Lecture 12 k-NN, Decision Tree and Random Forest

In previous lectures, we take linear regression and logistic regression as examples to form a (relatively) rigorous mathematical framework of **supervised learning**:

- 1. Define the **supervised learning** problem as function fitting problem $y \approx f(x)$:
 - Determining the function with **training data** (providing both true x and y), and with this f, making predictions on **test data** (only x is necessary, although sometimes y is also provided to evaluate the performace).
- 2. Making assumptions about the form of $f(x; \beta)$ by introducting parameters β (or w, W)-- assumptions lead to models;
- 1. Deriving the concrete form of Loss function $L(\beta)$ -- most common approach is maximum likelihood estimation, which measures "how good" $f(x; \beta)$ fits the actual y given the paramter β ;
- 1. Minimizing (analytically or numerically) the Loss function $L(\beta)$ on **training data**, to find a reasonable parameter $\hat{\beta}$; (this step is called "fit" in sklearn)
- 1. On the test data, making predictions (called "predict" in sklearn). If true labels are also known in test dataset, using metrics (R-squared,accuracy) to evaluate the performace (called "score" in sklearn).

Meanwhile, there exists other supervised learning approaches that might not strictly follow this guidline. Sometimes the formula f and loss function L is not explictly used. At first glance, these methods are rather heuristic or even "naive" -- while they can really give surprisingly good results. In this lecture, we are going to introduce some important algorithms of such style.

k-NN (k-nearest neighbor classifier) (https://en.wikipedia.org/wiki/K-nearest neighbors algorithm)

Intuitions: To make a prediction of test sample, we don't have to always derive the mapping formula explicitly -- we just look at its "close friends" in training dataset, and follow its friends' label!

Mathematical Description: Given a test sample \mathbf{x} from **test** dataset, the kNN classifier first identifies the neighbors k points in the **training** data that are closest to \mathbf{x} , whose indices are represented by \mathcal{N}_x . It then estimates the probability that \mathbf{x} belongs to class j by $P(y=j|\mathbf{x})$ computing the fraction of points in \mathcal{N} whose label(s) actually equal j:

$$P(y = j | \mathbf{x}) \approx \frac{1}{k} \sum_{i \in \mathcal{N}_x} 1\{y^{(i)} = j\}.$$

We finally determine its class by picking up the class with largest probability.

Remark: The similar philosophy can also extend to regression problem.

```
In [1]: from sklearn.datasets import load_iris
    X,y = load_iris(return_X_y = True)

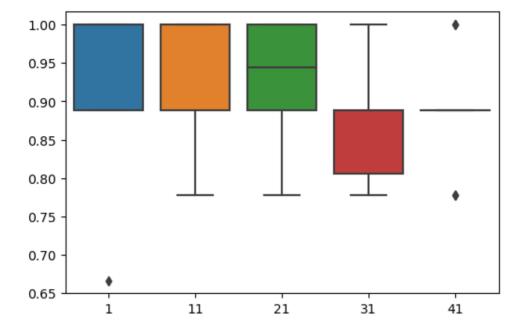
In [2]: from sklearn.model_selection import train_test_split
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.4, random_state = 42)
```

In practice, the challenging question is always choosing the correct *k* (parameter tuning). Recall that a powerful strategy is to use <u>crosms validation (https://scikit-learn.org/stable/modules/cross_validation.html</u>).

```
In [3]: from sklearn.neighbors import KNeighborsClassifier
         knn clf = KNeighborsClassifier(n neighbors = 20)
         knn_clf.fit(X_train, y_train)
         knn clf.score(X test,y test)
Out[3]: 1.0
In [4]:
         import pandas as pd
         from sklearn.model_selection import cross val score
         k list = list(range(1,50,10))
         # creating dataframe of cv scores and test scores -- of course you can also use Numpy
         arrav
         cv scores = pd.DataFrame()
         test scores = pd.Series(dtype = 'float64')
         # perform 10-fold cross validation
         for k in k list:
             knn_clf.set_params(n_neighbors=k) # update the object
             scores = cross val score(knn clf, X train, y train, cv=10, scoring='accuracy')
             cv scores[str(k)] = scores
             test_scores[str(k)] = knn_clf.score(X_test,y test)
In [5]:
         cv_scores
Out[5]:
                 1
                         11
                                 21
                                         31
                                                 41
          0 0.888889
                    0.777778 0.777778
                                    0.777778
                                            0.777778
          1 1.000000
                   1.000000 1.000000
                                    0.888889
                                            0.888889
          2 1.000000
                   0.888889
                            0.888889
                                    0.888889
                                            0.888889
          3 0.666667 0.777778 0.777778 0.777778
                                            0.888889
          4 0.888889
                    1.000000
                            0.888889
                                    0.888889
                                            0.888889
          5 1.000000
                   1.000000 1.000000
                                    0.888889
                                            0.888889
          6 1.000000
                   1.000000 1.000000
                                    1.000000
                                            1.000000
         7 1.000000
                    1.000000
                            1.000000
                                    1.000000
                                            1.000000
          8 1.000000
                   1.000000
                            1.000000
                                    0.777778 0.777778
          9 0.888889 0.888889 0.888889 0.888889
In [6]: cv scores.mean()
Out[6]: 1
               0.933333
               0.933333
         21
               0.922222
         31
               0.877778
               0.888889
         41
         dtype: float64
In [7]: cv_scores.std()
Out[7]: 1
               0.107344
         11
               0.093697
         21
               0.091475
         31
               0.081985
         41
               0.074074
         dtype: float64
```

```
In [8]: import seaborn as sns
   import matplotlib.pyplot as plt
   fig, ax = plt.subplots(dpi=100)
   sns.boxplot(data =cv_scores)
```

Out[8]: <AxesSubplot:>



<u>Decision Tree (https://en.wikipedia.org/wiki/Decision_tree_learning)</u>

How human-being make classifications? Instead of using mathematical equations, we actually make a series of "decisions" based on the important features that are drawn from our past experience.

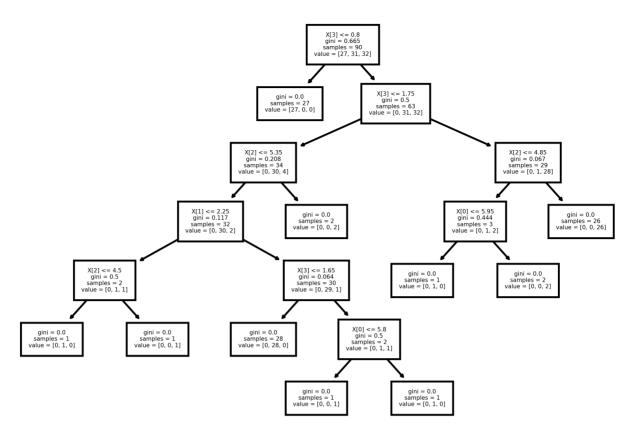
Intuitions: By repeatedly setting threshold for different features (multiple if-else conditions -- forming a flow-chart or decision tree structure), we can naturally achieve the classification task.

Mathematical Considerations: How to decide the appropriate thresholds and the order of if-else conditions? **Gini impurity** or **Entropy** (not required in this class). You only need to know that these tresholds/order of conditions are determined by the training dataset, using certain metrics to select. Different concerete strategies lead to various algorithms, known as ID3, CART, C4.5...

For the basic requirements, in this course we only ask you to call the package and understand how to interpret the results.

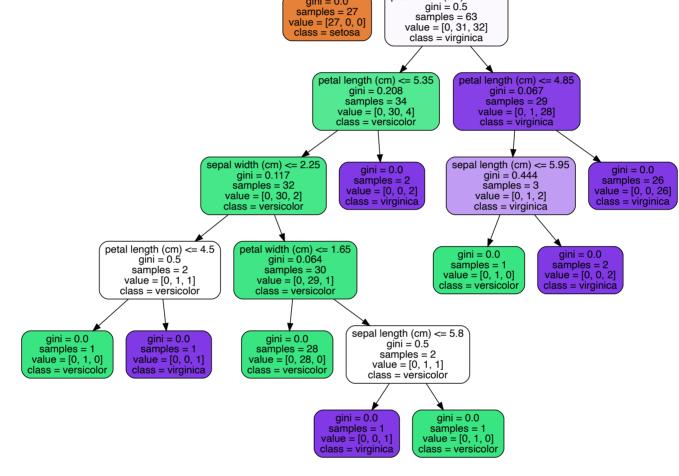
```
In [10]: from sklearn import tree
    dt_clf = tree.DecisionTreeClassifier()
    dt_clf.fit(X_train,y_train)
    dt_clf.score(X_test,y_test)
Out[10]: 0.98333333333333333
```

```
In [11]: fig, ax = plt.subplots(dpi=500)
    tree.plot_tree(dt_clf,fontsize=3)
    plt.show()
```



To visualize the trees more elegantly, we can use the graphviz package (<u>installment (https://scikit-learn.org/stable/modules/tree.html</u>) is not basic requirement of our course, and the easiest way is through <u>conda command line (https://tljh.jupyter.org/en/latest/howto/env/user-environment.html</u>)).

```
In [12]: from sklearn.datasets import load_iris
           iris = load iris()
           import graphviz
           dot data = tree.export graphviz(dt clf, out file=None, class names = iris.target names
            , feature names=iris.feature names, filled=True, rounded=True)
           graph = graphviz.Source(dot data)
           graph
Out[12]:
                                                             petal width (cm) <= 0.8
gini = 0.665
                                                                samples = 90
                                                              value = [27, 31, 32]
                                                                class = virginica
                                                                          False
                                                            True
                                                                      petal width (cm) <= 1.75
                                                         gini = 0.0
                                                                           gini = 0.5
                                                                          samples = 63
```



To get you more familiar with the concept of decision tree, let's try another dataset of breast cancer.

```
In [13]: from sklearn.datasets import load_breast_cancer
bc = load_breast_cancer()
X = bc.data
y = bc.target
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.5, random_state = 42)
dt_clf = tree.DecisionTreeClassifier()
dt_clf.fit(X_train,y_train)
dt_clf.score(X_test,y_test)
```

Out[13]: 0.9157894736842105

```
dot_data = tree.export_graphviz(dt_clf, out_file=None,class_names = bc.target_names,f
                         eature names=bc.feature names,filled=True, rounded=True)
                         graph = graphviz.Source(dot data)
                         graph
Out[14]:
                                                                                                                                                                     worst concave points <= 0.147
                                                                                                                                                                              gini = 0.481
samples = 284
value = [114, 170]
                                                                                                                                                                                 class = benian
                                                                                                                                                                        True
                                                                                                                                                                                                        False
                                                                                                                                                                            116.05
                                                                                                                                                                                             fractal dimension error <= 0.013
                                                                                                                                                 worst perimeter
                                                                                                                                                       gini = 0.197
samples = 190
value = [21, 169]
class = benign
                                                                                                                                                                                                          gini = 0.021
samples = 94
                                                                                                                                                                                                       value = [93, 1]
class = malignant
                                                                                                               area error <= 35.68
gini = 0.097
                                                                                                                                                     worst concavity <= 0.18
gini = 0.245
                                                                                                                                                                                                          gini = 0.0
                                                                                                                                                                                                                                        gini = 0.0
                                                                                                                                                                                                       samples = 93
value = [93, 0]
                                                                                                                  samples = 176
value = [9, 167]
class = benign
                                                                                                                                                            samples = 14
value = [12, 2]
                                                                                                                                                                                                                                     value = [0, 1]
class = benign
                                                                                                                                                                                                     class = malignan
                                                                                                                                                         class = malignant
                                                                orst texture <= 30.145
gini = 0.047
                                                                                                      fractal dimension error <= 0.003
gini = 0.496
                                                                                                                                                             gini = 0.0
samples = 2
value = [0, 2]
                                                                                                                                                                                             gini = 0.0
                                                                                                                                                                                          samples = 12
value = [12, 0]
                                                                  samples = 165
value = [4, 161]
class = benign
                                                                                                                    samples = 11
value = [5, 6]
                                                                                                                   class = benign
                                                         worst concave points <= 0.133
gini = 0.298
samples = 22
value = [4, 18]
class = benign
                                                                                                                     gini = 0.0
                                aini = 0.0
                                                                                                                                                   aini = 0.0
                                                                                                                samples = 5
value = [5, 0]
class = malignant
                            samples = 143
value = [0, 143]
class = benign
                                                                                                                                                samples = 6
value = [0, 6]
class = benign
                                                                   = 0.988
                                              texture error <
                                                                                          gini = 0.0
                                                     gini = 0.18
                                                                                        samples = 2
value = [2, 0]
                                                   samples = 20
value = [2, 18]
class = benign
                                                                                     class = malignant
                                                               perimeter error < gini = 0.1
                                                                      samples = 19
value = [1, 18]
class = benign
                                                  area error <= 17
gini = 0.375
samples = 4
value = [1, 3]
                                                                                      gini = 0.0
samples = 15
value = [0, 15]
                                          gini = 0.0
                                                                         aini = 0.0
                                        samples = 3 value = [0, 3]
                                                                      samples = 1
value = [1, 0]
```

Random Forest (https://en.wikipedia.org/wiki/Random_forest#:~:text=Random%20forests%20 and Ensemble Methods (https://scikitlearn.org/stable/modules/ensemble.html)

Despite that the idea of decision tree is very straightward, the method is notorious for its over-fitting and high variance.

To make the decision tree more robust, we can construct the "forest" of multiple trees, and let the forest of trees to "vote".

The each decision tree can be "random" (therefore different with each other) in two ways:

In [14]: import graphviz

- In each run, we only pick up a random subset of features as training dataset
- In each run, we only pick up a random subset of samples as training dataset

```
In [15]: from sklearn.ensemble import RandomForestClassifier
    rf_clf = RandomForestClassifier(n_estimators=1000, max_samples = 0.5, max_depth=5, ra
    ndom_state=0, n_jobs = -1) # make 1000 decision trees by random picking up 90% of the
    dataset, and each tree has the maximum depth of 5. njobs = -1 means you ask to use al
    l the processors of your computer
    rf_clf.fit(X_train, y_train) # note that we still work on the breast cancer dataset
    rf_clf.score(X_test, y_test)
Out[15]: 0.9614035087719298
```

The same idea can be applied to other supervised methods -- and the strategy is called "bagging" in machine learning.

```
In [16]: from sklearn.ensemble import BaggingClassifier
    bagging_knn_clf = BaggingClassifier(KNeighborsClassifier(), n_estimators=100,max_samp
    les=0.8, max_features=0.5, n_jobs = -1)
    bagging_knn_clf.fit(X_train,y_train)
    bagging_knn_clf.score(X_test,y_test)
```

Out[16]: 0.9543859649122807

Besides create random classifiers by subsetting the dataset, another clever strategy is to let different classifiers "vote" -- this relates to the <u>wisdom of crowds (https://www.geeksforgeeks.org/ensemble-methods-and-wisdom-of-the-crowd/)</u>.

```
In [ ]: from sklearn.ensemble import VotingClassifier
        from sklearn.linear model import LogisticRegression
        from sklearn.neighbors import KNeighborsClassifier
        from sklearn.svm import SVC
        clf1 = LogisticRegression(max iter=5000)
        clf2 = RandomForestClassifier(n estimators=50, random state=1)
        clf3 = SVC(kernel='rbf', probability=True)
        eclf = VotingClassifier(estimators=[('lr', clf1), ('rf', clf2), ('svm', clf3)],voting
        ='hard')
        for clf, label in zip([clf1, clf2, clf3, eclf], ['Logistic Regression', 'Random Fores
        t', 'Support Vector Machine', 'Ensemble']):
                scores_cv = cross_val_score(clf, X_train, y_train, scoring='accuracy', cv=5)
                clf.fit(X train,y train)
                score test = clf.score(X test,y test)
                print("Accuracy of CV: %0.2f (+/- %0.2f) [%s]" % (scores cv.mean(), scores cv
        .std(), label))
                print("Accuracy on Test: %0.2f [%s]" % (score_test, label))
```