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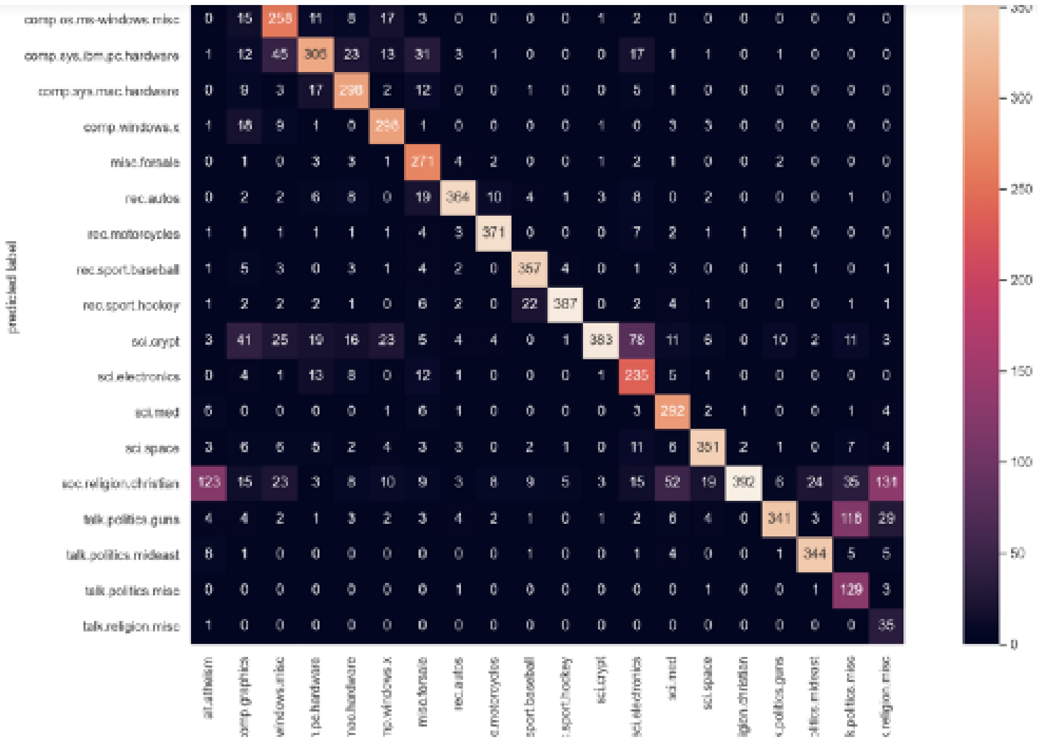
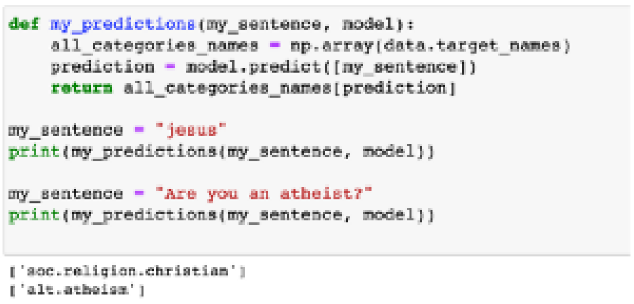
GETTING STARTED

Text Classification Using Naive Bayes: Theory & A Working Example

In this article, I explain how the Naive Bayes works and I implement a multi-class text classification problem step-by-step in Python.





```
def my_predictions(my_sentence, model):
    all_categories_names = np.array(data.target_names)
    prediction = model.predict([my_sentence])
    return all_categories_names[prediction]

my_sentence = "jesus"
print(my_predictions(my_sentence, model))

my_sentence = "Are you an atheist?"
print(my_predictions(my_sentence, model))
```

```
['soc.religion.christian']
['alt.atheism']
```

Figure created by the author.

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1. Introduction

Naive Bayes classifiers have been heavily used for **text classification** and **text analysis** machine learning **problems**.

Text Analysis is a major applicatio 178 3 ng algorithms. However the raw data, a sequence of symbols (i.e. strings) cannot be fed directly to the algorithms themselves as most of them expect numerical feature vectors with a fixed size rather than the raw text documents with variable length.

In this article I explain a) how **Naive Bayes** works, b) how we can use **text data** and **fit** them into a **model** after transforming them into a more appropriate form. Finally, I **implement** a **multi-class text classification problem step-by-step in Python**.

Let's get started !!!

2. The Naive Bayes algorithm

Naive Bayes classifiers are a collection of classification algorithms based on **Bayes' Theorem**. It is not a single algorithm but a family of algorithms where all of them share a common principle, i.e. every pair of features being classified is independent of each other.

The dataset is divided into two parts, namely, **feature matrix** and the **response/target vector**.

- The **Feature matrix** (X) contains all the vectors(rows) of the dataset in which each vector consists of the value of **dependent features.** The number of features is **d** i.e. **X = (x1,x2,x2, xd).**
- The **Response/target vector** (y) contains the value of **class/group variable** for **each row of feature matrix.**

2.1. The main two assumptions of Naive Bayes

Naive Bayes assumes that **each feature/variable** of the same class makes an:

- **independent**
- **equal**

contribution to the outcome.

Side Note: The assumptions made by Naive Bayes are not generally correct in real-world situations. In-fact, the independence assumption is often not met and this is why it is called event that has already occurred. Bayes' theorem is stated mathematically as follows:

$$P(A \mid B) = \frac{P(B \mid A)P(A)}{P(B)}$$

Figure created by the author.

where:

- A and **B** are called **events.**
- P(A | B) is the probability of event A, given the event B is true (has occured). Event B is also termed as **evidence**.
- P(A) is the **priori** of A (the prior independent probability, i.e. probability of event before evidence is seen).
- P(B | A) is the probability of B given event A, i.e. probability of event B after evidence A is seen.

Summary

$$\begin{aligned}
&A, B && = \text{events} \\
&P(A \mid B) && = \text{probability of A given B is true} \\
&P(B \mid A) && = \text{probability of } B \text{ given } A \text{ is true} \\
&P(A), P(B) && = \text{the independent probabilities of A and B}
\end{aligned}$$

Figure created by the author.

2.3. The Naive Bayes Model

Given a data matrix X and a target vector y, we state our problem as:

$$P(y \mid X) = \frac{}{P(X)}$$

Figure created by the author.

where, **y** is **class variable** and X is a **dependent feature vector with dimension d i.e.** X = **(x1,x2,x2, xd),** where **d** is the number of variables/features of the sample.

- P(y|X) is the probability of observing the class **y** given the sample **X** with **X = (x1,x2,x2, xd),** where **d** is the number of variables/features of the sample.

Now the "naïve" conditional independence assumptions come into play: assume that all features in **X** are mutually independent, conditional on the category **y:**

$$P(y \mid x_1, \ldots, x_d) = \frac{P(y) \prod_{i=1}^{d} P(x_i|y)}{P(x_1)P(x_2)\ldots P(x_d)}$$

The denominator remains constant for a given input, so we can remove that term:

$$P(y \mid x_1, \ldots, x_d) \propto P(y) \prod_{i=1}^{d} P(x_i \mid y)$$

Figure created by the author.

Finally, to find the probability of a given **sample** for all possible values of the class variable *y*, we just need to find the output with maximum probability:

$$y = \text{argmax}_y \, P(y) \prod_{i=1}^{n} P(x_i \mid y)$$

Figure created by the author.

3. Dealing with text data

One question that arises at this point is the following:

as most of them expect numerical feature vectors with a fixed size rather than the raw text documents with variable length.

In order to address this, scikit-learn provides utilities for the most common ways to extract numerical features from text content, namely:

- **tokenizing** strings and giving an integer id for each possible token, for instance by using white-spaces and punctuation as token separators.
- **counting** the occurrences of tokens in each document.

In this scheme, features and samples are defined as follows:

- each **individual token occurrence frequency** is treated as a **feature**.
- the vector of all the token frequencies for a given **document** is considered a multivariate **sample**.

"Counting" Example (to really understand this before we move on):

```
from sklearn.feature_extraction.text import CountVectorizer
corpus = [
    'This is the first document.',
    'This document is the second document.',
    'And this is the third one.',
    'Is this the first document?',
]

vectorizer = CountVectorizer()
X = vectorizer.fit_transform(corpus)

print(vectorizer.get_feature_names())
['and', 'document', 'first', 'is', 'one', 'second', 'the', 'third', 'this']

print(X.toarray())
[[0 1 1 1 0 0 1 0 1]
 [0 2 0 1 0 1 1 0 1]
 [1 0 0 1 1 0 1 1 1]
 [0 1 1 1 0 0 1 0 1]]
```

In the above toy example, we have a collection of strings stored into the variable **corpus.** Using the **text transformer**, we can see that we have a specific number of unique strings (vocabulary) in our data.

This can be seen by printing the **vectorizer.get_feature_names()** variable. We observe that we

- We have 4 rows in X as the number of our text strings (**we have the same number of samples after the transformation**).
- **We have the same number of columns** (features/variables) in the transformed data (**X**) **for all the samples** (this was not the case before that transformation i.e. the individual strings had different lengths).
- The values 0,1,2, encode the **frequency** of a **word** that **appeared** in the **initial text data.**

E.g. The first transformed row is **[0 1 1 1 0 0 1 0 1]** and the **unique vocabulary** is **['and', 'document', 'first', 'is', 'one', 'second', 'the', 'third', 'this'],** thus this means that the words "document", "first", "is", "the" and "this" appeared 1 time each in the initial text string (i.e. 'This is the first document.').

Side note: This is the counting approach. The term-frequency transform is nothing more than a transformation of a count matrix into a normalized term-frequency matrix.

Hope everything is clear now. If not, read this paragraph as many times as it is needed in order to really grasp the idea and understand this transformation. **It is a fundamental step.**

4. Working example in Python

Now that you understood how the Naive Bayes and the Text Transformation work, it's time to start coding !

Problem Statement

As a working example, we will use some **text data** and we will build a **Naive Bayes** model to **predict** the **categories** of the **texts.** This is a **multi-class (20 classes) text classification problem.**

Let's start (I will walk you through). First, we will **load all the necessary libraries:**

```
import numpy as np, pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.datasets import fetch_20newsgroups
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.naive_bayes import MultinomialNB
from sklearn.pipeline import make_pipeline
from sklearn.metrics import confusion_matrix, accuracy_score
```

```
# Load the dataset
data = fetch_20newsgroups()

# Get the text categories
text_categories = data.target_names

# define the training set
train_data = fetch_20newsgroups(subset="train", categories=text_categories)

# define the test set
test_data = fetch_20newsgroups(subset="test", categories=text_categories)
```

Let's find out **how many classes** and **samples** we have:

```
print("We have {} unique classes".format(len(text_categories)))
print("We have {} training samples".format(len(train_data.data)))
print("We have {} test samples".format(len(test_data.data)))
```

The above prints:

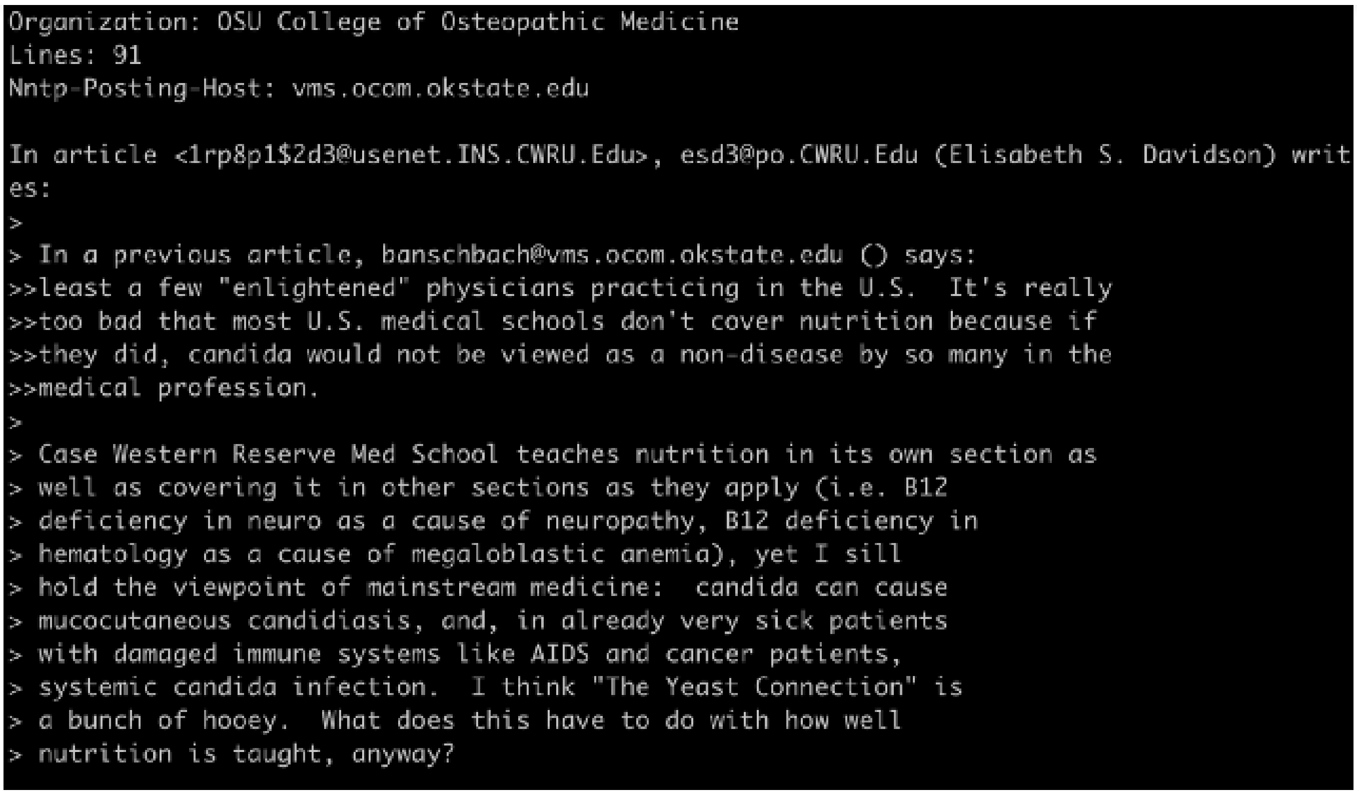
```
We have 20 unique classes
We have 11314 training samples
We have 7532 test samples
```

So, this is a **20-class text classification problem** with n_train = **11314 training samples** (text sentences) and n_test = **7532 test samples** (text sentences).

Let's visualize the 5th training sample:

```
# let's have a look as some training data
print(test_data.data[5])
```

As mentioned previously, our data are **texts** (more specifically, **emails**) so you should see something like the following printed out:



```
Organization: OSU College of Osteopathic Medicine
Lines: 91
Nntp-Posting-Host: vms.ocom.okstate.edu

In article <1rp8p1$2d3@usenet.INS.CWRU.Edu>, esd3@po.CWRU.Edu (Elisabeth S. Davidson) writ
es:
>
> In a previous article, banschbach@vms.ocom.okstate.edu () says:
>>least a few "enlightened" physicians practicing in the U.S.  It's really
>>too bad that most U.S. medical schools don't cover nutrition because if
>>they did, candida would not be viewed as a non-disease by so many in the
>>medical profession.
>
> Case Western Reserve Med School teaches nutrition in its own section as
> well as covering it in other sections as they apply (i.e. B12
> deficiency in neuro as a cause of neuropathy, B12 deficiency in
> hematology as a cause of megaloblastic anemia), yet I sill
> hold the viewpoint of mainstream medicine:  candida can cause
> mucocutaneous candidiasis, and, in already very sick patients
> with damaged immune systems like AIDS and cancer patients,
> systemic candida infection.  I think "The Yeast Connection" is
> a bunch of hooey.  What does this have to do with how well
> nutrition is taught, anyway?
```

Figure created by the author.

The next step consists of building the **Naive Bayes classifier** and finally **training** the **model.** In our example, we will convert the collection of text documents (train and test sets) into a matrix of token counts (I explained how this works in **Section 3**).

> *To implement that text transformation we will use the* ***make_pipeline*** *function. This will internally transform the text data and then the model will be fitted* ***using the transformed data.***

```
# Build the model
model = make_pipeline(TfidfVectorizer(), MultinomialNB())

# Train the model using the training data
model.fit(train_data.data, train_data.target)

# Predict the categories of the test data
predicted_categories = model.predict(test_data.data)
```

The last line of code **predicts the labels of the test set.**

Let’s see the predicted categories names:

```
print(np.array(test_data.target_names)[predicted_categories])
```

predicts correctly only specific text categories.

```
# plot the confusion matrix
mat = confusion_matrix(test_data.target, predicted_categories)
sns.heatmap(mat.T, square = True, annot=True, fmt = "d",
xticklabels=train_data.target_names,yticklabels=train_data.target_names)
plt.xlabel("true labels")
plt.ylabel("predicted label")
plt.show()

print("The accuracy is {}".format(accuracy_score(test_data.target,
predicted_categories)))
```

```
The accuracy is 0.7738980350504514
```

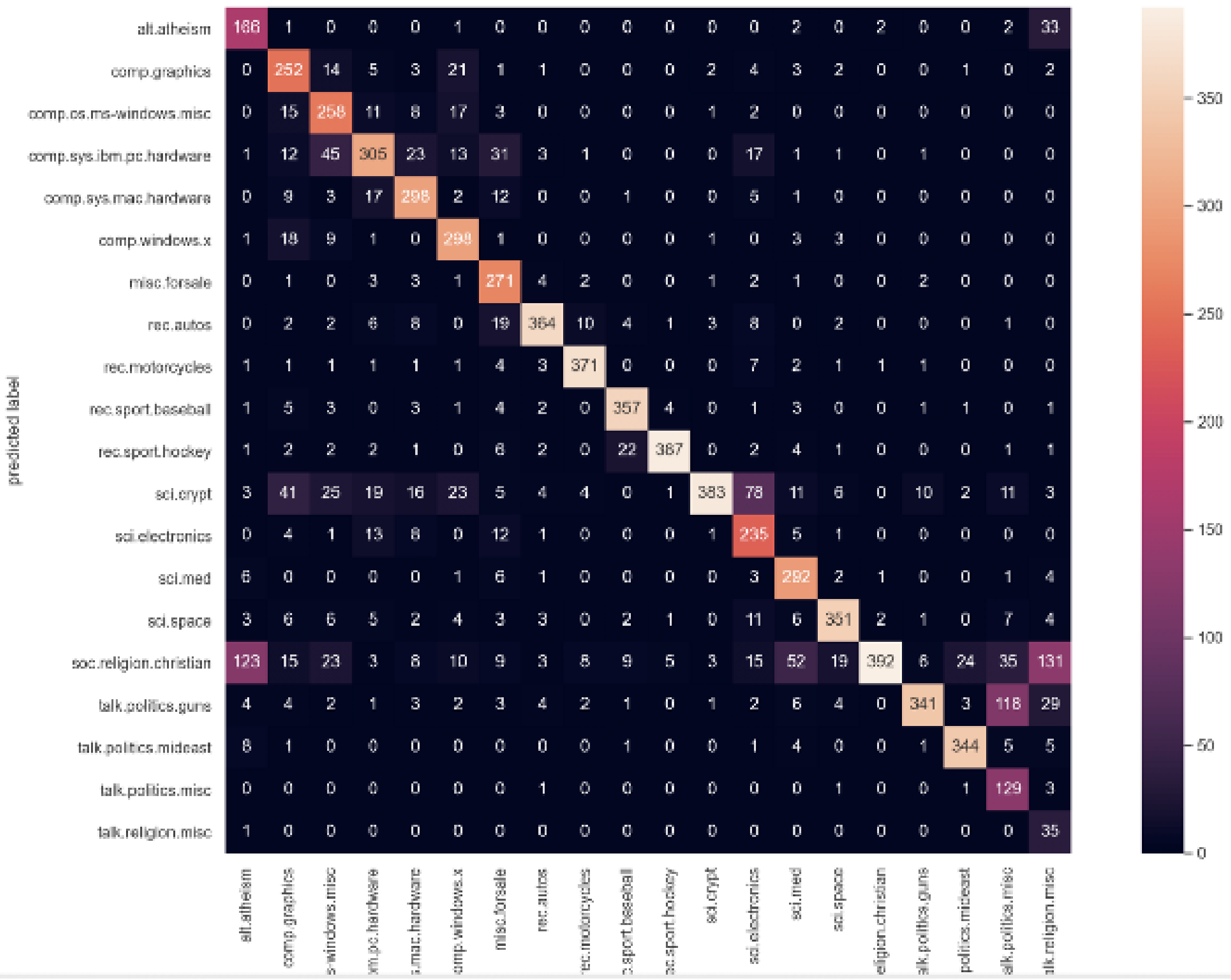


Figure created by the author.

5. Bonus: Having fun with the model

```
    all_categories_names = np.array(data.target_names)
    prediction = model.predict([my_sentence])
    return all_categories_names[prediction]


my_sentence = “jesus”
print(my_predictions(my_sentence, model))
['soc.religion.christian']

my_sentence = "Are you an atheist?"
print(my_predictions(my_sentence, model))
['alt.atheism']
```

We inserted the string “jesus” to the model and it predicted the class “[‘soc.religion.christian’]”.

Change the “my_sentence” into other stings and **play with the model** 😉.

6. Conclusions

We saw that **Naive Bayes is a very powerful algorithm** for **multi-class text classification problems.**

Side Note: *If you want to know more about the confusion matrix (and the ROC curve) read this:*

ROC Curve Explained using a COVID-19 hypothetical example: Binary & Multi-Class Classification...

In this post I clearly explain what a ROC curve is and how to read it. I use a COVID-19 example to make my point and I...

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Interpreting the confusion matrix

From the above **confusion matrix**, we can verify that the model is really good.

- It is able to correctly predict all 20 classes of the text data (most values are on the diagonal and few are off-the-diagonal).
- We also notice that the highest miss-classification (value off-the-diagonal) is **131** (5 lines from the end, last column at the right). The value 131 means that 131 documents that belonged to the “**religion miscellaneous** ” category were miss-classified as belonging to

Finally, the **accuracy** on the **test** set is **0.7739** which is quite good for a **20-class text classification problem** 🚀.

That's all folks! Hope you liked this article.

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