

# Machine Learning

## Decision Trees & Decision Trees-Based Models

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# Decision Trees – Introduction

- Also called Classification And Regression Trees or CART models
- The input space is recursively partitioned, and a local model is defined in each resulting region.
- We can represent this structure with a tree, with one leaf per region.
- A mean output is associated with each of these regions
- We then have a piecewise constant surface.
- The model can be written as

$$f(\mathbf{x}) = \mathbb{E}[y|\mathbf{x}] = \sum_{m=1}^M w_m \mathbb{I}(\mathbf{x} \in \mathbb{R}_m) = \sum_{m=1}^M w_m \phi(\mathbf{x}; \mathbf{v}_m)$$

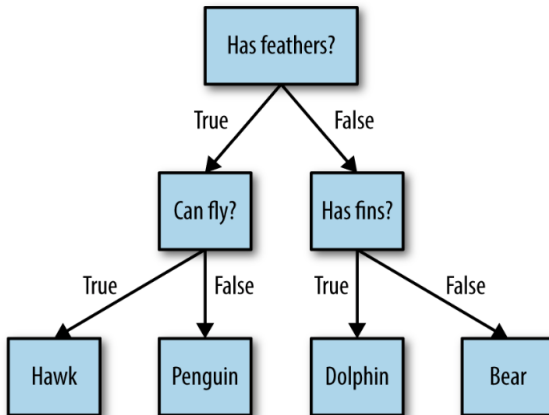
$R_m$  is the  $m$ 'th region,  $w_m$  is the mean output in this region,  $\mathbf{v}_m$  encodes the choice of variable to split on and the threshold value, on the path from the root to the  $m$ 'th leaf.

# Decision Trees – Introduction

- Imagine you want to distinguish between the following four animals: bears, hawks, penguins, and dolphins.
- Your goal is to get to the right answer by asking as few if/else questions as possible.
- You might start off by asking whether the animal has feathers, a question that narrows down your possible animals to just two.
- If the answer is “yes,” you can ask another question that could help you distinguish between hawks and penguins.
- For example, you could ask whether the animal can fly.
- If the animal doesn’t have feathers, your possible animal choices are dolphins and bears, and you will need to ask a question to distinguish between these two animals—for example, asking whether the animal has fins.

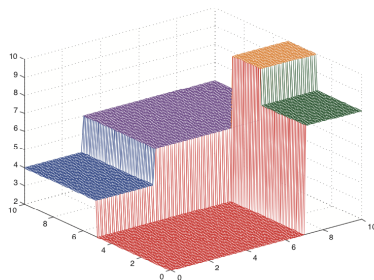
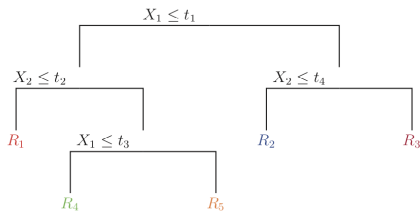
# Decision Trees - Example 1

**Figure:** A decision tree to distinguish among several animals. (Source: Müller & Guido [1])



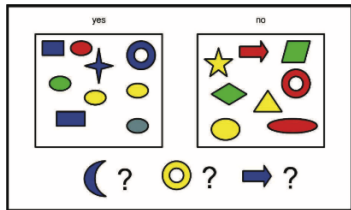
# Decision Trees - Example 2

Figure: Decision Trees. (Source: K. Murphy [2])



# Decision Trees

Figure: Some labeled training examples of colored shapes, along with 3 unlabeled test cases. (Source: K. Murphy [1])



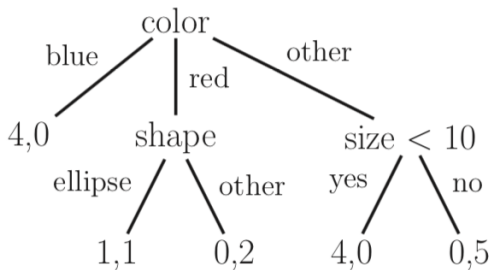
(a)

| D features (attributes) |         |           | Label |
|-------------------------|---------|-----------|-------|
| Color                   | Shape   | Size (cm) |       |
| Blue                    | Square  | 10        |       |
| Red                     | Ellipse | 2.4       |       |
| Red                     | Ellipse | 20.7      | 0     |

(b)

# Decision Trees

**Figure:** A simple decision tree for the data in Figure 7. A leaf labeled as  $(n_1, n_0)$  means that there are  $n_1$  positive examples that match this path, and  $n_0$  negative examples. In this tree, most of the leaves are “pure”, meaning they only have examples of one class or the other; the only exception is leaf representing red ellipses, which has a label distribution of  $(1, 1)$ . We could distinguish positive from negative red ellipses by adding a further test based on size. However, it is not always desirable to construct trees that perfectly model the training data, due to overfitting. (Source: K. Murphy [1])





- We split a tree so as to minimize a cost function
- Finding the optimal partitioning of the data is NP-complete
- A greedy approach is as follows
- The split function chooses the best feature, and the best value for that feature:

$$(j^*, t^*) = \arg \min_{j \in \{1, \dots, D\}} \min_{t \in \mathcal{T}_j} \text{cost}(\{\mathbf{x}_i, y_i : x_{ij} \leq t\}) + \text{cost}(\{\mathbf{x}_i, y_i : x_{ij} > t\}) \quad (1)$$

- A normalized measure of the reduction in cost

$$\Delta \triangleq \text{cost}(\mathcal{D}) - \left( \frac{|\mathcal{D}_L|}{|\mathcal{D}|} \text{cost}(\mathcal{D}_L) + \frac{|\mathcal{D}_R|}{|\mathcal{D}|} \text{cost}(\mathcal{D}_R) \right) \quad (2)$$

- The cost can be written as

$$C(\mathcal{D}) = \sum_{i \in \mathcal{D}} (y_i - \bar{y})^2$$

where  $\bar{y} = \frac{1}{|\mathcal{D}|} \sum_{i \in \mathcal{D}} y_i$  is the mean output in set  $\mathcal{D}$

- Alternatively, we can also use a linear regression model for each leaf, using the features that have been used on the path from the root to the leaf and calculate the residual errors.

- The class-conditional probabilities are given as

$$\hat{\pi}_c = \frac{1}{|\mathcal{D}|} \sum_{i \in \mathcal{D}} \mathbb{I}\{y_i = c\}$$

- The most probable class label is given by  $\hat{y}_c = \operatorname{argmax}_c \hat{\pi}_c$

Given these definitions, there are several common error measures for evaluating a proposed partition.

- Misclassification rate:

$$\frac{1}{|\mathcal{D}|} \sum_{i \in \mathcal{D}} \mathbb{I}\{y_i \neq \hat{y}\} = 1 - \hat{\pi}_c$$

- Entropy

$$\mathbb{H}(\hat{\pi}) = - \sum_{c=1}^C \hat{\pi}_c \log \hat{\pi}_c$$

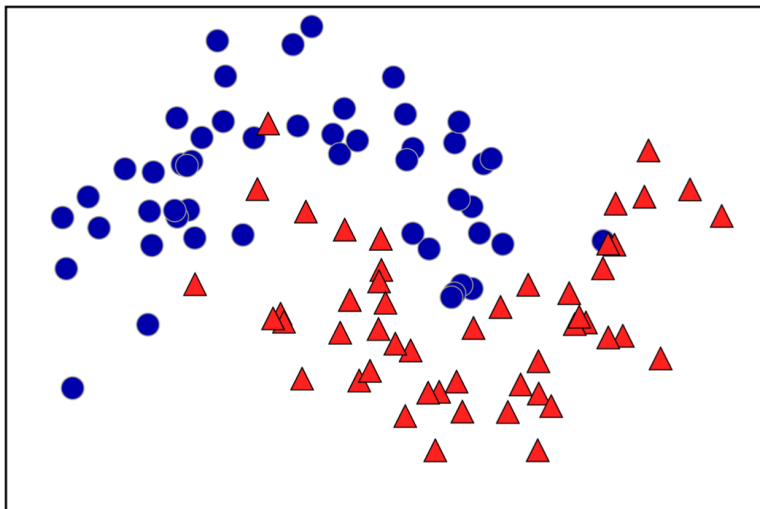
- Gini index:

$$\sum_{c=1}^C \hat{\pi}_c (1 - \hat{\pi}_c) = 1 - \sum_{c=1}^C \hat{\pi}_c^2$$

# Building decision trees

- Let's go through the process of building a decision tree for the 2D classification dataset.
- The dataset consists of two half-moon shapes, with each class consisting of 50 data points.
- We will refer to this dataset as `two_moons`.
- Learning a decision tree means learning the sequence of if/else questions that gets us to the true answer most quickly.
- In the machine learning setting, these questions are called tests
- Usually data does not come in the form of binary yes/no features as in the animal example, but is instead represented as continuous features such as in the 2D dataset shown.
- The tests that are used on continuous data are of the form “Is feature  $i$  larger than value  $a$ ?”

Figure: Two\_moons dataset. (Source: Müller & Guido [1])

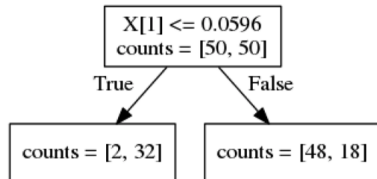
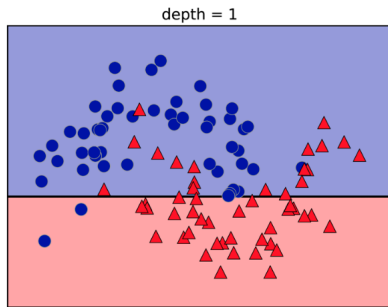


# Building decision trees

- To build a tree, the algorithm searches over all possible tests and finds the one that is most informative about the target variable.
- Splitting the dataset vertically at  $x[1]=0.0596$  yields the most information; it best separates the points in class 1 from the points in class 2.
- The top node, also called the root, represents the whole dataset, consisting of 50 points belonging to class 0 and 50 points belonging to class 1.
- The split is done by testing whether  $x[1] \leq 0.0596$ , indicated by a black line.
- If the test is true, a point is assigned to the left node, which contains 2 points belonging to class 0 and 32 points belonging to class 1.
- Otherwise the point is assigned to the right node, which contains 48 points belonging to class 0 and 18 points belonging to class 1.

# Building decision trees

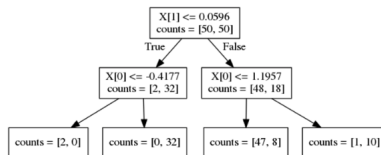
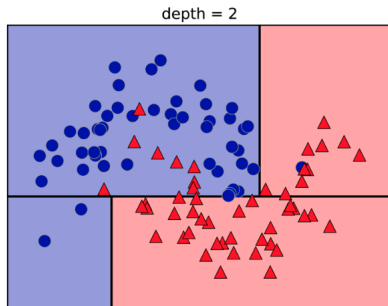
Figure: Two\_moons dataset. (Source: Müller & Guido [1])





# Building decision trees

**Figure:** Decision boundary of tree with depth 2 (left) and corresponding decision tree (right). (Source: Müller & Guido [1])

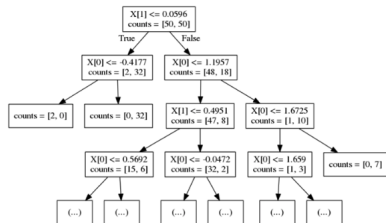
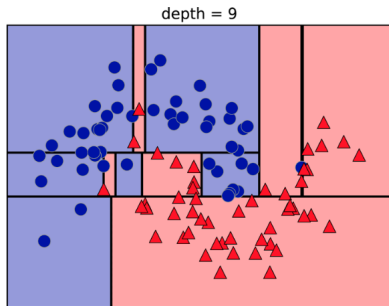


# Building decision trees

- The recursive partitioning of the data is repeated until each region in the partition (each leaf in the decision tree) only contains a single target value (a single class or a single regression value).
- A leaf of the tree that contains data points that all share the same target value is called pure. The final partitioning for this dataset is shown in the next slide

# Building decision trees

**Figure:** Decision boundary of tree with depth 9 (left) and part of the corresponding tree (right) (Source: Müller & Guido [1])



# Decision Trees - Classification examples

Residential status has three attributes with the numbers of goods and bads in each attribute in a sample of a previous customer, shown in Table. If one wants to split the tree on this characteristic, what should the split be?

| Residential status | Owner | Tenant | With Parents |
|--------------------|-------|--------|--------------|
| Number of goods    | 1000  | 400    | 80           |
| Number of bads     | 200   | 200    | 120          |
| Good:bad odds      | 5 : 1 | 2 : 1  | 0.67 : 1     |

# Decision Trees - Using entropy for classification cost

$l$  = parent,  $r$  = owner + tenant:

$$i(v) = - \left( \frac{520}{2000} \right) \ln \left( \frac{520}{2000} \right) - \left( \frac{1480}{2000} \right) \ln \left( \frac{1480}{2000} \right) = 0.573,$$

$$p(l) = \frac{200}{2000} = 0.1, \quad i(l) = - \left( \frac{80}{200} \right) \ln \left( \frac{80}{200} \right) - \left( \frac{120}{200} \right) \ln \left( \frac{120}{200} \right) = 0.673,$$

$$p(r) = \frac{1800}{2000} = 0.9, \quad i(r) = - \left( \frac{400}{1800} \right) \ln \left( \frac{400}{1800} \right) - \left( \frac{1400}{1800} \right) \ln \left( \frac{1400}{1800} \right) = 0.530,$$

$$I = 0.573 - 0.1(0.673) - 0.9(0.530) = 0.0287;$$

# Decision Trees - Using entropy for classification cost

$l$  = parent + tenant,  $r$  = owner:

$$i(v) = -\left(\frac{520}{2000}\right) \ln\left(\frac{520}{2000}\right) - \left(\frac{1480}{2000}\right) \ln\left(\frac{1480}{2000}\right) = 0.573,$$

$$p(l) = \frac{800}{2000} = 0.4, \quad i(l) = -\left(\frac{320}{800}\right) \ln\left(\frac{320}{800}\right) - \left(\frac{480}{800}\right) \ln\left(\frac{480}{800}\right) = 0.673,$$

$$p(r) = \frac{1200}{2000} = 0.6, \quad i(r) = -\left(\frac{200}{1200}\right) \ln\left(\frac{200}{1200}\right) - \left(\frac{1000}{1200}\right) \ln\left(\frac{1000}{1200}\right) = 0.451,$$

$$I = 0.573 - 0.4(0.673) - 0.6(0.451) = 0.0332.$$

$l = \text{parent}, \quad r = \text{owner} + \text{tenant}:$

$$i(v) = \left( \frac{1480}{2000} \right) \left( \frac{520}{2000} \right) = 0.1924,$$

$$p(l) = \frac{200}{2000} = 0.1, \quad i(l) = \left( \frac{80}{200} \right) \left( \frac{120}{200} \right) = 0.24,$$

$$p(r) = \frac{1800}{2000} = 0.9, \quad i(r) = \left( \frac{400}{1800} \right) \left( \frac{1400}{1800} \right) = 0.1728,$$

$$I = 0.1924 - 0.1(0.24) - 0.9(0.1728) = 0.01288;$$

$l$  = parent + tenant,  $r$  = owner:

$$i(v) = \left(\frac{520}{2000}\right) \left(\frac{1480}{2000}\right) = 0.1924,$$

$$p(l) = \frac{800}{2000} = 0.4, \quad i(l) = \left(\frac{320}{800}\right) \left(\frac{480}{800}\right) = 0.24,$$

$$p(r) = \frac{1200}{2000} = 0.6, \quad i(r) = \left(\frac{200}{1200}\right) \left(\frac{1000}{1200}\right) = 0.1389,$$

$$I = 0.1924 - 0.4(0.24) - 0.6(0.1389) \approx 0.01306.$$



```
# Splitting the dataset
from sklearn.model_selection\
    import train_test_split
X_train, X_test, y_train, y_test\
    = train_test_split(X, y, test_size = 0.25,\
        random_state = 0)
```

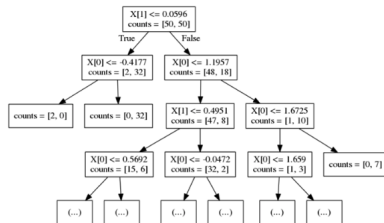
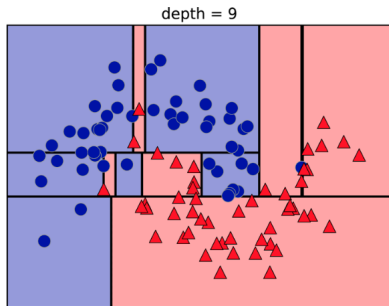
# Decision Tree Classification

```
# Fitting Decision Tree Classifier to the test set
from sklearn.tree import DecisionTreeClassifier
classifier = DecisionTreeClassifier(
    criterion = 'entropy',
    random_state = 0)
classifier.fit(X_train, y_train)

# Predicting the test set
y_pred = classifier.predict(X_test)
```

# Building decision trees

**Figure:** Decision boundary of tree with depth 9 (left) and part of the corresponding tree (right) (Source: Müller & Guido [1])



# Controlling complexity of decision trees

- Typically, building a tree as described here and continuing until all leaves are pure leads to models that are very complex and highly overfit to the training data.
- The presence of pure leaves mean that a tree is 100% accurate on the training set; each data point in the training set is in a leaf that has the correct majority class.
- The overfitting can be seen on the left.
- The regions determined to belong to class 1 in the middle of all the points belonging to class 0.
- On the other hand, there is a small strip predicted as class 0 around the point belonging to class 0 to the very right.
- This is not how one would imagine the decision boundary to look, and the decision boundary focuses a lot on single outlier points that are far away from the other points in that class.

# Preventing overfitting

- There are two common strategies to prevent overfitting:
  - Stopping the creation of the tree early (also called pre-pruning),
  - Building the tree but then removing or collapsing nodes that contain little information (also called post-pruning or just pruning).
- Possible criteria for pre-pruning include limiting the maximum depth of the tree, limiting the maximum number of leaves, or requiring a minimum number of points in a node to keep splitting it.
- Decision trees in scikit-learn are implemented in the `DecisionTreeRegressor` and `DecisionTreeClassifier` classes. scikit-learn only implements pre-pruning, not post-pruning.

# Preventing overfitting

- Let's look at the effect of pre-pruning in more detail on the Breast Cancer dataset.
- We import the dataset and split it into a training and a test part.
- Then we build a model using the default setting of fully developing the tree (growing the tree until all leaves are pure).

## No pre-pruning

```
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection\
    import train_test_split
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)
tree = DecisionTreeClassifier(random_state=0)
tree.fit(X_train, y_train)
print("Accuracy on training set: {:.3f}".format(
    tree.score(X_train, y_train)))
print("Accuracy on test set: {:.3f}".format(
    tree.score(X_test, y_test)))
```

Accuracy on training set: 1.000

Accuracy on test set: 0.937

- If we don't restrict the depth of a decision tree, the tree can become arbitrarily deep and complex.
- Unpruned trees are therefore prone to overfitting and not generalizing well to new data.
- Now let's apply pre-pruning to the tree, which will stop developing the tree before we perfectly fit to the training data.
- One option is to stop building the tree after a certain depth has been reached. Here we set `max_depth=4`, meaning only four consecutive questions can be asked.
- Limiting the depth of the tree decreases overfitting.
- This leads to a lower accuracy on the training set, but an improvement on the test set:



# With pre-pruning

```
tree = DecisionTreeClassifier(max_depth=4,  
                              random_state=0) tree.fit(  
                                X_train, y_train)  
print("Accuracy on training set: {:.3f}".format(  
      tree.score(X_train, y_train)))  
print("Accuracy on test set: {:.3f}".format(  
      tree.score(X_test, y_test)))
```

Accuracy on training set: 0.988

Accuracy on test set: 0.951

# Analyzing decision trees

- We can visualize the tree using the `export_graphviz` function from the `tree` module.
- This writes a file in the `.dot` file format, which is a text file format for storing graphs.

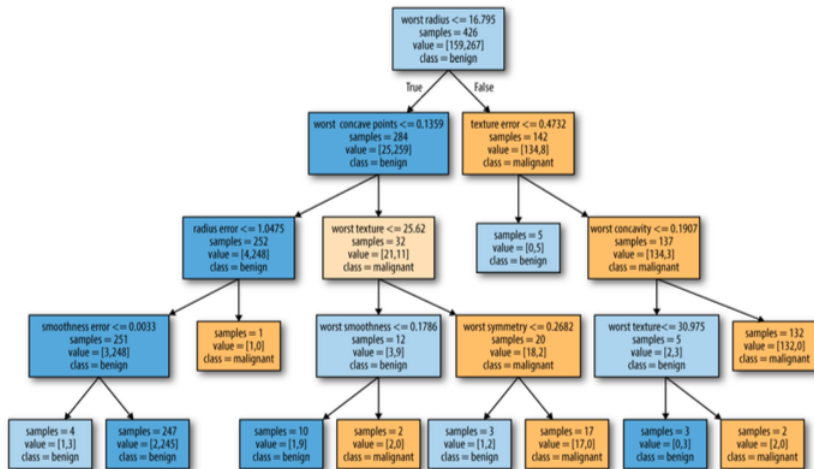
```
from sklearn.tree import export_graphviz
export_graphviz(tree, out_file="tree.dot",
                 class_names=["malignant", "benign"],
                 feature_names=cancer.feature_names,
                 impurity=False,
                 filled=True)
```

- We can read this file and visualize it using the graphviz module

```
import graphviz
with open("tree.dot") as f: dot_graph = f.read()
graphviz.Source(dot_graph)
```

# Analyzing decision trees

Figure: Analyzing decision trees (Source: Müller & Guido [1])



# Feature importance in trees

- Instead of looking at the whole tree, which can be taxing, there are some useful properties that we can derive to summarize the workings of the tree.
- The most commonly used summary is feature importance, which rates how important each feature is for the decision a tree makes.
- 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.” The feature importances always sum to 1

# Feature importances

In[62]:

```
print("Feature importances:\n{}".format(tree.feature_importances_))
```

Out[62]:

Feature importances:

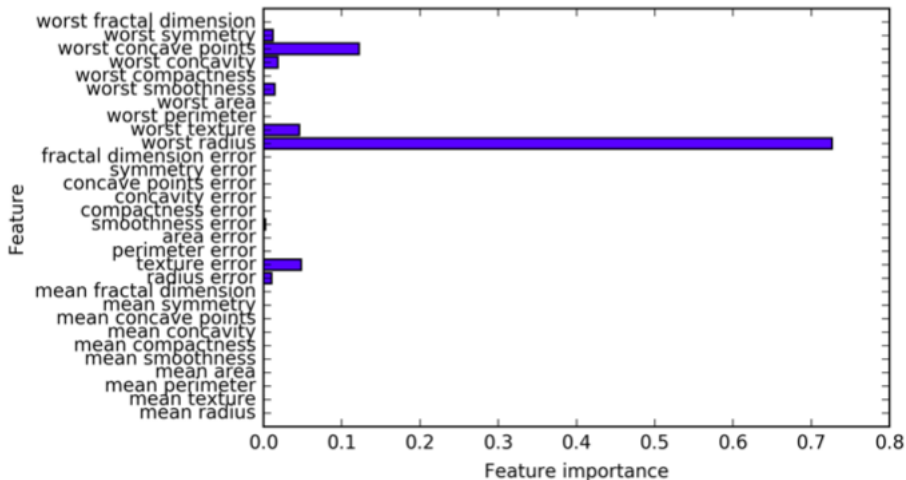
```
[ 0.      0.      0.      0.      0.      0.      0.      0.      0.      0.      0.01
  0.048  0.      0.      0.002  0.      0.      0.      0.      0.      0.727  0.046
  0.      0.      0.014  0.      0.018  0.122  0.012  0. ]
```

# Feature importances

```
def plot_feature_importances_cancer(model):  
    n_features = cancer.data.shape[1]  
    plt.barh(range(n_features),  
             model.feature_importances_, align='center')  
    plt.yticks(np.arange(n_features),  
               cancer.feature_names)  
    plt.xlabel("Feature importance")  
    plt.ylabel("Feature")  
    plot_feature_importances_cancer(tree)
```

# Feature importances

**Figure:** Feature importances computed from a decision tree learned on the Breast Cancer dataset (Source: Müller & Guido [1])





# Decision Tree Classification – Some parameters

- **criterion** : string, optional (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.
- **max\_depth** : int or None, optional (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.
- **min\_samples\_split** : int, float, optional (default=2) The minimum number of samples required to split an internal node:  
If int, then consider `min_samples_split` as the minimum number. If float, then `min_samples_split` is a fraction and  $\text{ceil}(\text{min\_samples\_split} * n\_samples)$  are the minimum number of samples for each split.

# Decision Tree Classification – Some parameters

- **min\_samples\_leaf** : int, float, optional (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  $\text{ceil}(\text{min\_samples\_leaf} * n\_samples)$  are the minimum number of samples for each node. Changed in version 0.18: Added float values for fractions.
- **min\_weight\_fraction\_leaf** : float, optional (default=0.) The minimum weighted fraction of the sum total of weights (of all the input samples) required to be at a leaf node. Samples have equal weight when sample\_weight is not provided.
- **max\_features** : int, float, string or None, optional (default=None) The number of features to consider when looking for the best split:

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- We can reduce the variance (without increasing the bias) of an estimate by averaging together multiple estimates.
- While the predictions of a single tree are highly sensitive to noise in its training set, the average of many trees is not, as long as the trees are not correlated (Wikipedia).
- For example, we can train  $N$  different trees on different subsets of the data, chosen randomly with replacement, and then compute the ensemble

$$f(\mathbf{x}) = \sum_{n=1}^N \frac{1}{N} f_n(\mathbf{x})$$

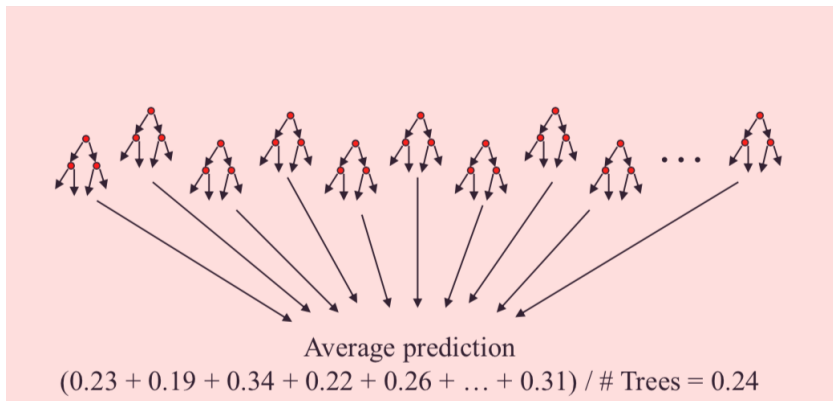
where  $f_m$  is the  $m$ 'th tree.

- This technique is known as **bagging**, which stands for “bootstrap aggregating”.

# Bagging

- Draw 100 bootstrap samples of data
- Train a tree on each sample (100 trees)
- Average prediction of trees on out-of-bag samples

Figure: An example of bagging. (Source: UIUC CS446 Lecture notes)



- Unfortunately, simply re-running the same learning algorithm on different subsets of the data can result in highly correlated predictors, which limits the amount of variance reduction that is possible.
- The technique known as random forests tries to decorrelate the base learners by learning trees based on a randomly chosen subset of features, as well as a randomly chosen subset of data cases.
- This process is sometimes called "feature bagging". The reason for doing this is the correlation of the trees in an ordinary bootstrap sample: if one or a few features are very strong predictors for the response variable (target output), these features will be selected in many of the trees, causing them to become correlated (Wikipedia).
- Such models often have very good predictive accuracy, and have been widely used in many applications

- Draw  $N$  bootstrap samples of data
- Draw sample of available attributes at each split
- Train trees on each sample/attribute set ( $N$  trees)
- Average prediction of trees on out-of-bag samples

# Random Forest Classification

```
# Fitting Random Forest Classifier  
# to the training set  
from sklearn.ensemble import\  
    RandomForestClassifier  
classifier = RandomForestClassifier(  
    n_estimators = 10,  
    criterion = 'entropy',  
    random_state = 0)  
classifier.fit(X_train, y_train)  
  
# Predicting the test set  
y_pred = classifier.predict(X_test)
```



# Random Forest Classification – Some parameters

- **n\_estimators** : integer, optional (default=10) The number of trees in the forest.
- **criterion** : string, optional (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. Note: this parameter is tree-specific.
- **max\_depth** : integer or None, optional (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.
- **min\_samples\_split** : int, float, optional (default=2) The minimum number of samples required to split an internal node: If int, then consider min\_samples\_split as the minimum number. If float, then min\_samples\_split is a fraction and  $\text{ceil}(\text{min\_samples\_split} * n\_samples)$  are the minimum number of samples for each split.

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- An **adaptive basis-function model** (ABM) is a model of the form

$$f(x) = w_0 + \sum_{m=1}^M w_m \phi_m(x)$$

where  $\phi_m(x)$  is the  $m$ 's basis function, which is learned from data

- In **boosting**,  $\phi_m$  are generated by an algorithm called a **weak learner** or a **base learner**.
- This weak learner can be any classification or regression algorithm, but it is common to use a CART model.

- Initialization:
  - Weigh all training samples equally
- Iteration Step:
  - Train model on (weighted) train set
  - Compute error of model on train set
  - Increase weights on training cases model gets wrong
- Typically requires 100's to 1000's of iterations
- Return final model:
  - Carefully weighted prediction of each model

```
# Fitting XGBoost to the training set  
from xgboost import XGBClassifier  
classifier = XGBClassifier()  
classifier.fit(X_train, y_train)  
  
# Predicting the test set  
y_pred = classifier.predict(X_test)
```

# XGBoost Classification – Some parameters

- **loss** : 'deviance', 'exponential', optional (default='deviance') loss function to be optimized. 'deviance' refers to deviance (= logistic regression) for classification with probabilistic outputs. For loss 'exponential' gradient boosting recovers the AdaBoost algorithm.
- **learning\_rate** : float, optional (default=0.1) learning rate shrinks the contribution of each tree by learning\_rate. There is a trade-off between learning\_rate and n\_estimators.
- **n\_estimators** : int (default=100) The number of boosting stages to perform. Gradient boosting is fairly robust to over-fitting so a large number usually results in better performance.
- **subsample** : float, optional (default=1.0) The fraction of samples to be used for fitting the individual base learners. If smaller than 1.0 this results in Stochastic Gradient Boosting. subsample interacts with the parameter n\_estimators. Choosing subsample  $\leq$  1.0 leads to a reduction of variance and an increase in bias.

- 1 Decision Trees
- 2 Random Forest
- 3 Boosting
- 4 References**

- [1] K. P. Murphy – Machine Learning – A Probabilistic Perspective, MIT Press, 2012.
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