Poisonous Mushrooms

January 8, 2018

Importing the libraries

```
In [1]: import numpy as np
        import matplotlib.pyplot as plt
        import pandas as pd
        import os
        from keras.models import Sequential
        from keras.layers import Dense
Using TensorFlow backend.
In [2]: dataset = pd.read_csv('data/mushrooms.csv')
In [3]: X = dataset.iloc[:, 1:23].values
        y = dataset.iloc[:, 0].values
   Encoding the variables
```

```
In [4]: from sklearn.preprocessing import LabelEncoder, OneHotEncoder
        #class: 2
        labelencoder_y = LabelEncoder()
        y[:] = labelencoder_y.fit_transform(y[:])
        print(labelencoder_y.inverse_transform([0,1]))
        print("--> 0,1\n")
['e' 'p']
--> 0,1
In [5]: #cap-shape: 6
        labelencoder0 = LabelEncoder()
        X[:,0] = labelencoderO.fit_transform(X[:,0])
        print(labelencoder0.inverse_transform([0,1,2,3,4,5]))
        print("--> 0,1,2,3,4,5\n")
```

```
['b' 'c' 'f' 'k' 's' 'x']
--> 0,1,2,3,4,5
In [6]: #cap-surface: 4
       labelencoder1 = LabelEncoder()
       X[:,1] = labelencoder1.fit_transform(X[:,1])
        print(labelencoder1.inverse_transform([0,1,2,3]))
       print("--> 0,1,2,3\n")
['f' 'g' 's' 'y']
--> 0,1,2,3
In [7]: #cap-color: 10
       labelencoder2 = LabelEncoder()
       X[:,2] = labelencoder2.fit_transform(X[:,2])
        print(labelencoder2.inverse_transform([0,1,2,3,4,5,6,7,8,9]))
       print("--> 0,1,2,3,4,5,6,7,8,9\n")
['b' 'c' 'e' 'g' 'n' 'p' 'r' 'u' 'w' 'y']
--> 0,1,2,3,4,5,6,7,8,9
In [8]: #bruises:2
       labelencoder3 = LabelEncoder()
       X[:,3] = labelencoder3.fit_transform(X[:,3])
       print(labelencoder3.inverse_transform([0,1]))
       print("--> 0,1\n")
['f' 't']
--> 0,1
In [9]: #odor:9
        labelencoder4 = LabelEncoder()
       X[:,4] = labelencoder4.fit_transform(X[:,4])
        print(labelencoder4.inverse_transform([0,1,2,3,4,5,6,7,8]))
       print("--> 0,1,2,3,4,5,6,7,8\n")
['a' 'c' 'f' 'l' 'm' 'n' 'p' 's' 'y']
--> 0,1,2,3,4,5,6,7,8
```

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In [10]: #gill-attachment:2
         labelencoder5 = LabelEncoder()
         X[:,5] = labelencoder5.fit_transform(X[:,5])
         print(labelencoder5.inverse_transform([0,1]))
         print("--> 0,1\n")
['a' 'f']
--> 0,1
In [11]: #gill-spacing:2
         labelencoder6 = LabelEncoder()
         X[:,6] = labelencoder6.fit_transform(X[:,6])
         print(labelencoder6.inverse_transform([0,1]))
         print("--> 0,1\n")
['c' 'w']
--> 0,1
In [12]: #gill-size:2
         labelencoder7 = LabelEncoder()
         X[:,7] = labelencoder7.fit_transform(X[:,7])
         print(labelencoder7.inverse_transform([0,1]))
         print("--> 0,1\n")
['b' 'n']
--> 0,1
In [13]: #gill-color:12
         labelencoder8 = LabelEncoder()
         X[:,8] = labelencoder8.fit_transform(X[:,8])
         print(labelencoder8.inverse_transform([0,1,2,3,4,5,6,7,8,9,10,11]))
         print("--> 0,1,2,3,4,5,6,7,8,9,10,11\n")
['b' 'e' 'g' 'h' 'k' 'n' 'o' 'p' 'r' 'u' 'w' 'y']
--> 0,1,2,3,4,5,6,7,8,9,10,11
In [14]: #sta; l-shape:2
         labelencoder9 = LabelEncoder()
         X[:,9] = labelencoder9.fit_transform(X[:,9])
         print(labelencoder9.inverse_transform([0,1]))
         print("--> 0,1\n")
```

```
['e' 't']
--> 0,1
In [15]: #stalk-root:5
         labelencoder10 = LabelEncoder()
         X[:,10] = labelencoder10.fit_transform(X[:,10])
         print(labelencoder10.inverse_transform([0,1,2,3,4]))
         print("--> 0,1,2,3,4\n")
['?' 'b' 'c' 'e' 'r']
--> 0,1,2,3,4
In [16]: #stalk-surface-above-ring: 4
         labelencoder11 = LabelEncoder()
         X[:,11] = labelencoder11.fit_transform(X[:,11])
         print(labelencoder11.inverse_transform([0,1,2,3]))
         print("--> 0,1,2,3\n")
['f' 'k' 's' 'y']
--> 0,1,2,3
In [17]: #stalk-surface-below-ring: 3
         labelencoder12 = LabelEncoder()
         X[:,12] = labelencoder12.fit_transform(X[:,12])
         print(labelencoder12.inverse_transform([0,1,2]))
         print("--> 0,1,2\n")
['f' 'k' 's']
--> 0,1,2
In [18]: #stalk-color-above-ring: 9
         labelencoder13 = LabelEncoder()
         X[:,13] = labelencoder13.fit_transform(X[:,13])
         print(labelencoder13.inverse_transform([0,1,2,3,4,5,6,7,8]))
         print("--> 0,1,2,3,4,5,6,7,8\n")
['b' 'c' 'e' 'g' 'n' 'o' 'p' 'w' 'y']
--> 0,1,2,3,4,5,6,7,8
```

```
In [19]: #stalk-color-below-ring: 9
         labelencoder14 = LabelEncoder()
         X[:,14] = labelencoder14.fit_transform(X[:,14])
         print(labelencoder14.inverse_transform([0,1,2,3,4,5,6,7,8]))
         print("--> 0,1,2,3,4,5,6,7,8\n")
['b' 'c' 'e' 'g' 'n' 'o' 'p' 'w' 'y']
--> 0,1,2,3,4,5,6,7,8
In [20]: #veil-type: 1
         labelencoder15 = LabelEncoder()
         X[:,15] = labelencoder15.fit_transform(X[:,15])
         print(labelencoder15.inverse_transform([0]))
         print("--> 0\n")
['p']
--> 0
In [21]: #veil-color: 4
         labelencoder16 = LabelEncoder()
         X[:,16] = labelencoder16.fit_transform(X[:,16])
         print(labelencoder16.inverse_transform([0,1,2,3]))
         print("--> 0,1,2,3\n")
['n' 'o' 'w' 'y']
--> 0,1,2,3
In [22]: #ring-number: 3
         labelencoder17 = LabelEncoder()
         X[:,17] = labelencoder17.fit_transform(X[:,17])
         print(labelencoder17.inverse_transform([0,1,2]))
         print("--> 0,1,2\n")
['n' 'o' 't']
--> 0,1,2
In [23]: #ring-type: 5
         labelencoder18 = LabelEncoder()
         X[:,18] = labelencoder18.fit_transform(X[:,18])
         print(labelencoder18.inverse_transform([0,1,2,3,4]))
         print("--> 0,1,2,3,4\n")
```

```
['e' 'f' 'l' 'n' 'p']
--> 0,1,2,3,4
In [24]: #spore-print-color: 9
         labelencoder19 = LabelEncoder()
         X[:,19] = labelencoder19.fit_transform(X[:,19])
         print(labelencoder19.inverse_transform([0,1,2,3,4,5,6,7,8]))
         print("--> 0,1,2,3,4,5,6,7,8\n")
['b' 'h' 'k' 'n' 'o' 'r' 'u' 'w' 'y']
--> 0,1,2,3,4,5,6,7,8
In [25]: #population: 6
         labelencoder20 = LabelEncoder()
         X[:,20] = labelencoder20.fit_transform(X[:,20])
         print(labelencoder20.inverse_transform([0,1,2,3,4,5]))
         print("--> 0,1,2,3,4,5\n")
['a' 'c' 'n' 's' 'v' 'y']
--> 0,1,2,3,4,5
In [26]: #habitat: 6
        labelencoder21 = LabelEncoder()
         X[:,21] = labelencoder21.fit_transform(X[:,21])
         print(labelencoder21.inverse_transform([0,1,2,3,4,5,6]))
         print("--> 0,1,2,3,4,5\n")
['d' 'g' 'l' 'm' 'p' 'u' 'w']
--> 0,1,2,3,4,5
```

3 Splitting the dataset into the Training set and Test set

In [27]: from sklearn.cross_validation import train_test_split

4 Create model

- ReLU tends to converge better than sigmoid activation functions for when calculating gradients the sigmoid function is saturated and tends to take longer.
- Sigmoid function is good for classification at the final layer.

5 Compile model

6 Fit the model

```
In [30]: model.fit(X_train, y_train, epochs=20, batch_size=10)
Epoch 1/20
6093/6093 [=============== ] - 3s - loss: 0.3348 - acc: 0.8628
Epoch 2/20
Epoch 3/20
Epoch 4/20
Epoch 5/20
Epoch 6/20
Epoch 7/20
6093/6093 [=============== ] - 2s - loss: 0.0210 - acc: 0.9962
Epoch 8/20
6093/6093 [=============== ] - 2s - loss: 0.0154 - acc: 0.9962
Epoch 9/20
6093/6093 [=============== ] - 2s - loss: 0.0084 - acc: 0.9985
Epoch 10/20
6093/6093 [=============== ] - 2s - loss: 0.0056 - acc: 0.9995
Epoch 11/20
Epoch 12/20
6093/6093 [=============== ] - 2s - loss: 0.0046 - acc: 0.9993
Epoch 13/20
6093/6093 [=============== ] - 2s - loss: 0.0040 - acc: 0.9993
Epoch 14/20
```

Out[30]: <keras.callbacks.History at 0x26c20715550>

7 Verify the accuracy

8 Conclusion

- Here we dealt with 22 categorical features with over 8000 entries.
- After variable encoding and splitting the data into training and test sets, we ran the deep learning model with RELU and Sigmoid activation functions.
- After twenty epochs, the training data displayed that the model had achieved 100% accuracy, as well as the test data following the verification.
- Although this model may be overfitted, because it was able to predict the test data with high accuracy, we can be comfortable using this model in the future.
- It may be beneficial to test this model on a more diverse/ larger dataset, as high accuracies throw red flags for overfitting, and could be disastrous when we least expect it. However, since the model performs well on both training and test data, we can be fairly confident that the distinguishing features between poisonous and edible mushrooms are much more distinct than not.