8,
                                       CV = 2,
                                       NCores = 1,
                                       NewData = NULL)
```

ModelMetrics	<i>Model metrics</i>
--------------	----------------------

Description

A function to extract the confusion matrix information.

Usage

```
ModelMetrics(Model)
```

Arguments

Model	A trained model.
-------	------------------

Value

A list

Examples

```
xgboost <- XGBoostModel(SplitRatio = 0.2,  
                        CV = 2,  
                        NCores = 1,  
                        NewData = NULL)  
ModelMetrics(Model = xgboost)
```

NaiveBayesModel	<i>Naive bayes model</i>
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Description

A function to train a Naive Bayes model to classify medulloblastoma subgroups using DNA methylation beta values (Illumina Infinium HumanMethylation450). Prediction is followed by training if new data is provided.

Arguments

SplitRatio	Train and test split ratio. A value greater or equal to zero and less than one.
CV	The number of folds for cross-validation. It should be greater than one.
Threshold	The threshold for deciding class probability. A value greater or equal to zero and less than one.
NCores	The number of cores for parallel computing.
NewData	A methylation beta values input from the ReadMethylFile function.

Value

A list

Examples

```
set.seed(123)
nb <- NaiveBayesModel(SplitRatio = 0.8,
                      CV = 2,
                      Threshold = 0.8,
                      NCores = 1,
                      NewData = NULL)
```

NeuralNetworkModel	<i>Artificial neural network model</i>
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Description

A function to train an artificial neural network model to classify medulloblastoma subgroups using DNA methylation beta values (Illumina Infinium HumanMethylation450). Prediction is followed by training if new data is provided.

Arguments

Epochs	The number of epochs.
NewData	A methylation beta values input from the ReadMethylFile function.
InstallTensorFlow	Logical. Running this function for the first time, you need to install TensorFlow library (V 2.10-cpu). Default is TRUE.

Value

A list

Examples

```
## Not run:
set.seed(1234)
ann <- NeuralNetworkModel(Epochs = 100,
                          NewData = NULL,
                          InstallTensorFlow = TRUE)

## End(Not run)
```

`NewDataPredictionResult`*New data prediction result*

Description

A function to output the predicted medulloblastoma subgroups by trained models.

Usage

```
NewDataPredictionResult(Model)
```

Arguments

`Model` A trained model

Value

A data frame

Examples

```
set.seed(10)
fac <- ncol(Data1)
NewData <- sample(data.frame(t(Data1[, -fac])), 10)
NewData <- cbind(rownames(NewData), NewData)
colnames(NewData)[1] <- "ID"
xgboost <- XGBoostModel(SplitRatio = 0.2,
                        CV = 2,
                        NCores = 1,
                        NewData = NewData)
NewDataPredictionResult(Model = xgboost)
```

`RandomForestModel`*Random forest model*

Description

A function to train a random forest model to classify medulloblastoma subgroups using DNA methylation beta values (Illumina Infinium HumanMethylation450). Prediction is followed by training if new data is provided.

Arguments

SplitRatio	Train and test split ratio. A value greater or equal to zero and less than one.
CV	The number of folds for cross-validation. It should be greater than one.
NTree	The number of trees to be grown.
NCores	The number of cores for parallel computing.
NewData	A methylation beta values input from the ReadMethylFile function.

Value

A list

Examples

```
set.seed(21)
rf <- RandomForestModel(SplitRatio = 0.8,
                        CV = 3,
                        NTree = 10,
                        NCores = 1,
                        NewData = NULL)
```

ReadMethylFile	<i>Input file for prediction</i>
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Description

A function to read DNA methylation files. It can be used as the new data for prediction by every model.

Usage

```
ReadMethylFile(File)
```

Arguments

File	A data frame with tsv or csv file extension. The first column of the data frame is the CpG methylation probe that starts with cg characters and is followed by a number (e.g., cg100091). Other columns are samples with methylation beta values. All columns in the data frame should have a name.
------	---

Value

A data frame

Examples

```
## Not run:
methyl <- ReadMethylFile(File = "file.csv")

## End(Not run)
```

ReadSNFData*Input file for similarity network fusion (SNF)*

Description

A function to read user-provided file feeding into the SNF function (from the SNFtools package).

Usage

```
ReadSNFData(File)
```

Arguments

File	A data frame with tsv or csv file extension. The first column of the data frame is the CpG methylation probe that starts with cg characters and is followed by a number (e.g., cg100091). Other columns are samples with methylation beta values. All columns in the data frame should have a name.
------	---

Value

A data frame

Examples

```
## Not run:  
data <- ReadSNFData(File = "file.csv")  
  
## End(Not run)
```

RLabels*RLabels*

Description

The actual labels from the medulloblastoma DNA methylation beta values (GSE85212, 50 samples) that was used for similarity network fusion.

Value

Factor

Source

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE85212>

References

Cavalli FMG, Remke M, Rampasek L, Peacock J et al. Intertumoral Heterogeneity within Medulloblastoma Subgroups. *Cancer Cell* 2017 Jun 12;31(6):737-754.e6. PMID: 28609654

Examples

```
data(RLabels)
```

```
SimilarityNetworkFusion
```

```
Similarity network fusion (SNF)
```

Description

A function to perform SNF function (from SNFtool package) and output clusters.

Usage

```
SimilarityNetworkFusion(  
  Files = NULL,  
  NNeighbors,  
  Sigma,  
  NClusters,  
  CLabels = NULL,  
  RLabels = NULL,  
  Niterations  
)
```

Arguments

Files	A list of data frames created using the ReadSNFData function or matrices.
NNeighbors	The number of nearest neighbors.
Sigma	The variance for local model.
NClusters	The number of clusters.
CLabels	A string vector to name the clusters. Optional.
RLabels	The actual label of samples to calculate the Normalized Mutual Information (NMI) score. Optional.
Niterations	The number of iterations for the diffusion process.

Value

Factor

Examples

```

data(RLabels) # Real labels
data(Data2) # Methylation
data(Data3) # Gene expression
snf <- SimilarityNetworkFusion(Files = list(Data2, Data3),
                              NNeighbors = 13,
                              Sigma = 0.75,
                              NClusters = 4,
                              CLabels = c("Group4", "SHH", "WNT", "Group3"),
                              RLabels = RLabels,
                              Niterations = 10)

snf

```

SupportVectorMachineModel

Support vector machine model

Description

A function to train a support vector machine model to classify medulloblastoma subgroups using DNA methylation beta values (Illumina Infinium HumanMethylation450). Prediction is followed by training if new data is provided.

Arguments

SplitRatio	Train and test split ratio. A value greater or equal to zero and less than one.
CV	The number of folds for cross-validation. It should be greater than one.
NCores	The number of cores for parallel computing.
NewData	A methylation beta values input from the ReadMethylFile function.

Value

A list

Examples

```

set.seed(56)
svm <- SupportVectorMachineModel(SplitRatio = 0.8,
                                CV = 3,
                                NCores = 1,
                                NewData = NULL)

```

TSNEPlot	<i>t-SNE 3D plot</i>
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Description

A function to draw a 3D t-SNE plot for DNA methylation beta values using the K-means clustering technique.

Usage

```
TSNEPlot(File, NCluster = 4)
```

Arguments

File	The output of ReadMethylFile function.
NCluster	The number of cluster.

Value

Objects of rgl

Examples

```
set.seed(123)
data <- Data2[1:100,]
data <- data.frame(t(data))
data <- cbind(rownames(data), data)
colnames(data)[1] <- "ID"
TSNEPlot(File = data, NCluster = 4)
```

XGBoostModel	<i>XGBoost model</i>
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Description

A function to train an XGBoost model to classify medulloblastoma subgroups using DNA methylation beta values (Illumina Infinium HumanMethylation450). Prediction is followed by training if new data is provided.

Arguments

SplitRatio	Train and test split ratio. A value greater or equal to zero and less than one.
CV	The number of folds for cross-validation. It should be greater than one.
NCores	The number of cores for parallel computing.
NewData	A methylation beta values input from the ReadMethylFile function.

Value

A list

Examples

```
set.seed(123)
xgboost <- XGBoostModel(SplitRatio = 0.2,
                        CV = 2,
                        NCores = 1,
                        NewData = NULL)
```

Index

BoxPlot, [2](#)

ConfusionMatrix, [3](#)

Data1, [4](#)

Data2, [4](#)

Data3, [5](#)

dataset1 (Data1), [4](#)

dataset2 (Data2), [4](#)

dataset3 (Data3), [5](#)

KNearestNeighborModel, [5](#)

LinearDiscriminantAnalysisModel, [6](#)

ModelMetrics, [7](#)

NaiveBayesModel, [7](#)

NeuralNetworkModel, [8](#)

NewDataPredictionResult, [9](#)

RandomForestModel, [9](#)

ReadMethylFile, [10](#)

ReadSNFData, [11](#)

RLabels, [11](#)

SimilarityNetworkFusion, [12](#)

Subgroups (RLabels), [11](#)

SupportVectorMachineModel, [13](#)

TSNEPlot, [14](#)

XGBoostModel, [14](#)