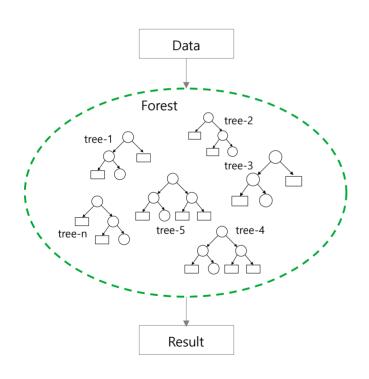


[MXML-8] Machine Learning / Random Forest





8. Random Forest

- Boostrap Aggregation (Bagging)
- Out-Of-Bag (OOB) score (error rate)
- Missing value, Outlier Detection using Proximity Matrix

www.youtube.com/@meanxai



	1. Overview of Random Forest		6. Missing value
	2. Boostrap Aggregation (Bagging)		- Proximity Matrix
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	- row (data instance) sub sampling		- Missing value imputation : test data
	- column (feature) sub sampling [MXML-8-05]		- Coding practice: Implementing missing value imputation
(4. Implementing Random Forest		7. Outlier Detection
[MXML-8-02] {	- Implementing Random Forest from scratch	[MXML-8-06] <	- Outlier detection using Proximity Matrix
	- scikit-learn's DecisionTreeClassifier and		- Coding practice: Implementing outlier detection
	Random Forest Classifier.		- Interpretation of the outlier detection result
	5. Out-Of-Bag (OOB) score (error rate)		8. Isolation Forest
[MXML-8-03]	- OOB details with example		- Outlier detection using Binary Search Tree (BST)
	- Coding practice: Implementing OOB	[MXML-8-07] <	- Coding practice: Implementing Isolation Forest
[MXML-8-01] 3. Data sub sampling - row (data instance) sub sampling - column (feature) sub sampling 4. Implementing Random Forest - Implementing Random Forest from scratch - scikit-learn's DecisionTreeClassifier and RandomForestClassifier. 5. Out-Of-Bag (OOB) score (error rate) - OOB details with example		- Interpretation of the outlier detection result	

MX-AI

* Reference [3]

Random Forest: Overview

• The first algorithm for random decision forests was created in 1995 by Tin Kam Ho. An extension of the algorithm was developed by Leo Breiman and Adele Cutler [Wikipedia]. Random Forest is a type of bagging ensemble that has many advantages, including less variance, less overfitting, and better overall performance, etc. I referred to the following two documents [1], [2], and a video [3].

* Reference [2]

* Reference [1] RANDOM FORESTS

Leo Breiman Statistics Department University of California Berkeley, CA 94720, January 2001

Abstract

Random forests are a combination of tree predictors such that each tree depends on the values of a random vector sampled independently and with the same distribution for all trees in the forest. The generalization error for forests converges a.s. to a limit as the number of trees in the forest becomes large. The generalization error of a forest of tree classifiers depends on the strength of the individual trees in the forest and the correlation between them. Using a random selection of features to split each node yields error rates that compare favorably to Adaboost (Freund and Schapire[1996]), but are more robust with respect to noise. Internal estimates monitor error, strength, and correlation and these are used to show the response to increasing the number of features used in the splitting. Internal estimates are also used to measure variable importance. These ideas are also applicable to regression

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- V- . . t. . l-

StatQuest: Random Forests Part 1: Building, Using and Evaluating

StatQuest: Random Forests Part 2: Missing data and clustering



Youtube:

3

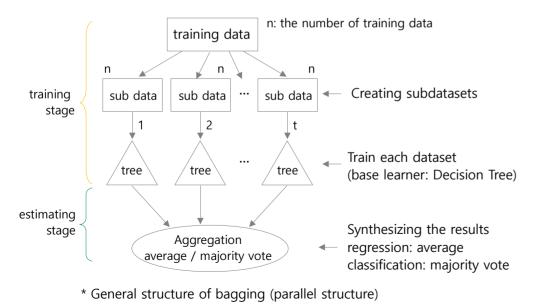
Missing values for the training set Missing values for the test set

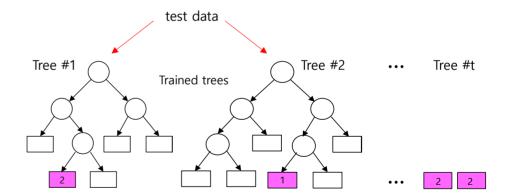
[MXML-8-01] Machine Learning / 8. Random Forest - Bagging



Random Forest : Bootstrap Aggregation (Bagging)

- Random Forest uses multiple Decision Trees. Each tree is then built based on randomly and uniformly drawn samples with replacement for the training data.
- Subdatasets are created from samples extracted from the training data. And the size of each subdataset is equal to the size of the training data.
- In the figure below, the number of subdatasets and the number of trees is t, and the number of the training data is n.
- Samples are drawn from rows and columns of the training data. Column sampling is the random selection of features. This results in lower correlation between trees.
- Each tree is grown to the largest extent possible. There is no pruning. (Reference [2]). Random Forest uses multiple deep decision trees, but it is less prone to overfitting because it uses sample data, and average the results of the trees. This is why pruning is not necessary.
- After training, test data is inserted into each tree and the results are synthesized. For regression, it is estimated as the average of each tree's results, and for classification, it is estimated as the most frequent class of each tree's results. (majority voting).





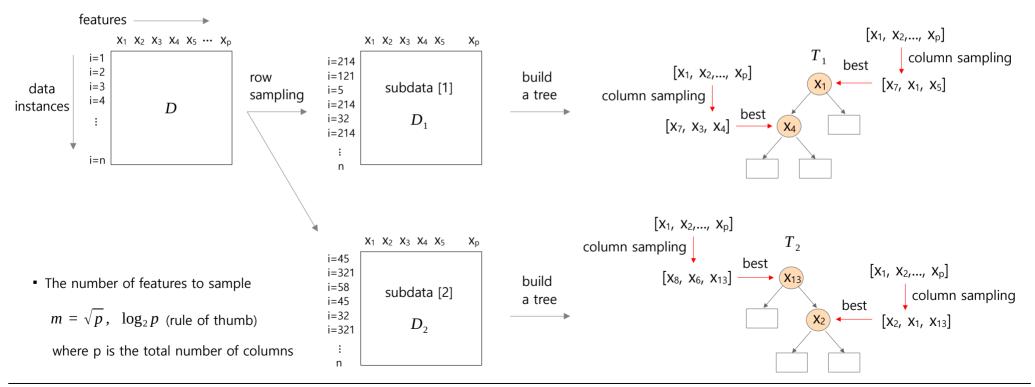
- If you insert one test data point into T trained trees, you can get t results.
- In classification, if the results are [2, 1, 2, 2, ...] as shown above, the class of the test data point is assumed to be 2 because 2 is the majority.
- In regression, it is estimated as the average value of the results.

[MXML-8-01] Machine Learning / 8. Random Forest - Sampling



Data Sampling: row (data instances) and column (features) sampling

- The training data (D) is sampled row-wise and column-wise. The reason for sampling is to reduce the correlation between each tree, thus reducing the estimation variance.
- Row sampling is done with replacement, and column sampling is done without replacement, but after sampling, all are replaced for the next sampling. That is, column sampling for node splitting is done without replacement, but with replacement within an individual tree.
- The number of columns (features) to sample is calculated as m=sqrt(p) or m=log2(p) by a rule of thumb, where p is the total number of columns.



[MXML-8-01] Machine Learning / 8. Random Forest - Sampling

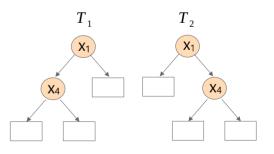


- Data Sampling : row (data instance) and column (feature) sampling
- Row sampling with replacement (bootstrap samples) reduces the correlation between the decision trees. Without row sampling, the results of many trees can be similar, reducing ensemble effects. Column sampling (sampling features) can further reduce correlation between trees. Without column sampling, if there are a few key features, these features are selected from many trees, making the trees similar (correlated) again.

$$\begin{split} \hat{y} &= \frac{1}{t} \sum_{i=1}^{t} T_{i}(x) \\ Var(\hat{y}) &= Var(\frac{1}{t} \sum_{i=1}^{t} T_{i}(x)) \\ &= \frac{1}{t^{2}} \sum_{i=1}^{t} \sum_{j=1}^{t} Cov(T_{i}(x), T_{j}(x)) \\ &= \frac{1}{t^{2}} \sum_{i=1}^{t} \left(\sum_{j \neq i}^{t} Cov(T_{i}(x), T_{j}(x)) + Var(T_{i}(x)) \right) \\ &= \frac{1}{t^{2}} \sum_{i=1}^{t} \left((t-1)\sigma^{2}\rho + \sigma^{2} \right) \leftarrow \rho = \frac{Cov(x, y)}{\sigma_{x}\sigma_{y}} \\ &= \frac{t(t-1)\rho\sigma^{2} + t\sigma^{2}}{\sigma_{x}\sigma_{y}} \end{split}$$

$$Var(\hat{y}) = \rho \,\sigma^2 + \sigma^2 \frac{1 - \rho}{t}$$

- Row/column sampling reduces ρ between trees, making Var(y) smaller. Also, the larger the number of trees, t, the smaller Var(y) becomes.
- The smaller m is, the smaller ρ is.
- Without column sampling:
- If x1 is the most important feature, it is likely to be used as the first split point for many trees, even if the data varies depending on row sampling. Then the trees will be similar.



Reference: https://stat.ethz.ch/education/semesters/ss2012/ams/slides/v10.2.pdf (Applied Multivariate Statistics – Spring 2012)



```
# MyDTreeClassifierRF.py: Create a tree for Random Forest.
# This code is an upgraded version of MyDTreeClassifier
# shown in [MXML-2-07] video.
# Features: subsampling by rows and columns,
           predict Out-Of-Bag (OOB) data points
import numpy as np
from collections import Counter
import copy
# Implement a simplified Random Forest using binary tree.
class MyDTreeClassifierRF:
   def init (self, max depth, max samples, max features):
        self.max depth = max depth
        self.max samples = max samples
        self.max features = max features
       self.u class = None
                              # unique class (target v value)
       self.estimator1 = dict() # tree result-1
       self.estimator2 = dict() # tree result-2
       self.feature = None
                                # feature data
       self.target = None  # target class data
       self.iob pred=None # predicted classes of train data points
        self.oob pred=None # predicted classes of OOB data points
   # Calculate Gini index of a leaf node
   def gini index(self, leaf):
        n = leaf.shape[0]
       if n > 1:
           gini = 1.0
           for c in self.u class:
               cnt = (self.target[leaf] == c).sum()
               gini -= (cnt / n) ** 2
            return gini
       else:
            return 0.0
```

```
# Split a node into left and right.
# Find the best split point with highest information gain,
# and split node with it.
# did: data index on the leaf node.
def node split(self, did):
   n = did.shape[0]
   # Gini index of parent node before splitting.
   p gini = self.gini index(did)
   # perform column subsampling without replacement
   p = self.feature.shape[1]
   m = self.max features
   f list = np.random.choice(np.arange(0, p), m,
                              replace=False)
   # Split the node into all candidates for all features
   # and find the best feature and the best split point with
   # the highest information gain.
   # fid: feature id
   max ig = -9999999
   for fid in f list:
        # feature data to be split
       x feat = self.feature[did, fid].copy()
        # split x feat using the best feature and the best
        # split point. Note: The code below is inefficient
        # because it sorts x feat every time it is split.
        # Future improvements are needed.
```



```
# remove duplicates of x feat and sort in ascending order
x uniq = np.unique(x feat)
# list up all the candidates, which are the midpoints of
# adjacent data points.
s point = [np.mean([x_uniq[i-1], x_uniq[i]]) \
           for i in range(1, len(x unig))]
# len(s point) > 1: Calculate the information gain for all
# candidates, and find the candidate with the largest
# information gain.
# len(s point) < 1: skip the for-loop. x feat either has
# only one data point or has all the same values.
# No need to split.
for p in s point:
    # split x feat into the left and the right node.
   left = did[np.where(x_feat <= p)[0]]
    right = did[np.where(x feat > p)[0]]
    # calculate Gini index after splitting.
    l gini = self.gini index(left)
    r gini = self.gini index(right)
    # calculate information gain
    ig = p_gini - (l_gini * left.shape[0] / n)
                - (r gini * right.shape[0] / n)
    # find where the information gain is greatest.
    if ig > max ig:
       max ig = ig
       b fid = fid
                       # best feature id
       b point = p # best split point
       b left = left
                       # data index on the left node.
       b right = right # data index on the right node.
```

```
if max_ig > 0.:
                       # split
        return {'fid':b fid, 'split point':b point,
                'left':b left, 'right':b right}
    else:
                        # No split
        return None
# Create a binary tree using recursion
def recursive split(self, node, curr depth):
    left = node['left']
   right = node['right']
    # exit recursion
   if curr depth >= self.max depth:
        return
    # recursion
    s = self.node split(left)
   if isinstance(s, dict): # splitting to the left done.
        node['left'] = s
        self.recursive split(node['left'], curr depth+1)
    s = self.node split(right)
   if isinstance(s, dict): # splitting to the right done.
        node['right'] = s
        self.recursive split(node['right'], curr depth+1)
# majority vote
def majority vote(self, did):
   c = Counter(self.target[did])
   return c.most common(1)[0][0]
```



```
# Change the data in the leaf node to majority class.
def update leaf(self, d):
    if isinstance(d, dict):
       for key, value in d.items():
            if key == 'left' or key == 'right':
                rtn = self.update leaf(value)
                if rtn[0] == 1:
                                     # leaf node
                    d[\bar{k}e\bar{y}] = rtn[1]
       return 0, 0 # the first 0 means this is not a leaf node.
                     # leaf node
    else:
        # the first 1 means this is a leaf node.
        return 1, self.majority vote(d)
# create a tree using training data
# x : feature data, y: target data
def fit(self, x, y):
    # perform row subsampling with replacement
   n = x.shape[0]
   i_rows = np.random.choice(np.arange(0, n), self.max_samples,
                              replace=True)
    self.feature = x[i rows, :]
   self.target = v[i rows]
   self.u class = np.unique(v)
    # Initially, the root node holds all data points IDs.
    root = self.node split(np.arange(x.shape[0]))
   if isinstance(root, dict):
        self.recursive split(root, curr depth=1)
   # tree result-1. Every leaf node has data point IDs.
   self.estimator1 = root
   # tree result-2. Every leaf node has the majority class.
    self.estimator2 = copy.deepcopy(self.estimator1)
    self.update leaf(self.estimator2)
                                              # tree result-2
```

```
# predict Out-Of-Bag (OOB) data points
   # initialize the predicted classes of OOB
   # and train data points
   self.iob_pred = np.ones(shape=(x.shape[0],), dtype=int) * -1
   self.oob_pred = np.ones(shape=(x.shape[0],), dtype=int) * -1
   # predict training dataset
   v pred = self.predict(x)
   # predict training and OOB dataset
   i train = set(np.arange(0, x.shape[0]))
   i oobs = list(i train - set(i rows)) # 00B data point IDs
   self.iob_pred[i_rows] = y_pred[i_rows] # for training data
   self.oob pred[i oobs] = y pred[i oobs] # for OOB data
   return self.iob pred, self.oob pred
# Estimate the target class of a test data.
def x predict(self, p, x):
   if x[p['fid']] <= p['split point']:</pre>
      if isinstance(p['left'], dict): # recursion if not leaf.
         return self.x predict(p['left'], x) # recursion
      else:
                      # return the value in the leaf, if leaf.
         return p['left']
   else:
      if isinstance(p['right'], dict) # recursion if not leaf.
         return self.x_predict(p['right'], x) # recursion
                       # return the value in the leaf, if leaf.
       else:
         return p['right']
# Estimate the target class of a x test.
def predict(self, x test):
   p = self.estimator2 # predictor
   y pred = [self.x predict(p, x) for x in x test]
   return np.array(y pred)
```



```
# [MXML-8-02]: 1.RF(titanic).py
# Implement Random Forest using MyDTreeClassifierRF
import numpy as np
import pandas as pd
from MyDTreeClassifierRF import MyDTreeClassifierRF
from sklearn.model selection import train test split
# Read preprocessed Titanic data.
df = pd.read csv('data/titanic clean.csv')
# Survived Pclass Sex Age SibSp Parch
                                           Fare Embarked Title
                       22.0
                                            3.62
                                        0 35.64
                     0 38.0
                    0 26.0
                                        0 7.92
                                        0 26.55
                     0 35.0
                     1 35.0
                                        0 8.05
                                                         3
y = np.array(df['Survived'])
x = np.array(df.drop('Survived', axis=1))
x train, x test, y train, y test = train test split(x, y)
n = 100
n_features = round(np.sqrt(x.shape[1])) # the number of features
                                      # for column sampling
n depth = 3
                                      # max depth of tree
models = [] # base model list
for i in range(n estimators):
   # Create a tree for Random Forest
   model = MyDTreeClassifierRF(max depth=n depth,
                              max samples = x train.shape[0],
                              max features=n features)
```

```
# train the tree
    # subsampling by rows and columns is performed within the
    # model
    model.fit(x train, y train)
    # save trained tree
    models.append(model)
# prediction
y estimates = np.zeros(shape=(x test.shape[0], n estimators))
for i, model in enumerate(models):
    y estimates[:, i] = model.predict(x test)
# synthesizing the estimation results
y prob = y estimates.mean(axis=1)
y \text{ pred} = (y \text{ prob} >= 0.5) * 1
print('\nAccuracy = \{:.4f\}'.format((y pred == y test).mean()))
Result:
Accuracy = 0.8027
Accuracy = 0.8161
                      Result of running
Accuracy = 0.7982
                      multiple times
Accuracy = 0.8296
```

[MXML-8-02] Machine Learning / 8. Random Forest – Implementation



```
models
[<MyDTreeClassifierRF.MyDTreeClassifierRF at 0x7f7c89047bb0>,
 <MyDTreeClassifierRF.MyDTreeClassifierRF at 0x7f7c89047a30>,
 <MyDTreeClassifierRF.MyDTreeClassifierRF at 0x7f7c89044ee0>,
 <MyDTreeClassifierRF.MyDTreeClassifierRF at 0x7f7c89046a40>,
v estimates.shape
(223, 100)
y estimates
array([[0., 0., 0., ..., 0., 0., 0.],
       [0., 1., 1., ..., 1., 0., 0.],
       [1., 1., 1., ..., 1., 0., 0.],
       . . . ,
y estimates[0, :]
array([0., 0., 0., 0., 1., 0., 0., 1., 0., 1., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 1., 0., 0., 0., 1., 1., 1., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 1., 0., 0., 0., 1., 0., 1., 0., 0.,
       1., 0., 0., 0., 0., 0., 0., 0., 0., 0., 1., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 1., 0., 0., 0., 1., 1., 0., 0., 0.,
       0., 0., 0., 1., 0., 0., 1., 0., 0., 0., 0., 1., 1., 1., 0.,
       0., 1., 1., 0., 0., 0., 0., 0., 0., 0.)
```



```
models[1].estimator2
Out[4]:
{'fid': 0,
 'split point': 1.5,
 'left': {'fid': 7,
  'split point': 1.5,
  'left': {'fid': 5, 'split_point': 38.43, 'left': 1, 'right': 1},
  'right': {'fid': 2,
   'split point': 28.84,
   'left': 0.
   'right': 1}},
 'right': {'fid': 1,
  'split point': 0.5,
  'left': {'fid': 0, 'split point': 2.5, 'left': 1, 'right': 0},
  'right': {'fid': 7, 'split point': 1.0, 'left': 1, 'right': 0}}}
                                 x[0] \le 1.5
                   x[7] \le 1.5
                                              x[1] \le 0.5
                        (x[2] \le 28.84)
                                       x[0] \le 2.5
          x[5] \leq 38.43
                                                     x[7] \le 1.0
                          0
                                              0
```

```
models[3].estimator2
Out[6]:
{'fid': 7,
 'split point': 2.5,
 'left': {'fid': 6.
  'split point': 2.5,
  'left': {'fid': 1, 'split point': 0.5, 'left': 1, 'right': 0},
  'right': {'fid': 7, 'split point': 1.5, 'left': 1, 'right': 0}},
 'right': {'fid': 5.
  'split point': 3.60,
  'left': 0.
  'right': {'fid': 2, 'split point': 66.5, 'left': 1, 'right': 0}}}
                                  x[7] \le 2.5
                   x[6] \le 2.5
                                               x[5] \le 3.6
           x[1] \le 0.5
                          x[7] \le 1.5
                                                     x[2] \le 66.5
                                             0
                   0
```



Coding practice: Implement Random Forest using DecisionTreeClassifier & RandomForestClassifier

```
# [MXML-8-02]: 2.RF(sklearn).pv
# Implement Random Forest using scikit-learn.
import numpy as np
import pandas as pd
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.model selection import train test split
# Read preprocessed Titanic data.
df = pd.read csv('data/titanic clean.csv')
v = np.array(df['Survived'])
x = np.array(df.drop('Survived', axis=1))
x train, x test, y train, y test = train test split(x, y)
n = 100
n depth = 3 # max depth of tree
# Implement Random Forest using DecisionTreeClassifier
models = [] # base model list
n = x train.shape[0] # the number of train data points
for i in range(n estimators):
    # row subsampling
    i_row = np.random.choice(np.arange(0, n), n, replace=True)
    x sample = x train[i row, :]
    y sample = y train[i row]
    # Create a tree for Random Forest
    # Column subsampling for each split is performed within the
    # model.
    model = DecisionTreeClassifier(max depth=n depth,
                                  max features="sqrt")
```

```
# train the tree.
    model.fit(x sample, y sample)
    # save trained tree
    models.append(model)
# prediction
y estimates = np.zeros(shape=(x test.shape[0], n estimators))
for i, model in enumerate(models):
    y estimates[:, i] = model.predict(x test)
# synthesizing the estimation results
v prob = v estimates.mean(axis=1)
y \text{ pred} = (y \text{ prob} >= 0.5) * 1
print('\nAccuracy1 = {:.4f}'.format((v pred == v test).mean()))
# Implement Random Forest using RandomForestClassifier
model = RandomForestClassifier(n estimators=n estimators,
                                max depth=n depth,
                                max samples=n,
                                                     # default
                                max features="sqrt") # default
model.fit(x train, y train)
y pred = model.predict(x test)
print('\nAccuracy2 = {:.4f}'.format((y pred == y test).mean()))
model.estimators
# [DecisionTreeClassifier(max depth=3, max features='sqrt',
                          random state=1090277217),
   DecisionTreeClassifier(max depth=3, max features='sqrt',
                           random state=1758239483),
   DecisionTreeClassifier(max depth=3, max features='sqrt',
                           random state=1420256802) ...
```

[MXML-8-03] Machine Learning / 8. Random Forest – Out-Of-Bag (OOB) score

- Out-Of-Bag (OOB) score (or error rate)
- Data points that are not selected by row subsampling are called Out-of-Bag (OOB) data. OOB data can be used to evaluate the performance of the model.
- Using OOB score eliminates the need for cross-validation. No need to use a validation dataset.
- If you have a lot of data available, you can use a separate validation dataset to evaluate your model's performance, but if you have less data, you can use OOB data to evaluate its performance. OOB increases the efficiency of data use.

	Training data								
	X ₁ X ₂ X ₃ X ₄								
i=1									
i=2									
i=3									
i=4									

Data points selected for each tree

T ₁	T ₂	T ₃	T ₄	T ₅	T ₆
4	1	3	1	3	5
2	5	3	5	2	5
3	5	2	1	1	1
2	1	2	2	1	2
4	1	4	2	5	2

OOB data points

T ₁	T ₂	T ₃	T ₄	T ₅	T ₆
1	2	1	3	4	3
5	3	5	4		4
	4				

OOB tree list

		Tree	list	
i=1	T ₁	Тз		
i=2	T ₂			
i=3	T_2	T ₄	T ₆	
i=4	T ₂	T ₄	T ₅	T ₆
i=5	T ₁	T ₃		

i=1 data point is used to evaluate T₁ and T₃ i=2 data point is used to evaluate T₂

i=3 data point is used to evaluate T₂, T₄, T₆

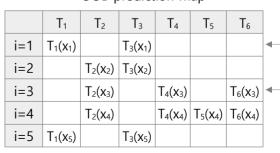
i=4 data point is used for T₂, T₄, T₅, T₆

i=5 data point is used for T_1 , T_3

- The probability that the subset does not contain the original data. (Out-Of-Bag probability)
- the number of subsets is n, and the number of data points in a subset is also n.
- The probability that data instance i will be selected when selecting a sample: $\frac{1}{2}$ data instance i will not be selected when selecting a sample: $1-\frac{1}{2}$ data instance i will not be selected at all while selecting n samples: $(1-\frac{1}{n})^n$
- If n is large enough: $\lim_{n \to \infty} \left(1 \frac{1}{n}\right)^n = \frac{1}{e} = 0.3679$ OOB probability

					•	
	T ₁	T ₂	T ₃	T ₄	T ₅	T ₆
i=1	1		1			
i=2		1				
i=3		1		1		1
i=4		1		1	1	1
i=5	1		1			

OOB prediction map



prediction



Implement Random Forest from scratch and measure OOB score

```
# This code is a part of MyDTreeClassifierRF class.
# You can find the full code at [MXML-8-02] video.
# In this video, we'll just look at the fit() function.
      self.iob_pred
                                        -1
                                                        -1
                   y_pred
                                              3
      self.oob pred
                                             -1
                                                        0
                                                  -1
                   y_pred
# create a tree using training data
# x : feature data, y: target data
def fit(self, x, v):
    # perform row subsampling with replacement
   n = x.shape[0]
   i rows = np.random.choice(np.arange(0, n), self.max_samples,
                              replace=True)
    self.feature = x[i rows, :]
   self.target = v[i rows]
    self.u class = np.unique(v)
    # Initially, the root node holds all data points IDs.
    root = self.node split(np.arange(x.shape[0]))
   if isinstance(root, dict):
        self.recursive split(root, curr depth=1)
   # tree result-1. Every leaf node has data point IDs.
    self.estimator1 = root
   # tree result-2. Every leaf node has the majority class.
    self.estimator2 = copy.deepcopy(self.estimator1)
    self.update leaf(self.estimator2)
                                              # tree result-2
```

```
# predict In-Of-Bag (IOB) and Out-Of-Bag (OOB) data points
   # initialize the predicted classes of IOB and OOB data points
   self.iob pred = np.ones(shape=(x.shape[0],), dtype=int) * -1
   self.oob_pred = np.ones(shape=(x.shape[0],), dtype=int) * -1
   # predict training dataset
   v pred = self.predict(x)
   # predict IOB and OOB data points
   i train = set(np.arange(0, x.shape[0]))
   i oobs = list(i train - set(i rows)) # 00B data point IDs
   self.iob pred[i rows] = y pred[i rows] # for IOB data
   self.oob pred[i oobs] = y pred[i oobs] # for OOB data
   return self.iob pred, self.oob pred
# Estimate the target class of a test data.
def x_predict(self, p, x):
   if x[p['fid']] <= p['split_point']:</pre>
      if isinstance(p['left'], dict): # recursion if not leaf.
          return self.x predict(p['left'], x) # recursion
                       # return the value in the leaf, if leaf.
       else:
         return p['left']
    else:
      if isinstance(p['right'], dict) # recursion if not leaf.
         return self.x predict(p['right'], x) # recursion
                       # return the value in the leaf, if leaf.
       else:
         return p['right']
# Estimate the target class of a x test.
def predict(self, x test):
   p = self.estimator2
                          # predictor
   y pred = [self.x predict(p, x) for x in x test]
   return np.array(v pred)
```

[MXML-8-03] Machine Learning / 8. Random Forest – Out-Of-Bag (OOB) score



Implement Random Forest from scratch and measure OOB score

```
# [MXML-8-03] 3.RF_00B.py
# Add Out-Of-Bag (OOB) score feature to 2.RF(titanic).py.
import numpy as np
import pandas as pd
from MyDTreeClassifierRF import MyDTreeClassifierRF
from sklearn.model selection import train test split
import matplotlib.pyplot as plt
# Read preprocessed Titanic data.
df = pd.read csv('data/titanic clean.csv')
# Survived Pclass Sex
                         Age SibSp Parch
                                           Fare
                                                  Embarked Title
                        22.0
                                            3.62
                        38.0
                                        0 35.64
                     0 26.0
                                           7.92
                        35.0
                                         0 26.55
N = x train.shape[0] # the number of train data points
y = np.array(df['Survived'])
x = np.array(df.drop('Survived', axis=1))
x train, x test, y train, y test = train test split(x, y)
n = 50
n depth = 5
                  # max depth of tree
max features = round(np.sqrt(x train.shape[1])) # for column sampling
# majority vote for iob pred, or oob pred (p = iob pred or oob pred)
def majority vote(p):
   cnt 0 = (p == 0).sum(axis=1)
   cnt 1 = (p == 1).sum(axis=1)
   cnts = np.array([cnt 0, cnt 1])
                                    # shape = (2, 668)
   return np.argmax(cnts, axis=0)
```

```
models = []
                # base model list
iob score = [] # Error rate measured with IOB
oob score = [] # Error rate measured with OOB
# initialize IOB and OOB prediction map
iob pred = np.ones(shape=(N, n estimators)) * -1
oob pred = np.ones(shape=(N, n estimators)) * -1
                                                     iob pred
# Create n estimators models
                                                     T_2 \mid T_3 \mid T_4 \mid T_5 \mid T_6
for i in range(n estimators):
    # Create a tree for Random Forest
    model = MyDTreeClassifierRF(
                                                            0
               max depth=n depth,
                                               i=3
                                                            0
               max samples = N,
               max features = max features)
                                               i=4 1 1
                                                        1 0
                                               i=5 1
    p1, p2 = model.fit(x train, y train)
                                                     oob pred
    # save trained tree
    models.append(model)
                                                     T_2 T_3 T_4 T_5 T_6
    # Create IOB and OOB prediction map
                                               i=1 0
    iob_pred[:, i] = p1
                                               i=2 .
    oob pred[:, i] = p2
                                                        0
                                               i=3 0
    # Calculate IOB and OOB score
                                               i=4
                                                           0
    y trn = majority vote(iob pred)
                                               i=5 .
    y oob = majority vote(oob pred)
    iob score.append((y trn != y train).mean())
    oob score.append((y oob != y train).mean())
```



Implement Random Forest from scratch and measure OOB score

```
# Visualize TOB and OOB score
plt.figure(figsize=(6, 4))
plt.plot(iob score, color='blue', lw=1.0, label='IOB error')
plt.plot(oob score, color='red', lw=1.0, label='00B error')
plt.legend()
plt.xlabel('n estimators')
plt.ylabel('00B error rate')
plt.show()
# prediction
y estimates = np.zeros(shape=(x test.shape[0], n estimators))
for i, model in enumerate(models):
   y estimates[:, i] = model.predict(x test)
# synthesizing the estimation results
y prob = y estimates.mean(axis=1)
v \text{ pred} = (v \text{ prob} >= 0.5) * 1
accuracy = (y pred == y test).mean()
print('\nAccuracy of test data = {:.4f}'.format(accuracy))
print('final 00B error rate = {:.4f}'.format(oob score[-1]))
# 00B probability
# In theory, it would be 0.3679.
# This means that x_train is selected with probability 0.6321
# by row subsampling. (1.0 - 0.3679 = 0.6321)
oob percent = ((oob pred >= 0).sum(axis=0) / N).mean()
print('00B probability = {:.4f}'.format(oob percent))
```

```
IOB error
          0.300
                                        OOB error
          0.275
         0.250
         0.225
          0.200
          0.175
          0.150
         0.125
                    10
                          20
                           n estimators
Accuracy of test data = 0.8251
Final OOB error rate = 0.1811
00B probability = 0.3644
oob_pred[:8, :10]
array([[-1., -1., 0., -1., 0., -1., -1., 1., 0., 0.],
      [0., 1., 1., -1., -1., 1., -1., 0., 1., -1.],
      [ 0., -1., -1., -1., -1., -1., 0., -1., -1., -1.],
      [-1., -1., -1., -1., 0., -1., 0., -1., 0., 0.],
      [-1., -1., 0., -1., 0., -1., -1., -1., -1., -1.]
```

[-1., -1., -1., -1., -1., -1., -1., 1., 1., -1.]



• Implement Random Forest using DecisionTreeClassifier and RandomForestClassifier and measure OOB score

```
# [MXML-8-03] 4.RF 00B(sklearn).pv
# Add Out-Of-Bag (OOB) score feature to 2.RF(sklearn).pv
import numpy as np
import pandas as pd
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.model selection import train test split
import matplotlib.pyplot as plt
# Read preprocessed Titanic data.
df = pd.read csv('data/titanic clean.csv')
v = np.array(df['Survived'])
x = np.array(df.drop('Survived', axis=1))
x train, x test, y train, y test = train test split(x, y)
N = x train.shape[0] # the number of train data points
n = 50
n depth = 5
                                              # tree의 max depth
max_features= round(np.sqrt(x_train.shape[1])) # for column sampling
# Implement Random Forest using DecisionTreeClassifier
# majority vote for iob pred, or oob pred
# p = iob pred or oob pred
def majority vote(p):
    cnt 0 = (p == 0).sum(axis=1)
    cnt 1 = (p == 1).sum(axis=1)
    cnts = np.array([cnt 0, cnt 1]) # shape = (2, 668)
    return np.argmax(cnts, axis=0)
```

```
sk models = [] # base model list
iob score = [] # Error rate measured with IOB
oob score = [] # Error rate measured with OOB
# initialize IOB and OOB prediction map
iob pred = np.ones(shape=(N, n estimators)) * -1
oob pred = np.ones(shape=(N, n estimators)) * -1
i train = set(np.arange(0, N))
# Create n estimators models
for i in range(n estimators):
   # row subsampling
    i_row = np.random.choice(np.arange(0, N), N, replace=True)
   x sample = x train[i row, :] # bootstrapped data
   y sample = y train[i row]
    # Create a Decision Tree for Random Forest
    # Column sampling for each split is performed within the model.
   model = DecisionTreeClassifier(max depth=n depth,
                                   max features="sqrt")
    # Training
   model.fit(x sample, y sample)
    sk models.append(model)
   # Create IOB and OOB prediction map
    i oob = list(i train - set(i row)) # 00B index
    iob pred[i row, i] = model.predict(x train[i row])
   oob pred[i oob, i] = model.predict(x train[i oob])
```



• Implement Random Forest using DecisionTreeClassifier and RandomForestClassifier and measure OOB score

```
# Calculate TOB and OOB score
    y trn = majority vote(iob pred)
    y oob = majority vote(oob pred)
    iob score.append((v trn != v train).mean())
    oob score.append((y oob != y train).mean())
# Visualize IOB and OOB score
plt.figure(figsize=(6, 4))
plt.plot(iob score, color='blue', lw=1.0, label='IOB error')
plt.plot(oob score, color='red', lw=1.0, label='00B error')
plt.legend()
plt.xlabel('n estimators')
plt.ylabel('00B error rate')
plt.show()
# prediction
y estimates = np.zeros(shape=(x test.shape[0], n estimators))
for i, model in enumerate(sk models):
   y estimates[:, i] = model.predict(x test)
# synthesizing the estimation results
y prob = y estimates.mean(axis=1)
y \text{ pred} = (y \text{ prob} >= 0.5) * 1
accuracy = (v pred == v test).mean()
print('\nThe result from DecisionTreeClassifier:')
print('Accuracy of test data = {:.4f}'.format(accuracy))
print('Final OOB error rate = {:.4f}'.format(oob score[-1]))
```

```
# OOB probability: In theory, it would be 0.3679.
# This means that x train is selected with probability 0.6321
# by row subsampling. (1.0 - 0.3679 = 0.6321)
oob percent = ((oob pred >= 0).sum(axis=0) / N).mean()
print('00B probability = {:.4f}'.format(oob percent))
# Implement Random Forest using RandomForestClassifier
rf model = RandomForestClassifier(n estimators=n estimators,
                                   max depth=n depth,
                                   max features="sqrt",
                                                          # default
                                   max samples=N,
                                                          # default
                                   oob score=True)
rf model.fit(x train, y train)
v pred1 = rf model.predict(x test)
print('\nThe result from RandomForestClassifier:')
print('Accuracy of test data = {:.4f}'\
       .format((y pred1 == y test).mean()))
print('Final OOB error rate = {:.4f}'\
                                            0.300
       .format(1 - rf model.oob score ))
                                            0.275
The result from DecisionTreeClassifier:
                                            0.250
Accuracy of test data = 0.7937
                                           0.225
Final OOB error rate = 0.1692
                                           E 0.200
                                          8 <sub>0.175</sub>
OOB probability = 0.3685
                                            0.150
The result from RandomForestClassifier:
                                            0.125
Accuracy of test data = 0.8117
Final OOB error rate = 0.1677
                                                            n estimators
```

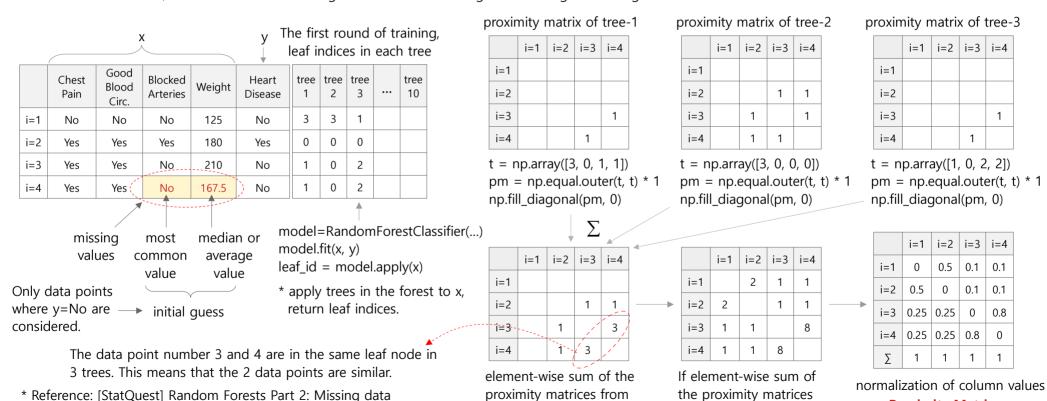
[MXML-8-04] Machine Learning / 8. Random Forest – Missing value

MX-AI

• Missing value : Proximity Matrix

and clustering

- If there are missing values in the data, they can be estimated through Random Forest. The idea is to estimate the missing values in data points by referring to the values in similar data points. Proximity matrix (PM) is used to measure the similarity. (1 PM) is distance matrix.
- Proximity matrix (PM) is generated by the following procedure. When normalizing PM, it is divided by the number of trees. Here, it is normalized so that the sum of the columns is 1, as shown in the bottom right. This is to create weights for a weighted average to be used later.



Proximity Matrix

from tree-1 to tree-10 is:

tree-1 to tree-3.

[MXML-8-04] Machine Learning / 8. Random Forest – Missing value

Missing value imputation – training data

- Missing values are estimated using the proximity matrix (PM).
- Continuous variable is estimated as a weighted average using PM, and categorical variable is estimated as a category with a large probability times weight.
- Update the proximity matrix using the estimated missing values and repeat this process until there are no changes.

	X						
	Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease		
i=1	No	No	No	125	No		
i=2	Yes	Yes	Yes	180	Yes		
i=3	Yes	Yes	No	210	No		
i=4	Yes	Yes	No	167.5) No		
	missing values initial guess						

Proximity Matrix (pm)

	i=1	i=2	i=3	i=4
i=1	0	0.5	0.1	0.1
i=2	0.5	0	0.1	0.1
i=3	0.25	0.25	0	0.8
i=4	0.25	0.25	0.8	0
Σ	1	1	1	1

Continuous variable: Weight

The "weight" value for data point number 4 is assumed to be this value.

Categorical variable: Blocked Arteries

Yes: $\frac{1}{3} \times \frac{0.1}{0.1 + 0.1 + 0.8} = 0.033$ No: $\frac{2}{3} \times \frac{0.1 + 0.8}{0.1 + 0.1 + 0.8} = 0.6$ Since it is larger, the missing value is assumed to be "No".

Because of normalization, the denominator is always 1.

^{*} Reference: [StatQuest] Random Forests Part 2: Missing data and clustering

[MXML-8-04] Machine Learning/ 8. Random Forest–Missing value

* Reference: [StatQuest] Random Forests Part 2: Missing data and clustering

Missing value imputation – test data

* Reference [2] in [MXML-8-01]

Proximities

<skipped>

When a test set is present, the proximities of each case in the test set with each case in the training set can also be computed. The amount of additional computing is moderate.

Missing value replacement for the test set

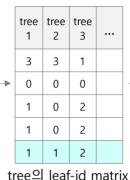
When there is a test set, there are two different methods of replacement depending on whether labels exist for the test set.

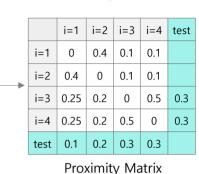
If they do, then the fills derived from the training set are used as replacements. If labels no not exist, then each case in the test set is replicated nclass times (nclass= number of classes). The first replicate of a case is assumed to be class 1 and the class one fills used to replace missing values. The 2nd replicate is assumed class 2 and the class 2 fills used on it.

This augmented test set is run down the tree. In each set of replicates, the one receiving the most votes determines the class of the original case.

• Continuous variable: (No detailed explanation in the documentation. This is my quess.)

					•		
		Chest Pain	Good Blood Circ.	Blocked Arteries	Weight	Heart Disease	
•	i=1	No	No	No	125	No	
	i=2	Yes	Yes	Yes	180	Yes	-
	i=3	Yes	Yes	No	210	No	
	i=4	Yes	Yes	No	198.5	No	
	test	Yes	No	No	178.4	?	
					A		

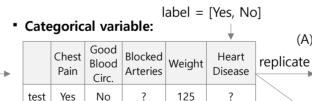




missing value 1. Initial guess. There is no y in the test data, so all data points, including the training data, are used.

(B)

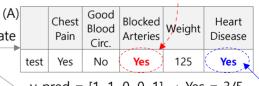
- 2. Create a proximity matrix using all data points, including the training data.
- 3. Estimate the missing value using proximity matrix
- * Please see the code in the following video for more details.



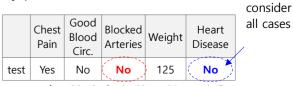
Example from above reference

Use the model to predict replicated data, A and B, then select the one with higher accuracy in y_pred. In this example, the missing value is assumed to be "yes".

Since we have y, we estimate it in the same way as the train data.



 $y_pred = [1, 1, 0, 0, 1] \rightarrow Yes = 3/5$



 $y_pred = [1, 1, 0, 1, 1] \rightarrow No = 1/5$

test



• Implement of Missing value imputation using Proximity Matrix

```
# [MXML-8-05] 5.RF proximity.py
# Add missing value estimation functionality to
# RandomForestClassifier.
# To understand this code, you need to learn about the
# proximity matrix from the previous video, [MXML-8-04].
import numpy as np
import pandas as pd
from sklearn.ensemble import RandomForestClassifier
from sklearn.model selection import train test split
import matplotlib.pyplot as plt
# Read Titanic dataset
df = pd.read csv('data/titanic.csv')
df['Embarked'].fillna('N', inplace = True) # Replace with 'N'
df['Sex'] = df['Sex'].factorize()[0]
                                              # encoding
df['Embarked'] = df['Embarked'].factorize()[0] # encoding
df.drop(['PassengerId', 'Name', 'Ticket', 'Cabin'], axis=1,
       inplace=True)
df.info()
# RangeIndex: 891 entries, 0 to 890
# Data columns (total 8 columns):
       Column
                 Non-Null Count Dtype
      Survived 891 non-null
                                int64
      Pclass
                 891 non-null
                                int64
  2
      Sex
                 891 non-null
                                int64
  3
                714 non-null
                                float64
      Age
  4
      SibSp
                891 non-null
                                int64
 5
      Parch
                 891 non-null
                                int64
  6
                 891 non-null
                                float64
      Fare
       Embarked 891 non-null
                                int64
```

```
Survived Pclass Sex
                            Age SibSp Parch
                                                  Fare
                                                        Embarked
# 0
                            22.0
                                                7.2500
            0
                           35.0
                                               53,1000
                            35.0
# 4
                                                8.0500
# 5
                            NaN
                                                8.4583
# 6
                           54.0
                                            0 51.8625
# 8
                         1 27.0
                                            2 11.1333
# create training and test data
v = np.array(df['Survived'])
x = np.array(df.drop('Survived', axis=1))
x train, x test, y train, y test = train test split(x, y, test size=0.2)
# Initially, missing values in 'Age' are replaced with the average value.
AGE = 2 # column number of 'Age' feature
# the position of missing values. It is for later use.
i train = np.where(np.isnan(x train[:, AGE]))[0] # training data
i test = np.where(np.isnan(x test[:, AGE]))[0]
                                                 # test data
# indices where y train=0, and y train=1
i y0 = np.where(y train == 0)[0]
i y1 = np.where(y train == 1)[0]
# the mean value of 'Age' where v train=0, and the same where v train=1.
y0 mean = np.nanmean(x train[i y0, AGE]) # where y train=0
y1 mean = np.nanmean(x train[i y1, AGE]) # where y train=1
# replace nan in 'Age' where y_train = 0 to y0_mean
x train[i y0, AGE] = np.nan to num(x train[i y0, AGE], nan=y0 mean)
# replace nan in 'Age' where v train = 1 to v1 mean
x train[i y1, AGE] = np.nan to num(x train[i y1, AGE], nan=y1 mean)
```



Implement of Missing value imputation using Proximity Matrix

```
print('Before:\n', x train.round(2))
print('y0 mean=\{:.2f\}, y1 mean=\{:.2f\}'.format(y0 mean, y1 mean))
plt.plot(x train[i train, AGE], 'bo')
plt.title('Initial values for the missing values')
plt.show()
#i train = np.where(np.isnan(x train[:, AGE]))[0]
# Before: [[ 3.
                          36. ... 0.
                                            7.5
                         27.78 ... 0.
                                           16.1
                         25.
                              ... 0.
                                           13.
\# v0 mean = 30.82, y1_mean = 27.78
       Initial values for the missing values
                                   leaf node ID
 30.5
                                                           pm
30.0
                                      T2
                                          T3
                                                       i=1 | i=2 | i=3 | i=4
29.5
                                      3
                                                           0.5
                                  3
                                                   i=1
                                                               0.1
                                                                   0.1
                                      0
                                  0
                                          0
                                                  i=2
                                                       0.5
                                                            0
                                                               0.1
                                                                   0.1
28.5
                                  1
                                                  i=3 0.25 0.25
                                                                   0.8
                                          2
                                                   i=4 0.25 0.25 0.8
                                      0
# Create Proximity matrix
# normalize = 0: pm / n tree
# normalize # 0: Normalize columns to sum to 1
def proximity matrix(model, x, normalize=0):
    n tree = len(model.estimators )
    # Apply trees in the forest to X, return leaf indices.
    leaf = model.apply(x) # shape = (x.shape[0], n tree)
    pm = np.zeros(shape=(x.shape[0], x.shape[0]))
    for i in range(n tree):
        t = leaf[:, \overline{i}]
        pm += np.equal.outer(t, t) * 1.
```

```
np.fill diagonal(pm, 0)
   if normalize == 0:
        return pm / n tree
    else:
        return pm / pm.sum(axis=0, keepdims=True)
n = 50
n depth = 5
# Missing value imputation using the proximity matrix
for i in range(5):
                   # 5 iterations
    model = RandomForestClassifier(n estimators=n estimators,
                                   max depth=n depth,
                                   oob score=True)
   model.fit(x train, v train)
    # Create proximity matrix
    pm = proximity matrix(model, x train, normalize=1)
    # estimate the missing values of 'Age' using the proximity matrix
   x age = x train[:, AGE].copy()
    u age = np.dot(x_age, pm) # updated 'Age'
   x train[i train, AGE] = u age[i train]
                                               37.5
print('\nAfter:\n', x train.round(2))
plt.plot(x train[i train, AGE], 'ro')
plt.title('Estimated values for the missing val<sup>300</sup>
plt.show()
# After:
# [[ 3.
                36.
                                7.5
                                       0.
    3.
                26.45 ...
                                16.1
                                       0.
                25.
                                13.
                                       0.
```



Implement of Missing value imputation using Proximity Matrix

```
# Train a new model after imputing missing values of training data
model = RandomForestClassifier(n estimators=n estimators,
                               max depth=n depth,
                               oob score=True)
model.fit(x train, y train)
# Predict the test data. There are also missing values in 'Age' in the
# test data.
# [2] Proximities
# When a test set is present, the proximities of each case in the test
# set with each case in the training set can also be computed.
# Initially, there is no target value y in the test data, so the
# missing values are replaced with the mean value of the training data.
x test[i test, AGE] = x train[:, AGE].mean()
x_data = np.vstack([x_train, x_test]) # combine training and test data
pm = proximity matrix(model, x data, normalize=1)
x age = x data[:, AGE].copy()
                                      # 'Age' feature data
u age = np.dot(x age, pm)
                                      # updated 'Age' feature
u age = u age[-x test.shape[0]:]
                                      # 'Age' of test data
u test = x data[-x test.shape[0]:]
                                      # test data
u test[i test, AGE] = u age[i test]
                                      # update the missing values in
                                      # test data
# predict
y pred = model.predict(u test)
print('\nResults:')
print('Accuracy = {:.4f}'.format((y pred == y test).mean()))
print('Final OOB error rate = {:.4f}'.format(1 - model.oob score ))
```

```
Before:
 [[ 3.
                  36.
                                     16.1
    3.
                  27.78 ... 0.
    2.
                  25.
                                     13.
    3.
    3.
                  16.
                                      7.73
After:
                   36.
                                       7.5
                   26.45 ... 0.
                                      16.1
                                       8.05
                   16.
                                     7.73 2.
                                      27.
Results:
Accuracy = 0.8324
Final OOB error rate = 0.1812
PM (example in [MXML-8-04])
                                             Estimated values for the missing values
       i=1 | i=2 | i=3 | i=4 | test
                                     37.5
            0.4 | 0.1 | 0.1
   i=1
                                     35.0
                                     32.5
   i=2
                0.1
                     0.1
                                     30.0
   i=3 0.25 0.2
                     0.5 0.3
                                     27.5
      0.25 0.2
                0.5
                                     25.0
                                     22.5
            0.2 0.3 0.3
       0.1
   test
```



Outlier Detection: Algorithm

- Random Forest's proximity matrix can be used to detect outliers.
- It is an outlier detection algorithm in the form of supervised learning.

Reference [2]: Outliers

Outliers are generally defined as cases that are removed from the main body of the data. Translate this as: outliers are cases whose proximities to all other cases in the data are generally small. A useful revision is to define outliers relative to their class. Thus, an outlier in class j is a case whose proximities to all other class j cases are small.

(1)

Define the average proximity from case n in class i to the rest of the training data class i as:

$$\bar{P}(n) = \sum_{class(k)=j} prox^2(n,k)$$

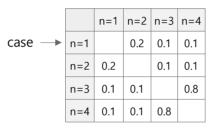
(2)

The raw outlier measure for case n is defined as

$$r(n) = \frac{nsample}{\bar{P}(n)}$$

This will be large if the average proximity is small. Within each class find the median of these raw measures, and their absolute deviation from the median. Subtract the median from each raw measure, and divide by the absolute deviation to arrive at the final outlier measure. (3)

Proximity matrix (normalized by the number of trees)



1) Average proximity

$$\bar{P}(n=1) = \sum_{class(k)=0} prox^{2}(1,k)$$

$$= \sum_{k=[3,4]} prox^{2}(1,k) = 0.1^{2} + 0.1^{2} = 0.02$$

$$\bar{P}(n=2) = \sum_{class(k)=1} prox^{2}(2,k) = 0$$

$$\bar{P}(n=3) = 0.1^{2} + 0.8^{2} = 0.65$$

$$\bar{P}(n=4) = 0.1^{2} + 0.8^{2} = 0.65$$

2) Raw outlier measure

$$r(n=1) = \frac{4}{0.02} = 200$$
$$r(n=2) = \frac{4}{0} = \infty$$
$$r(n=3) = \frac{4}{0.65} = 6.15$$

$$r(n=3) = \frac{4}{0.65} = 6.15$$

$$r(n=4) = \frac{4}{0.65} = 6.15$$

3) Final outlier measure

class i

- Data with an excessively large r_f are considered outliers.

y=0
$$\[\begin{array}{c} \text{y=0} \[\begin{array}{c} \text{y=1} \[\begin{array}{c} \text{y=1}$$

^{*} Evaluate how far each data point is from the center of the normalized distribution.



Outlier Detection: Implemention

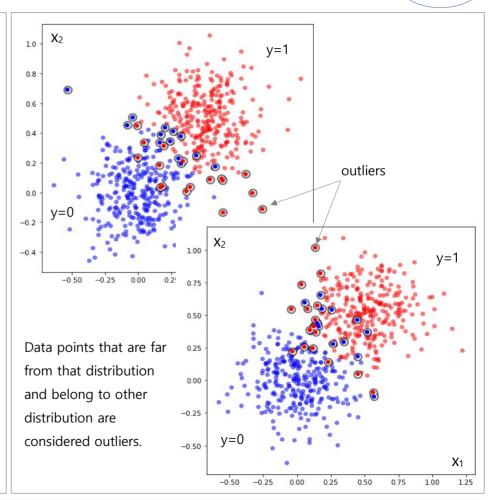
```
# [MXML-8-06] 6.RF outlier.py
# Outlier detection using Random Forest's proximity matrix
# Reference [2]:
# https://www.stat.berkeley.edu/~breiman/RandomForests/
          cc home.htm#outliers
import numpy as np
from sklearn.datasets import make blobs
from sklearn.ensemble import RandomForestClassifier
import matplotlib.pvplot as plt
# Generate training data
x, y = make blobs(n samples=600, n features=2,
                centers=[[0., 0.], [0.5, 0.5]],
                cluster std=0.2, center box=(-1., 1.)
# Create Proximity matrix
# normalize = 0: pm / n tree
# normalize ≠ 0: Normalize columns to sum to 1
def proximity matrix(model, x, normalize=0):
    n tree = len(model.estimators )
    # Apply trees in the forest to X, return leaf indices.
    leaf = model.apply(x) # shape = (x.shape[0], n tree)
    pm = np.zeros(shape=(x.shape[0], x.shape[0]))
    for i in range(n tree):
       t = leaf[:, i]
       p = np.equal.outer(t, t) * 1.
       pm += p
    np.fill diagonal(pm, 0)
```

```
if normalize == 0:
        return pm / n tree
    else:
        return pm / pm.sum(axis=0, keepdims=True)
n = 50
n depth = 5
# Detect outliers using a proximity matrix
model = RandomForestClassifier(n estimators=n estimators,
                                 max depth=n depth,
                                 max features="sqrt", # default
                                 bootstrap=True,
                                                        # default
                                 oob score=True)
                                                     PM
                                                                class i
model.fit(x, y)
                                               n=1 | n=2 | n=3 | n=4
# Create a proximity matrix
                                                    0.2 | 0.1 | 0.1
pm = proximity matrix(model, x)
                                           n=1
                                                       0.1
                                           n=2 0.2
                                                           0.1
i \ v0 = np.where(v == 0)[0]
                                           n=3 0.1
                                                   0.1
i y1 = np.where(y == 1)[0]
                                                           0.8
i y = [i y0, i y1]
                                           n=4 0.1
                                                   0.1 0.8
# 1) average proximity
                                          \bar{P}(n) = \sum_{n=0}^{\infty} prox^{2}(n,k)
pi bar = []
for i in range(pm.shape[0]):
    j class = y[i]
                           # the class of data instance i
    j same = i y[j class] # Data point IDs with the same class as
                           # data point i
    pi bar.append(np.sum(pm[i, j same] ** 2))
```



Outlier Detection: Implementation

```
# 2) raw outlier measure
o raw = x.shape[0] / np.array(pi bar)
# 3) final outlier measure
# For convenience of coding, the mean value was used instead of the
# median, and the standard deviation was used instead of the absolute
# deviation.
f measure = []
for i in range(o raw.shape[0]):
    i class = v[i]
                           # the class of the data instance i
    j same = i y[j class] # Data point IDs with the same class as
                           # data point i
    f measure.append((o raw[i] - o raw[j same].mean()) /\
                      o raw[i same].std())
# Data in the upper top rate percentage of f measure are considered
# outliers.
top rate = 0.05 # top 5%
top idx = np.argsort(f measure)[::-1][:int(top rate * x.shape[0])]
# Visualize normal data and outliers by color.
plt.figure(figsize=(7, 7))
color = [['blue', 'red'][i] for i in y]
color out = [['blue', 'red'][i] for i in y[top idx]]
plt.scatter(x[:, 0], x[:, 1], s=30, c=color, alpha=0.5)
plt.scatter(x[top_idx, 0], x[top_idx, 1], s=150, c='black', alpha=0.5)
plt.scatter(x[top idx, 0], x[top idx, 1], s=60, c='white')
plt.scatter(x[top idx, 0], x[top idx, 1], s=30, c=color out)
plt.show()
```





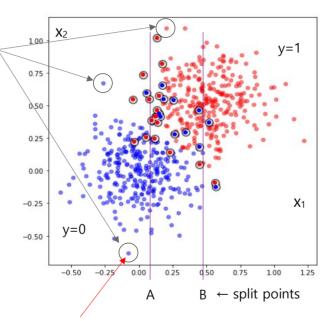
Outlier Detection: Interpretation of the result

Let's consider why outliers are near the decision boundary.

Outlier detection algorithms in the form of unsupervised learning consider these data to be outliers. This is because they are far from the entire distribution.

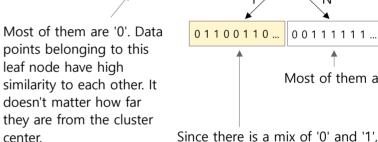
(ex: Isolation Forest, Auto Encoder, etc)

Random forest is a supervised learning method. Supervised learning type outlier detection algorithms take classes into account to determine outliers.

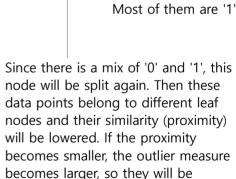


This data point is far from the y=0 cluster centroid, but belongs to the same leaf as the centroid, so it has high similarity to the centroid data. So it is not considered an outlier.

Within the decision boundary, no matter how far away from the center it is, it is not an error and therefore does not need to be treated as an outlier (in the "hinge loss" concept).



0000010...



considered as outliers.

 $x_1 < B$



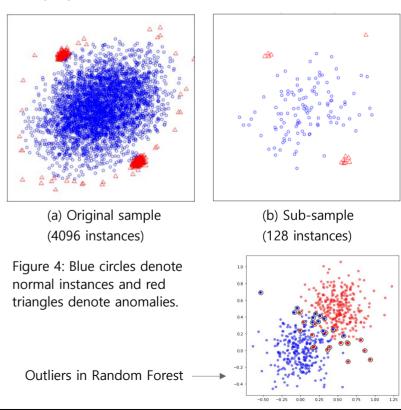
- Isolation Forest (iForest): Outlier Detection Overview
- Isolation Forest is not part of Random Forest. The purpose of this video is to compare the outlier detection result of Random Forest and Isolation Forest.
- iForest is an outlier detection algorithm in the form of unsupervised learning proposed by Fei Tony Liu, Kai Ming Ting, and Zhi-Hua Zhou in 2008.
- Like Random Forest, Isolation Forest uses multiple trees, performs row and column subsampling. However, row subsampling is performed with small sizes and without replacement. Column subsampling randomly selects only one column and randomly selects the split point.

Isolation Forest

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Abstract

Most existing model-based approaches to anomaly detection construct a profile of normal instances, then identify instances that do not conform to the normal profile as anomalies. This paper proposes a fundamentally different model-based method that explicitly isolates anomalies instead of profiles normal points. To our best knowledge, the concept of isolation has not been explored in current literature. The use of isolation enables the proposed method, iForest, to exploit sub-sampling to an extent that is not feasible in existing methods, creating an algorithm which has a linear time complexity with a low constant and a low memory requirement. Our empirical evaluation shows that iForest performs favourably to ORCA, a near-linear time complexity distance-based method, LOF and Random Forests in terms of AUC and processing time, and especially in large data sets. iForest also works well in high dimensional problems which have a large number of irrelevant attributes, and in situations where training set does not contain any anomalies.

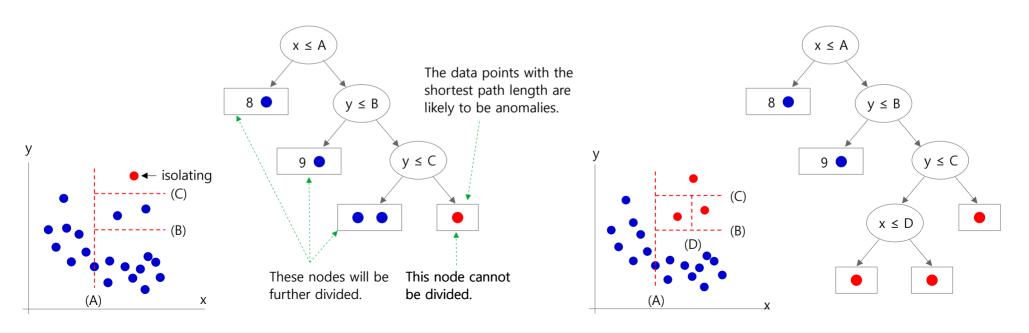


[MXML-8-07] Machine Learning / 8. Random Forest – Outlier



■ Isolation Forest (iForest): Outlier Detection – Basic idea

- Creating a binary tree from training data isolates outliers much faster than normal samples. Outliers have short decision depth, path length.
- Splitting the node with normal samples until one sample remains in a leaf node makes the tree deeper. That is because the normal data points are clustered in the distribution. Therefore, the path length for normal data points becomes large.
- In the picture on the left, the data point is left alone in the leaf node by the split point (C). Its path length is 3. Other data points require more splits and therefore have greater depth. In the picture on the right, dividing by (D) separates two additional data points, which are also likely outliers.
- In practice, we create multiple trees with sample data, calculate the anomaly score for each isolated leaf node, and calculate the average to determine the data points with larger scores as outliers.

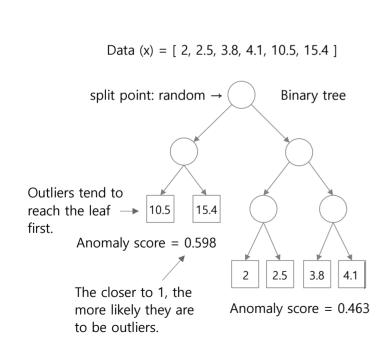


[MXML-8-07] Machine Learning / 8. Random Forest – Outlier



■ Isolation Forest (iForest): Outlier Detection – Algorithm

- Isolation Forest uses anomaly scores to detect outliers. The trees in Isolation Forest, iTrees, have the same structure as binary search trees (BST).
- The anomaly score is calculated as the average path length taken from the BST.
- The closer the Anomaly score is to '1', the more likely it is to be an outlier, and the closer it is to '0', the more likely it is to be normal data. The closer it is to 0.5, the less clear the distinction between normal and abnormal data is. For the data below, 10.5 and 15.4 are likely outliers.



: internal node (n-1 = 5)

: external node (n = 6)

1) average path length of unsuccessful search in BST- average depth of leaf nodes

$$c(n)=2H(n-1)-\frac{2(n-1)}{n}$$

$$H(i) = \log(i) + 0.5772156649$$
 (Euler's constant)

actual average depth: $\frac{2+2+3+3+3+3}{6} = 2.67$ similar $c(n) = 2(\log(5) + 0.577) - \frac{2 \times 5}{6} = 2.70$

2) Anomaly score

$$s(x,n)=2^{-\frac{E[h(x)]}{c(n)}}$$

h(x) – path length of data point x c(n) – average of h(x) given n. E[h(x)] – average of h(x) from all trees.

if the number of trees is just one, the left tree.

$$s(2,n=6)=2^{-\frac{3}{2.7}}=0.463$$

$$s(10.5, n=6)=2^{-\frac{2}{2.7}}=0.598$$

$$s(15.4, n=6)=2^{-\frac{2}{2.7}}=0.598$$

$$E[h(x)] \rightarrow c(n), s \rightarrow 0.5$$

$$E[h(x)] \rightarrow 0, s \rightarrow 1$$

$$E[h(x)] \rightarrow n-1, s \rightarrow 0$$



Coding practice: Implement Isolation Forest

```
# [MXML-8-07] 7.iForest test.pv
# Implementation of Isolation Forest using ExtraTreeRegressor
# sklearn's IsolationForest library makes it easy to implement
# Isolation Forest, but I used ExtraTreeRegressor to better
# understand how it works.
from sklearn.tree import ExtraTreeRegressor
import numpy as np
# simple dataset
x = np.array([2, 2.5, 3.8, 4.1, 10.5, 15.4],
             dtype=np.float32).reshape(-1, 1)
n = x.shape[0] # the number of data points
n trees = 10  # the number of trees in Isolation Forest
# H(i) is the harmonic number and it can be estimated
# by ln(i) + 0.5772156649 (Euler's constant).
def H(n):
    return np.log(n) + 0.5772156649
# average path length of unsuccessful search in BST
def C(n):
    return 2 * H(n-1) - (2 * (n-1) / n)
hx = np.zeros(n)
for t in range(n trees):
    # Create a tree using random split points
    model = ExtraTreeRegressor(max depth=3, max features=1)
    # Fit the model to training data.
    # Since it is unsupervised learning and there is no target
    # value, a binary tree is created by randomly generating
    # target values.
    model.fit(x, np.random.uniform(size=n))
```

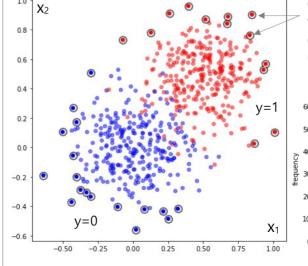
```
leaf id = model.apply(x) # indices of leaf nodes
   # depth of each node, internal and external nodes.
    node depth = model.tree .compute node depths()
   # h(x): accumulated path length of data points
   hx += node depth[leaf id] - 1.0
   print('Tree',t,':', (hx / (t+1)).round(1))
Ehx = hx / n trees
                           # Average of h(x)
S = 2 ** (-(Ehx / C(n)))
                          # Anomaly scores for each data point
i out = np.argsort(S)[-2:] # Top 2 anomaly scores
outliers = x[i out]
                           # outliers
print('\nAnomaly scores:'); print(S.round(3))
print('\nOutliers:'); print(outliers)
Tree 0: [3. 3. 3. 3. 2. 1.]
Tree 1: [3. 3. 3. 3. 2. 1.]
Tree 2: [3. 3. 3. 3. 2. 1.3]
Tree 3: [2.8 3. 3.
                     3. 2. 1.51
Tree 4: [2.8 \ 3. \ 3. \ 2. \ 1.6]
Tree 5 : [2.7 3. 3. 3. 2.2 1.7]
Tree 6: [2.7 3. 3. 3. 2.3 1.6]
Tree 7: [2.8 3. 3. 2.2 1.5]
Tree 8: [2.7 2.9 3. 3. 2.3 1.7]
Tree 9: [2.7 2.9 3. 3. 2.3 1.7]
Anomaly scores:
[0.501 0.476 0.464 0.464 0.555 0.647]
Outliers:
[[10.5]
 [15.4]]
```



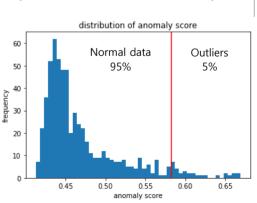
Isolation Forest (iForest): Outlier Detection

```
# [MXML-8-07] 8.iForest outlier.pv
# Outlier detection using Isolation Forest (iForest)
import numpy as np
from sklearn.datasets import make blobs
from sklearn.ensemble import IsolationForest
import matplotlib.pvplot as plt
                                                       Anomaly
# Create training dataset
x, y = make blobs(n samples=600, n features=2,
                                                       score top
                centers=[[0., 0.], [0.5, 0.5]],
                                                         5%
                cluster std=0.2, center box=(-1., 1.)
model = IsolationForest(n estimators=50, contamination=0.05)
model.fit(x)
outlier = model.predict(x) # Normal = 1, Outlier = -1
# Extract outliers
i outlier = np.where(outlier == -1)[0]
x outlier = x[i outlier, :]
# Visualize normal data points and outliers by color.
plt.figure(figsize=(7, 7))
color = [['blue', 'red'][i] for i in y]
color out = [['blue', 'red'][i] for i in y[i outlier]]
plt.scatter(x[:, 0], x[:, 1], s=30, c=color, alpha=0.5)
plt.scatter(x outlier[:, 0], x_outlier[:, 1], s=150, c='black',
            alpha=0.5) # outlier scatter
plt.scatter(x outlier[:, 0], x outlier[:, 1], s=60, c='white')
plt.scatter(x outlier[:, 0], x_outlier[:, 1], s=30, c=color_out)
plt.show()
```

```
# Check out the distribution of Anomaly score
score = abs(model.score_samples(x))
score[i_outlier].min()
plt.hist(score, bins = 50)
plt.title('distribution of anomaly score')
plt.xlabel('anomaly score')
plt.ylabel('frequency')
plt.axvline(x=score[i_outlier].min(), c='red')
plt.show()
```



Outlier detection algorithms in the form of unsupervised learning consider these data to be outliers. (far from the overall distribution)





Comparison of outlier detection results between Random Forest and Isolation Forest

