How To Build a Machine Learning Classifier in Python with Scikit-learn

Written by Michelle Morales Edited by Brian Hogan

In this tutorial, you'll implement a simple machine learning algorithm in Python using <u>Scikit-learn</u>, a machine learning tool for Python. Using a database of breast cancer tumor information, you'll use a <u>Naive Bayes</u> (NB) classifier that predicts whether or not a tumor is malignant or benign.

By the end of this tutorial, you'll know how to build your very own machine learning model in Python.

Prerequisites

To complete this tutorial, we'll use Jupyter Notebooks, which are a useful and interactive way to run machine learning experiments. With Jupyter Notebooks, you can run short blocks of code and see the results quickly, making it easy to test and debug your code.

To get up and running quickly, you can open up a web browser and navigate to the Try Jupyter website: jupyter.org/try. From there, click on Try Jupyter with Python, and you will be taken to an interactive Jupyter Notebook where you can start to write Python code.

If you would like to learn more about Jupyter Notebooks and how to set up your own Python programming environment to use with Jupyter, you can read our tutorial on <u>How To Set Up Jupyter Notebook for Python 3</u>.

Step 1 — Importing Scikit-learn

Let's begin by installing the Python module <u>Scikit-learn</u>, one of the best and most documented machine learning libraries for Python.

To begin our coding project, let's activate our Python 3 programming environment. Make sure you're in the directory where your environment is located, and run the following command:

```
. my env/bin/activate
```

With our programming environment activated, check to see if the Sckikit-learn module is already installed:

```
(my env) $ python -c "import sklearn"
```

If sklearn is installed, this command will complete with no error. If it is not installed, you will see the following error message:

Output

```
Traceback (most recent call last): File "<string>", line 1, in <module>
    ImportError: No module named 'sklearn'
```

The error message indicates that sklearn is not installed, so download the library using pip:

```
(my env) $ pip install scikit-learn[alldeps]
```

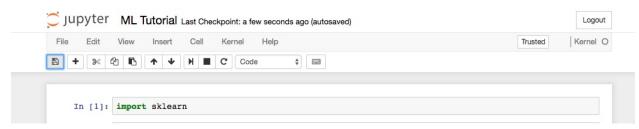
Once the installation completes, launch Jupyter Notebook:

In Jupyter, create a new Python Notebook called ML Tutorial. In the first cell of the Notebook, <u>import</u> the sklearn module:

ML Tutorial

import sklearn

Your notebook should look like the following figure:



Jupyter Notebook with one Python cell, which imports sklearn

Now that we have sklearn imported in our notebook, we can begin working with the dataset for our machine learning model.

Step 2 — Importing Scikit-learn's Dataset

The dataset we will be working with in this tutorial is the <u>Breast Cancer Wisconsin Diagnostic Database</u>. The dataset includes various information about breast cancer tumors, as well as classification labels of malignant or benign. The dataset has 569 instances, or data, on 569 tumors and includes information on 30 attributes, or features, such as the radius of the tumor, texture, smoothness, and area.

Using this dataset, we will build a machine learning model to use tumor information to predict whether or not a tumor is malignant or benign.

Scikit-learn comes installed with various datasets which we can load into Python, and the dataset we want is included. Import and load the dataset:

```
ML Tutorial
...
from sklearn.datasets import load_breast_cancer
# Load dataset

data = load breast cancer()
```

The data <u>variable</u> represents a Python object that works like a <u>dictionary</u>. The important dictionary keys to consider are the classification label names (target_names), the actual labels (target), the attribute/feature names (feature_names), and the attributes (data).

Attributes are a critical part of any classifier. Attributes capture important characteristics about the nature of the data. Given the label we are trying to predict (malignant versus benign tumor), possible useful attributes include the size, radius, and texture of the tumor.

Create new variables for each important set of information and assign the data:

```
ML Tutorial
...
# Organize our data
```

```
label_names = data['target_names']
labels = data['target']
feature_names = data['feature_names']
features = data['data']
```

We now have <u>lists</u> for each set of information. To get a better understanding of our dataset, let's take a look at our data by printing our class labels, the first data instance's label, our feature names, and the feature values for the first data instance:

```
ML Tutorial
...

# Look at our data
print(label_names)
print(labels[0])
print(feature_names[0])
print(features[0])
```

You'll see the following results if you run the code:

```
In [3]: # Look at our data
       print(label_names)
        print(labels[0])
       print(feature_names[0])
       print(features[0])
       ['malignant' 'benign']
       mean radius
        8.58900000e+00 1.5340000e+02
5.37300000e-02 1.58700000e-02
                                           6.39900000e-03
                                                           4.90400000e-02
                                          3.00300000e-02
                                                           6.19300000e-03
          2.53800000e+01
                          1.73300000e+01
                                           1.84600000e+02
                                                           2.01900000e+03
          1.62200000e-01 6.65600000e-01
4.60100000e-01 1.18900000e-01]
                                           7.11900000e-01
                                                           2.65400000e-01
```

Alt Jupyter Notebook with three Python cells, which prints the first instance in our dataset

As the image shows, our class names are malignant and benign, which are then mapped to binary values of 0 and 1, where 0 represents malignant tumors and 1 represents benign tumors. Therefore, our first data instance is a malignant tumor whose mean radius is 1.79900000e+01.

Now that we have our data loaded, we can work with our data to build our machine learning classifier.

Step 3 — Organizing Data into Sets

To evaluate how well a classifier is performing, you should always test the model on unseen data. Therefore, before building a model, split your data into two parts: a training set and a test set.

You use the training set to train and evaluate the model during the development stage. You then use the trained model to make predictions on the unseen test set. This approach gives you a sense of the model's performance and robustness.

Fortunately, sklearn has a function called train_test_split(), which divides your data into these sets. Import the function and then use it to split the data:

```
ML Tutorial
...
from sklearn.model_selection import train_test_split

# Split our data

train, test, train_labels, test_labels = train_test_split(features, labels,
```

```
test_size=0.33,
random state=42)
```

The function randomly splits the data using the test_size parameter. In this example, we now have a test set (test) that represents 33% of the original dataset. The remaining data (train) then makes up the training data. We also have the respective labels for both the train/test variables, i.e. train labels and test labels.

We can now move on to training our first model.

Step 4 — Building and Evaluating the Model

There are many models for machine learning, and each model has its own strengths and weaknesses. In this tutorial, we will focus on a simple algorithm that usually performs well in binary classification tasks, namely <u>Naive Bayes (NB)</u>.

First, import the GaussianNB module. Then initialize the model with the GaussianNB() function, then train the model by fitting it to the data using gnb.fit():

```
ML Tutorial
...
from sklearn.naive_bayes import GaussianNB
# Initialize our classifier
gnb = GaussianNB()
# Train our classifier
```

```
model = gnb.fit(train, train labels)
```

After we train the model, we can then use the trained model to make predictions on our test set, which we do using the predict() function. The predict() function returns an array of predictions for each data instance in the test set. We can then print our predictions to get a sense of what the model determined.

Use the predict () function with the test set and print the results:

```
ML Tutorial
...
# Make predictions
preds = gnb.predict(test)
print(preds)
```

Run the code and you'll see the following results:

Jupyter Notebook with Python cell that prints the predicted values of the Naive Bayes classifier on our test data

As you see in the Jupyter Notebook output, the predict() function returned an array of 0s and 1s which represent our predicted values for

the tumor class (malignant vs. benign).

Now that we have our predictions, let's evaluate how well our classifier is performing.

Step 5 — Evaluating the Model's Accuracy

Using the array of true class labels, we can evaluate the accuracy of our model's predicted values by comparing the two arrays (test_labels vs.preds). We will use the sklearn function accuracy_score() to determine the accuracy of our machine learning classifier.

```
ML Tutorial
...
from sklearn.metrics import accuracy_score
# Evaluate accuracy
print(accuracy_score(test_labels, preds))
```

You'll see the following results:

```
In [7]: from sklearn.metrics import accuracy_score
    # Evaluate accuracy
    print(accuracy_score(test_labels, preds))
    0.941489361702
```

Alt Jupyter Notebook with Python cell that prints the accuracy of our NB classifier

As you see in the output, the NB classifier is 94.15% accurate. This means that 94.15 percent of the time the classifier is able to make the correct prediction as to whether or not the tumor is malignant or benign.

These results suggest that our feature set of 30 attributes are good indicators of tumor class.

You have successfully built your first machine learning classifier. Let's reorganize the code by placing all import statements at the top of the Notebook or script. The final version of the code should look like this:

ML Tutorial

```
from sklearn.datasets import load breast cancer
from sklearn.model selection import train test split
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score
# Load dataset
data = load_breast_cancer()
# Organize our data
label_names = data['target_names']
labels = data['target']
feature names = data['feature names']
features = data['data']
# Look at our data
print(label names)
print('Class label = ', labels[0])
print(feature names)
print(features[0])
```

```
# Split our data
train, test, train labels, test labels = train test split(features,
                                                            labels,
test size=0.33,
random state=42)
# Initialize our classifier
gnb = GaussianNB()
# Train our classifier
model = gnb.fit(train, train labels)
# Make predictions
preds = gnb.predict(test)
print(preds)
# Evaluate accuracy
print(accuracy score(test labels, preds))
```

Now you can continue to work with your code to see if you can make your classifier perform even better. You could experiment with different subsets of features or even try completely different algorithms. Check out Scikit-learn's website at scikit-learn.org/stable for more machine learning ideas.

Conclusion

In this tutorial, you learned how to build a machine learning classifier in Python. Now you can load data, organize data, train, predict, and evaluate machine learning classifiers in Python using Scikit-learn. The steps in this tutorial should help you facilitate the process of working with your own data in Python.