Supervised Learning – Part 4

ESM3081 Programming for Data Science

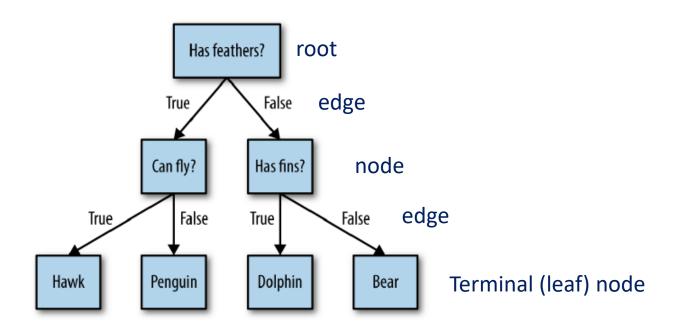
Seokho Kang



Learning algorithms covered in this course

- Supervised Learning (Classification/Regression)
 - K-Nearest Neighbors
 - Linear Models (Logistic/Linear Regression)
 - Decision Trees
 - Random Forests
 - Support Vector Machines
 - Neural Networks
 - * Many algorithms have a classification and a regression variant, and we will describe both.
 - * We will review the most popular machine learning algorithms, explain how they learn from data and how they make predictions, and examine the strengths and weaknesses of each algorithm.

- A decision tree is a hierarchy of if/else questions leading to a decision.
 - Each node either represents a question or a terminal node (also called a leaf) that contains the answer.
 - The edges connect the answers to a question with the next question you would ask.



Example – Skiing Classification

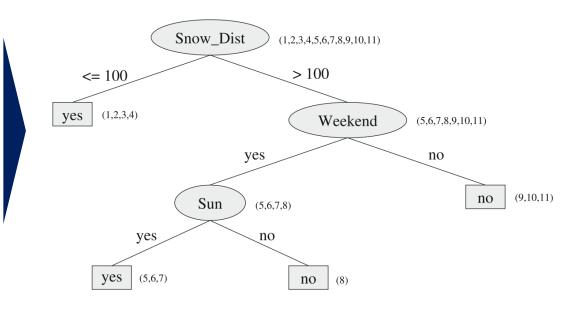
Features: "Snow_Dist", "Weekend", and "Sun".

- **Target**: "Skiing" = yes or no

Dataset

Day	Snow_Dist	Weekend	Sun	Skiing
1	≤100	yes	yes	yes
2	≤100	yes	yes	yes
3	≤100	yes	no	yes
4	≤100	no	yes	yes
5	>100	yes	yes	yes
6	>100	yes	yes	yes
7	>100	yes	yes	no
8	>100	yes	no	no
9	>100	no	yes	no
10	>100	no	yes	no
11	>100	no	no	no

Ski (goal variable)	yes, no	Should I drive to the nearest sk	
,-		resort with enough snow?	
Sun (feature)	yes, no	Is there sunshine today?	
Snow_Dist (feature)	≤ 100 , > 100	Distance to the nearest ski re-	
		sort with good snow conditions	
		(over/under 100 km)	
Weekend (feature)	yes, no	Is it the weekend today?	



- Instead of building the tree by hand, we can learn them from data
 - → the output is a set of if/else rules represented by a tree diagram
 - Each inner node represents a feature.
 - Each edge stands for the condition of a feature value.
 - At each leaf node, a prediction is given.
- The extracted knowledge can be easily understood, interpreted, and controlled by humans in the form of a readable decision tree
- Decision trees are widely used for classification and regression tasks

There are finitely many different decision trees.

- **Optimal algorithm** for the construction of a tree is to simply generate all possible trees and choose the best one.
- The obvious disadvantage of this algorithm is its unacceptably high computation time, as soon as the number of features becomes somewhat larger.

Decision Tree Learning

- We use **heuristic algorithms** with greedy strategy.
- Because greedy strategy is used for construction of the tree,
 the trees are in general sub-optimal.

- Given a (training) dataset $D = \{(x_1, y_1), (x_2, y_2), ..., (x_n, y_n)\}$ such that $x_i = (x_{i1}, ..., x_{id}) \in \mathbb{R}^d$ is the *i*-th input vector of *d* features and y_i is the corresponding target label.
- **General Procedure** Repeatedly split a node into two parts so as to minimize the impurity of outcome within the new parts.
 - The training dataset *D* constitutes the root node
 - Repeat the following process
 - Try all possible splits in all nodes and features to find the "best split"
 - Split the node

- How to determine the best split (for classification)
 - Nodes with low degree of impurity are preferred

C0: 5 C1: 5

C0: 9 C1: 1

High degree of impurity

Low degree of impurity

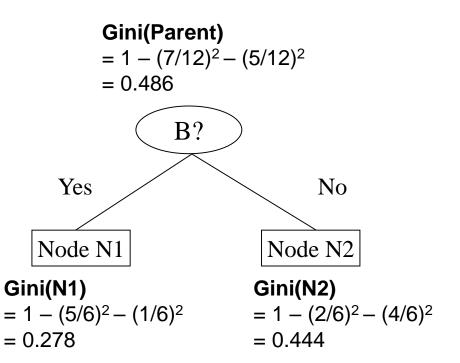
- Measures of node impurity
 - * p(j|t) is the fraction of class j at node t

GINI(t) =
$$1 - \sum_{j} [p(j|t)]^2$$

Entropy(t) = $-\sum_{j} p(j|t) \log p(j|t)$

- How to determine the best split (for classification)
 - 1. Compute impurity measure (P) before splitting
 - 2. Compute impurity measure (M) after splitting
 - Compute impurity measure of each child node
 - M is the weighted impurity of children
 - 3. Choose the feature that produces the highest gain or equivalently, lowest impurity measure after splitting (M)
 - Gain = P M

How to determine the best split (for classification)

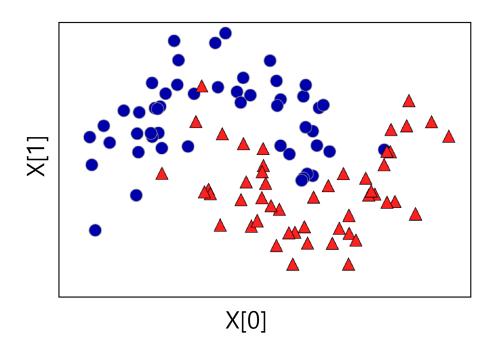


	Parent		
C1	7		
C2	5		
Gini = 0.486			

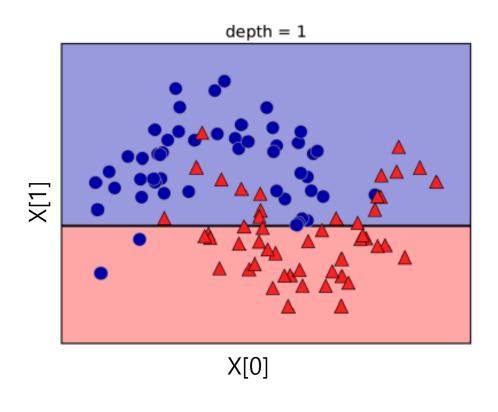
	N1	N2			
C1	5	2			
C2	1	4			
Gini=0.361					

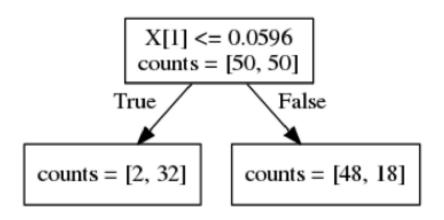
Weighted Gini of N1 and N2

- Example of building a decision tree (for classification)
 - The *two-moons* dataset consists of two half-moon shapes, with each class consisting of 50 data points.

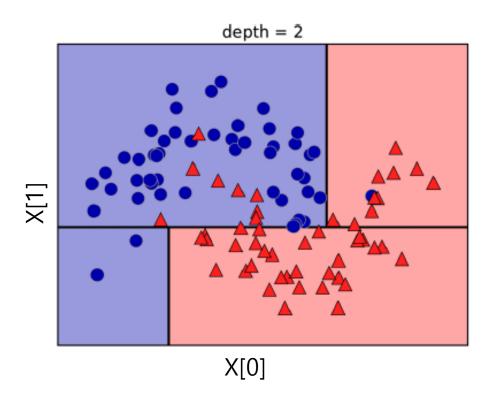


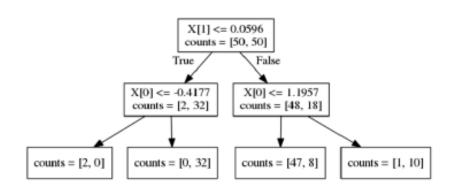
- Example of building a decision tree (for classification)
 - The algorithm searches over all possible tests and finds the one that is most informative about the target.



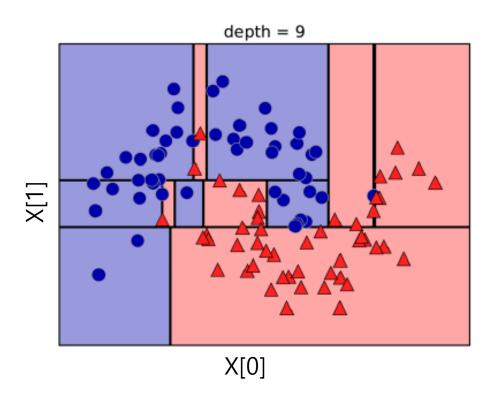


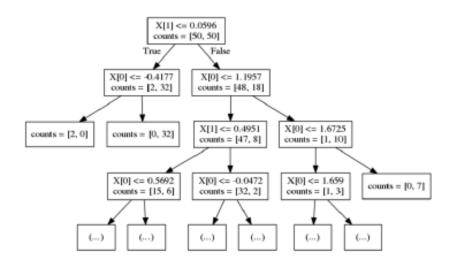
- Example of building a decision tree (for classification)
 - We can build a more accurate model by repeating the process of looking for the most informative next split for the left and the right region.





- Example of building a decision tree (for classification)
 - The recursive partitioning of the data is repeated until each region in the partition (each leaf in the tree) become homogeneous.





 To make a prediction for a new data point, we traverse the tree to find the leaf the data point falls into.

For Classification,

The output for the data point is the majority class of the training points in this leaf.

For Regression

The output for the data point is the mean target of the training points in this leaf.

- Building a tree typically leads to a model that is very complex and highly overfit to the training data.
 - Continuing until all leaves are pure means that a tree is 100% accurate on the training set,
 but fails to generalize on new data
- Two common strategies to prevent overfitting
 - Pre-pruning: stopping the creation of the tree early (e.g., below)
 - max_depth: limiting the maximum depth of the tree
 - min_sample_leaf: requiring a minimum number of points in a node to keep splitting it
 - max_leaf_nodes: limiting the maximum number of leaves
 - Post-pruning: building the tree but then removing or collapsing nodes that contain little information

https://scikit-learn.org/stable/modules/generated/sklearn.tree.DecisionTreeClassifier.html

sklearn.tree.DecisionTreeClassifier

class sklearn.tree. DecisionTreeClassifier(*, criterion='gini', splitter='best', max_depth=None, min_samples_split=2, min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features=None, random_state=None, max_leaf_nodes=None, min_impurity_decrease=0.0, min_impurity_split=None, class_weight=None, ccp_alpha=0.0)

[source]

A decision tree classifier.

* It only implements pre-pruning, not post-pruning.

Read more in the User Guide.

Parameters:

criterion: {"gini", "entropy"}, default="gini"

The function to measure the quality of a split. Supported criteria are "gini" for the Gini impurity and "entropy" for the information gain.

splitter: {"best", "random"}, default="best"

The strategy used to choose the split at each node. Supported strategies are "best" to choose the best split and "random" to choose the best random split.

max depth: int, default=None

The maximum depth of the tree. If None, then nodes are expanded until all leaves are pure or until all leaves contain less than min samples split samples.

https://scikit-learn.org/stable/modules/generated/sklearn.tree.DecisionTreeClassifier.html

min_samples_leaf: int or float, default=1

The minimum number of samples required to be at a leaf node. A split point at any depth will only be considered if it leaves at least min_samples_leaf training samples in each of the left and right branches. This may have the effect of smoothing the model, especially in regression.

- If int, then consider min samples leaf as the minimum number.
- If float, then min_samples_leaf is a fraction and ceil(min_samples_leaf * n_samples) are the minimum number of samples for each node.

Changed in version 0.18: Added float values for fractions.

max_leaf_nodes : int, default=None

Grow a tree with max_leaf_nodes

in best-first fashion. Best nodes are defined as relative reduction in impurity. If None then unlimited number of leaf nodes.

Example (breast_cancer dataset)

```
In [2]: from sklearn.datasets import load_breast_cancer
        cancer = load_breast_cancer()
In [3]: from sklearn.model_selection import train_test_split
        X_train, X_test, y_train, y_test = train_test_split(
            cancer.data, cancer.target, stratify=cancer.target, random_state=42)
In [4]: from sklearn.tree import DecisionTreeClassifier
        clf = DecisionTreeClassifier(random state=0)
        clf.fit(X train, y train)
Out[4]:
                  DecisionTreeClassifier
         DecisionTreeClassifier(random_state=0)
In [5]: from sklearn.metrics import accuracy score
        y train hat = clf.predict(X train)
        print('train accuracy: %.5f'%accuracy_score(y_train, y_train_hat))
        y_test_hat = clf.predict(X_test)
        print('test accuracy: %.5f'%accuracy score(y test, y test hat))
        train accuracy: 1.00000
        test accuracy: 0.93706
```

Example (breast_cancer dataset)

cancer = load breast cancer() X train, X test, y train, y test = train test split(cancer.data, cancer.target, stratify=cancer.target, random state=42) clf = DecisionTreeClassifier(random state=0) clf.fit(X train, y train) Training Data X_train clf Model Training Labels y_train y test hat = clf.predict(X test) Prediction X_test Test Data y_test_hat y_test Test Labels **Evaluation** accuracy_score(y_test, y_test_hat)

• Example (breast_cancer dataset): varying the hyperparameter min_samples_leaf

```
In [6]: from sklearn.datasets import load breast cancer
        from sklearn.model_selection import train_test_split
        from sklearn.tree import DecisionTreeClassifier
        from sklearn.metrics import accuracy score
        cancer = load_breast_cancer()
        X train, X test, y train, y test = train test split(
            cancer.data, cancer.target, stratify=cancer.target, random state=42)
In [7]: training_accuracy = []
        test accuracy = []
        m_{settings} = [1, 2, 5, 7, 10, 20]
        for m in m settings:
            # build the model
            clf = DecisionTreeClassifier(min_samples_leaf=m, random_state=0)
                                                                                     min_samples_leaf training accuracy test accuracy
            clf.fit(X train, y train)
                                                                                   0
                                                                                                            1.00000
                                                                                                                        0.93706
                                                                                                                        0.93706
                                                                                                            0.99061
            # accuracy on the training set
            y_train_hat = clf.predict(X_train)
                                                                                   2
                                                                                                            0.97653
                                                                                                                        0.93706
             training_accuracy.append(accuracy_score(y_train, y_train_hat))
                                                                                   3
                                                                                                            0.96244
                                                                                                                        0.95105
            # accuracy on the test set (generalization)
                                                                                                                        0.95105
                                                                                                 10
                                                                                                            0.96244
            y test hat = clf.predict(X test)
                                                                                                 20
                                                                                                            0.94601
                                                                                                                        0.91608
             test_accuracy.append(accuracy_score(y_test, y_test_hat))
```

Visualizing and Analyzing Decision Trees

 The visualization of the tree provides a great in-depth view of how the algorithm makes predictions

```
In [9]: from sklearn import tree
                               tree.plot tree(clf. precision=5)
     Out[9]: [Text(0.5833333333333334, 0.9, 'X[20] <= 16.795\( mgini = 0.46786\( msamples = 426\( msamples = 426\) (notation and the second of the 
                             Text(0.41666666666667, 0.7, 'X[27] <= 0.13595\mathrm{mgini} = 0.16056\mathrm{msamples} = 284\mathrm{mnvalue} = [25, 259]'),
                             Text(0.3333333333333333, 0.5, 'X[1] <= 21.56\text(0.33333333333333333, 0.5, 'X[1] <= 21.56\text(0.333333333333333333, 0.5, 'X[1] <= 21.56\text(0.3333333333333333333, 0.5, 'X[1] <= 21.56\text(0.333333333333333333)
                             Text(0.1666666666666666, 0.3, 'X[10] <= 0.40995\( mgini = 0.00945\( msamples = 210\) mvalue = [1, 209]').
                             Text(0.25. 0.1. 'gini = 0.095\mathref{m}nsamples = 20\mathref{m}nvalue = [1, 19]'),
                             Text(0.5, 0.3, 'X[18] <= 0.01888\mgini = 0.13265\msamples = 42\mvalue = [3, 39]'),
                             Text(0.416666666666667, 0.1, 'gini = 0.255\nsamples = 20\nvalue = [3, 17]'),
                             Text(0.583333333333334, 0.1, 'gini = 0.0\msamples = 22\mvalue = [0, 22]'),
                             Text(0.5, 0.5, 'gini = 0.45117\text(0.5 = 32\text{mvalue} = [21, 11]'),
                             Text(0.75, 0.7, 'X[21] <= 23.375\mgini = 0.10633\msamples = 142\mvalue = [134, 8]'),
                             Text(0.666666666666666, 0.5, 'gini = 0.455\nsamples = 20\nvalue = [13, 7]'),
                             Text(0.833333333333334, 0.5, 'X[5] <= 0.09352\text{\text{mgini}} = 0.01626\text{\text{msamples}} = 122\text{\text{mvalue}} = [121, 1]').
                             Text(0.75, 0.3, 'gini = 0.095\text{\text{msamples}} = 20\text{\text{myalue}} = [19, 1]').
                             Text(0.9166666666666666, 0.3, 'gini = 0.0\mathbb{W}nsamples = 102\mathbb{W}nvalue = [102, 0]')]
                                                                                                                                                                                                                                                                                                                                                                                                                                  ampire o 110
                                                                                                                                                                                                                                                                                                    samples = 284
                                                                                                                                                                                                                                                                                                      lan = (2%, 25%)
                                                                                                                                                                                                                                                               X1101 -- 1.50
                                                                                                                                                                                                                                                                                                                                        33737 vo 38.62
```

Feature Importance in Decision Trees

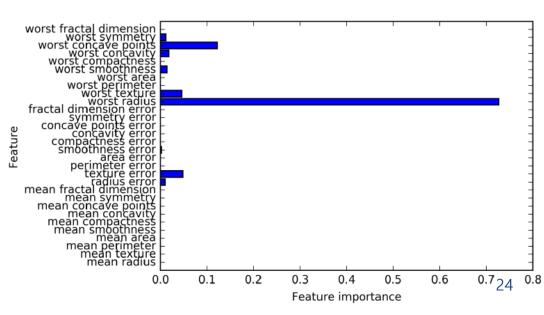
- feature importance summarizes the workings of a tree by rating how important each feature is for the decision the tree makes.
 - The importance of a feature is computed as the (normalized) total reduction of the criterion brought by that feature.
 - It is a number between 0 and 1 for each feature, where 0 means "not used at all" and 1 means "perfectly predicts the target."

Attributes:

feature_importances_: ndarray of shape (n_features,)

Return the feature importances.

```
In [10]: clf.feature_importances_
Out[10]: array([0.00000e+00, 1.86437e-03, 0.00000e+00, 0.00000e+00, 0.00000e+00, 5.01021e-04, 0.00000e+00, 0.00000e+00, 0.00000e+00, 0.00000e+00, 5.42188e-04, 0.00000e+00, 0.00000e+00])
```



scikit-learn Practice: DecisionTreeRegressor

https://scikit-learn.org/stable/modules/generated/sklearn.tree.DecisionTreeRegressor.html

sklearn.tree.DecisionTreeRegressor

class sklearn.tree. **DecisionTreeRegressor**(*, criterion='mse', splitter='best', max_depth=None, min_samples_split=2, min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features=None, random_state=None, max_leaf_nodes=None, min_impurity_decrease=0.0, min_impurity_split=None, ccp_alpha=0.0)

[source]

A decision tree regressor.

Read more in the User Guide.

Parameters:

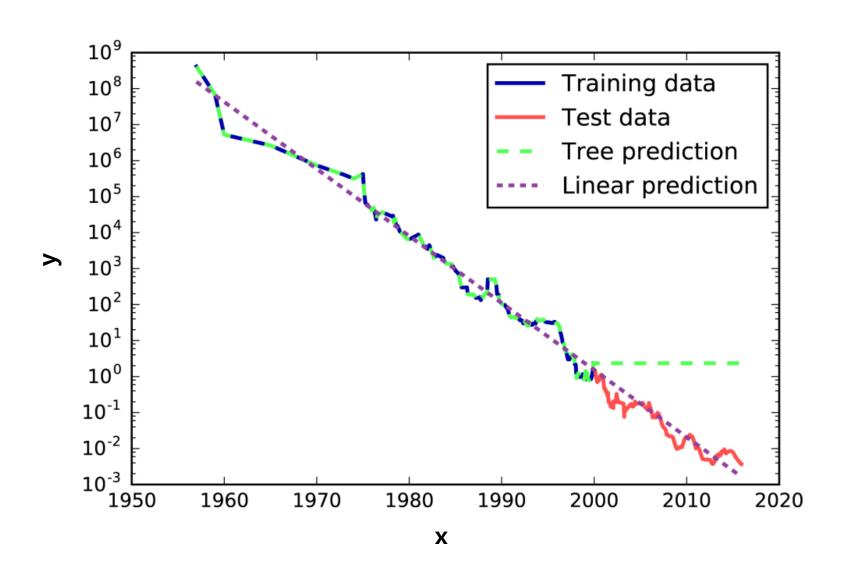
criterion: {"mse", "friedman mse", "mae", "poisson"}, default="mse"

The function to measure the quality of a split. Supported criteria are "mse" for the mean squared error, which is equal to variance reduction as feature selection criterion and minimizes the L2 loss using the mean of each terminal node, "friedman_mse", which uses mean squared error with Friedman's improvement score for potential splits, "mae" for the mean absolute error, which minimizes the L1 loss using the median of each terminal node, and "poisson" which uses reduction in Poisson deviance to find splits.

New in version 0.18: Mean Absolute Error (MAE) criterion.

New in version 0.24: Poisson deviance criterion.

scikit-learn Practice: DecisionTreeRegressor



The main hyperparameters of decision trees

- criterion: the function to measure the quality of a split (impurity measure)
- Picking one of the pre-pruning strategies—setting either max_depth, max_leaf_nodes, or min_samples_leaf—is sufficient to prevent overfitting.
- * Typically chosen to have the highest performance in validation data

Strengths

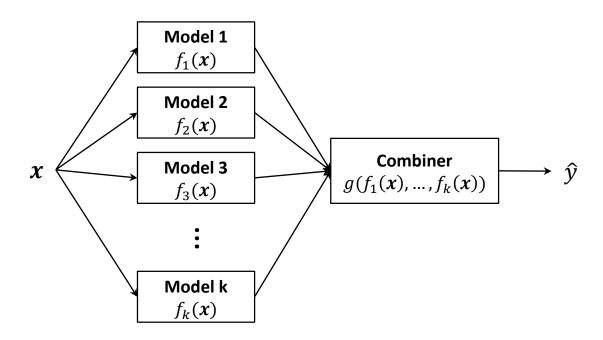
- Decision trees tend to work well when you have a mix of continuous and categorical features.
- The algorithm is completely invariant to the scales of features (no data scaling is needed)
- Feature selection & reduction is automatic.
- It is robust to outliers.
- The resulting model can easily be visualized and understood.

Weaknesses

- Even with the use of pre-pruning, they tend to overfit and provide poor generalization performance.
 - → the ensemble methods are usually used in place of a single decision tree.
- It does not take into account interactions between features.
- Space of possible decision trees is exponentially large. Greedy approaches are often unable to find the optimal tree.

Ensembles of Decision Trees

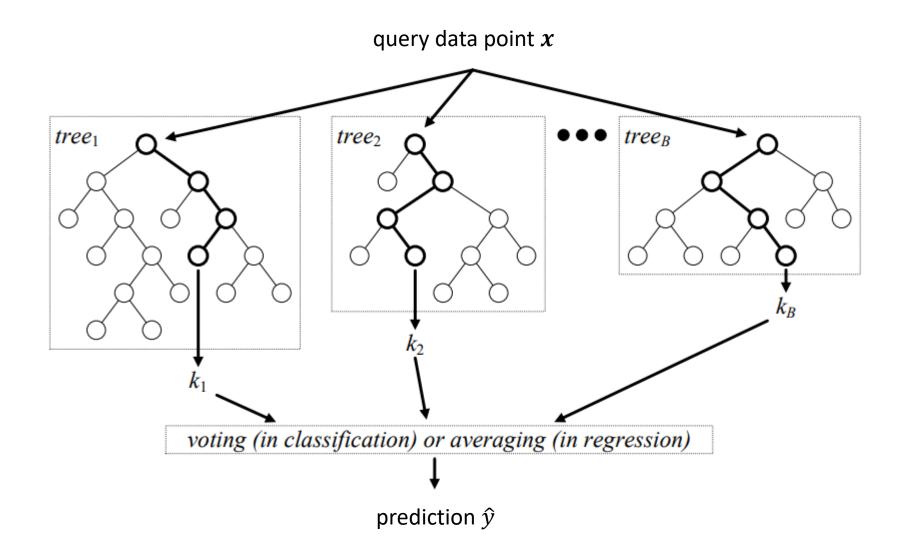
- Decision trees tend to overfit the training data
 - → Ensembles are one way to address this problem.
- Ensemble methods combine multiple machine learning models to create more powerful models.



- A random forest is an ensemble of decision trees, where each tree is slightly different from the others.
 - Each tree might do a relatively good job of predicting, but will likely overfit on part of the data in different ways.
 - If we build many trees, we can reduce the amount of overfitting by averaging their results while retaining the predictive power of the trees.
 - Random forests get their name from injecting randomness into the tree building to ensure each tree is different.

- Two ways in which the trees in a random forest are randomized
 - by selecting the data points used to build a tree
 - bootstrap: It leads to each decision tree in the random forest being built on a slightly different dataset.
 - From a list ['a', 'b', 'c', 'd'], possible examples of bootstrap samples are ['b', 'd', 'd', 'c'] and ['d', 'a', 'd', 'a'].
 - by selecting the features in each split test.
 - max_features: in each node, the algorithm randomly selects a subset of the features, and it looks for the best possible test involving one of these features
 - → each node in a tree can make a decision using a different subset of the features.
 - A high max_features means that the trees in the random forest will be quite similar, and they will be able to fit the data easily, using the most distinctive features.
 - A low max_features means that the trees in the random forest will be quite different, and that each tree might need to be very deep in order to fit the data well.

^{*} Typically, for a classification problem with p features, $\forall p$ (rounded down) features are used in each split. For regression problems the inventors recommend p/3 (rounded down) as the default. In practice the best value will depend on the problem.



 To make a prediction for a new data point, we first make a prediction for every tree in the forest.

For Classification,

- Each tree makes a "soft" prediction, providing a probability for each possible output label.
- The probabilities predicted by all the trees are averaged.
- The output for the data point is the class with the highest average probability.

For Regression

- The output for the data point is the mean prediction of the trees in the forest.

scikit-learn Practice: RandomForestClassifier

https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html

sklearn.ensemble.RandomForestClassifier

class sklearn.ensemble. RandomForestClassifier(n_estimators=100, *, criterion='gini', max_depth=None, min_samples_split=2, min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_impurity_decrease=0.0, min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=None, random_state=None, verbose=0, warm_start=False, class_weight=None, ccp_alpha=0.0, max_samples=None) [source]

A random forest classifier.

A random forest is a meta estimator that fits a number of decision tree classifiers on various sub-samples of the dataset and uses averaging to improve the predictive accuracy and control over-fitting. The sub-sample size is controlled with the max_samples parameter if bootstrap=True (default), otherwise the whole dataset is used to build each tree.

Read more in the User Guide.

Parameters:

n estimators: int, default=100

The number of trees in the forest.

Changed in version 0.22: The default value of n_estimators changed from 10 to 100 in 0.22.

scikit-learn Practice: RandomForestClassifier

https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html

max_features: {"auto", "sqrt", "log2"}, int or float, default="auto"

The number of features to consider when looking for the best split:

- If int, then consider max_features features at each split.
- If float, then max_features is a fraction and round(max_features * n_features) features are considered at each split.
- If "auto", then max_features=sqrt(n_features).
- If "sqrt", then max_features=sqrt(n_features) (same as "auto").
- If "log2", then max_features=log2(n_features).
- If None, then max features=n features.

Note: the search for a split does not stop until at least one valid partition of the node samples is found, even if it requires to effectively inspect more than max_features features.

bootstrap : bool, default=True

Whether bootstrap samples are used when building trees. If False, the whole dataset is used to build each tree.

scikit-learn Practice: RandomForestClassifier

Example (breast_cancer dataset): varying the hyperparameter n_estimators

```
In [11]: from sklearn.datasets import load_breast_cancer
         from sklearn.model selection import train test split
         from sklearn.ensemble import RandomForestClassifier
         from sklearn.metrics import accuracy_score
         cancer = load_breast_cancer()
         |X_train, X_test, y_train, y_test = train_test_split(
             cancer.data, cancer.target, stratify=cancer.target, random state=42)
In [12]:
         training_accuracy = []
         test accuracy = []
         n settings = [1, 2, 5, 10, 20, 50, 100]
                                                                                       n_estimators training accuracy test accuracy
         for n in n_settings:
                                                                                                           0.98357
                                                                                                                        0.93706
             # build the model
             clf = RandomForestClassifier(n_estimators=n)
                                                                                                           0.97887
                                                                                                                        0.91608
             clf.fit(X_train, y_train)
                                                                                                           0.98826
                                                                                                                        0.93706
             # accuracy on the training set
                                                                                                10
                                                                                                           0.99765
                                                                                                                        0.95105
             y_train_hat = clf.predict(X_train)
                                                                                                20
                                                                                                           1.00000
                                                                                                                        0.95105
             training accuracy.append(accuracy score(y train, y train hat))
                                                                                                50
                                                                                                           1.00000
                                                                                                                        0.95804
             # accuracy on the test set (generalization)
                                                                                               100
                                                                                                           1.00000
                                                                                                                        0.95804
             y_test_hat = clf.predict(X_test)
             test_accuracy.append(accuracy_score(y_test, y_test_hat))
```

How Many Trees in a Random Forest?



<u>International Workshop on Machine Learning and Data Mining in Pattern Recognition</u>

<u>MLDM 2012: Machine Learning and Data Mining in Pattern Recognition pp 154-168 | Cite as</u>

How Many Trees in a Random Forest?

Authors Authors and affiliations

Thais Mayumi Oshiro, Pedro Santoro Perez, José Augusto Baranauskas

Conference paper



Part of the <u>Lecture Notes in Computer Science</u> book series (LNCS, volume 7376)

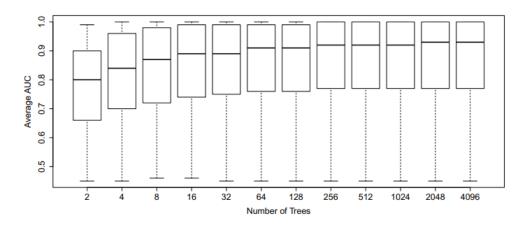
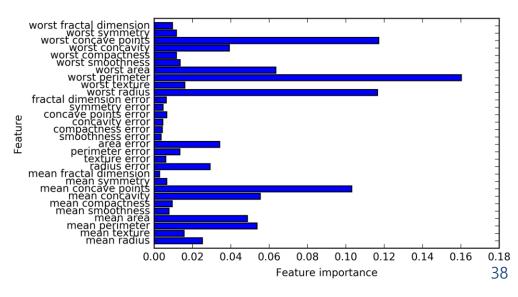


Fig. 1. AUC in all datasets

... ... The analysis of 29 datasets shows that from 128 trees there is no more significant difference between the forests using 256, 512, 1024, 2048 and 4096 trees. The mean and the median AUC values do not present major changes from 64 trees. Therefore, it is possible to suggest, based on the experiments, a range between 64 and 128 trees in a forest. With these numbers of trees it is possible to obtain a good balance between AUC, processing time, and memory usage.

Feature Importance in Random Forest

- Similarly to the decision tree, the random forest provides feature importances
 - Computed by aggregating the feature importances over the trees in the forest.
 - Typically, the feature importances provided by the random forest are more reliable than the ones provided by a single tree.



scikit-learn Practice: RandomForestRegressor

https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestRegressor.html

sklearn.ensemble.RandomForestRegressor

class sklearn.ensemble. RandomForestRegressor(n_estimators=100, *, criterion='mse', max_depth=None, min_samples_split=2, min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='auto', max_leaf_nodes=None, min_impurity_decrease=0.0, min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=None, random_state=None, verbose=0, warm_start=False, ccp_alpha=0.0, max_samples=None) [source]

A random forest regressor.

A random forest is a meta estimator that fits a number of classifying decision trees on various sub-samples of the dataset and uses averaging to improve the predictive accuracy and control over-fitting. The sub-sample size is controlled with the max_samples parameter if bootstrap=True (default), otherwise the whole dataset is used to build each tree.

Read more in the User Guide.

Parameters:

n_estimators : int, default=100

The number of trees in the forest.

Changed in version 0.22: The default value of n_estimators changed from 10 to 100 in 0.22.

max_features: {"auto", "sqrt", "log2"}, int or float, default="auto"

The number of features to consider when looking for the best split:

If "auto", then max_features=n_features.

The main hyperparameters of random forests

- n_estimators: larger is always better
- bootstrap: whether bootstrap samples are used
- max_features: how random each tree is, the default values in scikit-learn are sqrt(n_features) for classification and n_features for regression
- Plus, the main hyperparameters of decision trees
- * Typically chosen to have the highest performance in validation data

Strengths

They are very powerful, often work well without heavy tuning of the hyperparameters

Weaknesses

- It is basically impossible to interpret all the trees in detail
- Building random forests on large datasets might be somewhat time consuming
 but, it can be parallelized across multiple CPU (use n_jobs)

Journal of Machine Learning Research 15 (2014) 3133-3181

Submitted 11/13; Revised 4/14; Published 10/14

Do we Need Hundreds of Classifiers to Solve Real World Classification Problems?

Manuel Fernández-Delgado Eva Cernadas

MANUEL.FERNANDEZ.DELGADO@USC.ES EVA.CERNADAS@USC.ES

Senén Barro SENEN.BARRO@USC.ES CITIUS: Centro de Investigación en Tecnoloxías da Información da USC

University of Santiago de Compostela

Campus Vida, 15872, Santiago de Compostela, Spain

Dinani Amorim

DINANIAMORIM@GMAIL.COM

Departamento de Tecnologia e Ciências Sociais- DTCS Universidade do Estado da Bahia

Av. Edgard Chastinet S/N - São Geraldo - Juazeiro-BA, CEP: 48.305-680, Brasil

Editor: Russ Greiner

Abstract

We evaluate 179 classifiers arising from 17 families (discriminant analysis, Bayesian, neural networks, support vector machines, decision trees, rule-based classifiers, boosting, bagging, stacking, random forests and other ensembles, generalized linear models, nearestneighbors, partial least squares and principal component regression, logistic and multinomial regression, multiple adaptive regression splines and other methods), implemented in Weka, R (with and without the caret package), C and Matlab, including all the relevant classifiers available today. We use 121 data sets, which represent the whole UCI data base (excluding the large-scale problems) and other own real problems, in order to achieve significant conclusions about the classifier behavior, not dependent on the data set collection. The classifiers most likely to be the bests are the random forest (RF) versions, the best of which (implemented in R and accessed via caret) achieves 94.1% of the maximum accuracy overcoming 90% in the 84.3% of the data sets. However, the difference is not statistically significant with the second best, the SVM with Gaussian kernel implemented in C using LibSVM, which achieves 92.3% of the maximum accuracy. A few models are clearly better than the remaining ones: random forest, SVM with Gaussian and polynomial kernels, extreme learning machine with Gaussian kernel, C5.0 and avNNet (a committee of multi-layer perceptrons implemented in R with the caret package). The random forest is clearly the best family of classifiers (3 out of 5 bests classifiers are RF), followed by SVM (4 classifiers in the top-10), neural networks and boosting ensembles (5 and 3 members in the top-20, respectively).

Journal of Machine Learning Research 17 (2016) 1-5

Submitted 7/15; Revised 3/16; Published 7/16

Are Random Forests Truly the Best Classifiers?

Michael Wainberg

Department of Electrical and Computer Engineering University of Toronto, Toronto, ON M5S 3G4, Canada; Deep Genomics, Toronto, ON M5G 1L7, Canada

Babak Alipanahi

Department of Electrical and Computer Engineering University of Toronto, Toronto, ON M5S 3G4, Canada

Brendan J. Frey

Department of Electrical and Computer Engineering University of Toronto, Toronto, ON M5S 3G4, Canada; Deep Genomics, Toronto, ON M5G 1L7, Canada

Editor: Nando de Freitas

M.WAINBERG@UTORONTO.CA

BABAK@PSI.TORONTO.EDU

FREY@PSI.TORONTO.EDU

Abstract

The JMLR study Do we need hundreds of classifiers to solve real world classification problems? benchmarks 179 classifiers in 17 families on 121 data sets from the UCI repository and claims that "the random forest is clearly the best family of classifier". In this response, we show that the study's results are biased by the lack of a held-out test set and the exclusion of trials with errors. Further, the study's own statistical tests indicate that random forests do not have significantly higher percent accuracy than support vector machines and neural networks, calling into question the conclusion that random forests are the best classifiers.



