Machine Learning Applications for Biological Data

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Abstract

In this report consist the 50 samples from each of three species of Iris (Iris setosa, Iris virginica and Iris versicolor). Four features were measured from each sample: the length and the width of the sepals and petals, in centimeters.Overall,simple neural network model were applied to predict the species types using their features.

1 Introduction

This is perhaps the best known database to be found in the pattern recognition literature. Fisher's paper is a classic in the field and is referenced frequently to this day. (See Duda Hart, for example.) The data set contains 3 classes of 50 instances each, where each class refers to a type of iris plant. One class is linearly separable from the other 2; the latter are NOT linearly separable from each other.

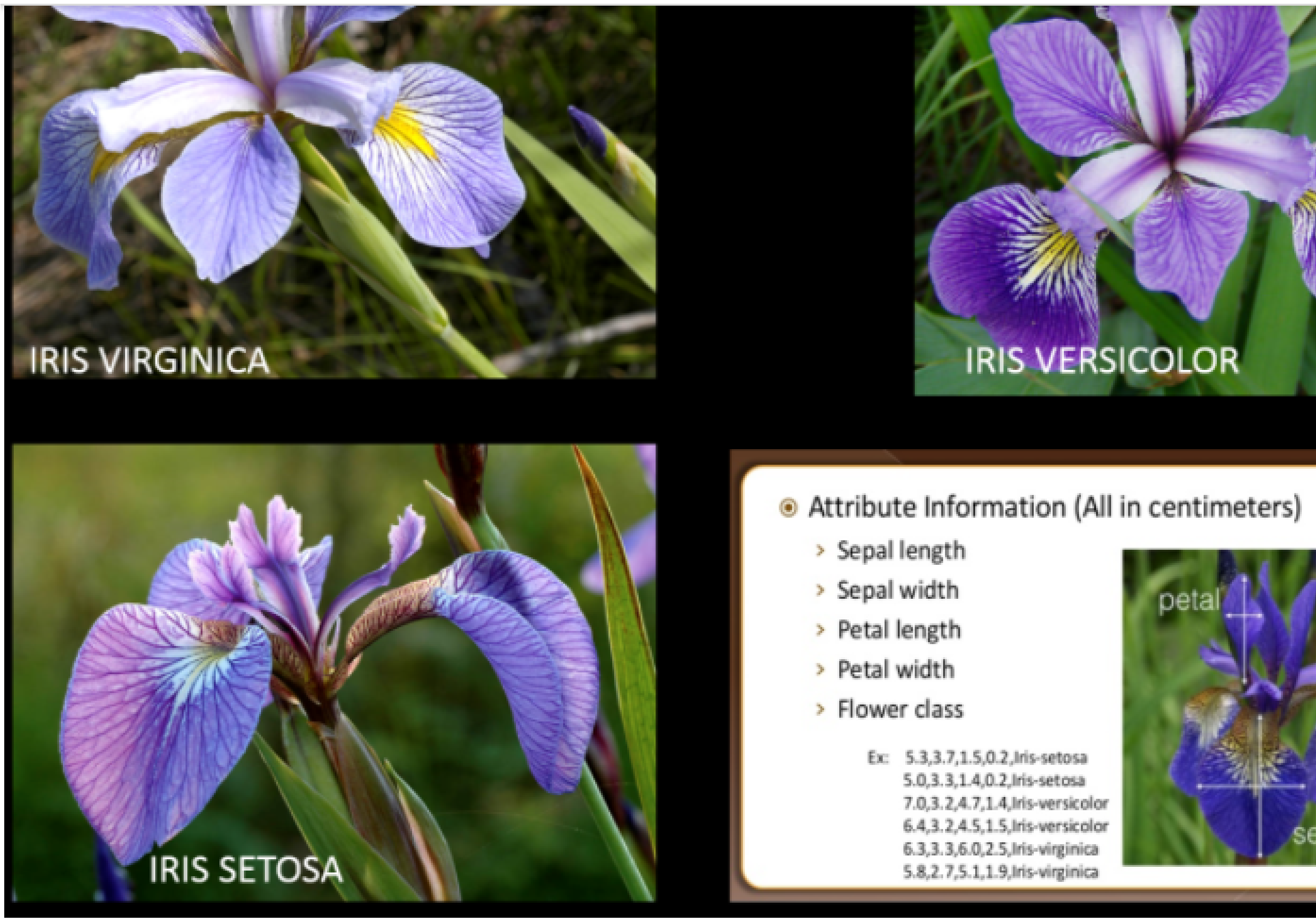
Predicted attribute: class of iris plant.

This is an exceedingly simple domain.

This data differs from the data presented in Fishers article (identified by Steve Chadwick, spchadwick '@' espeedaz.net). The 35th sample should be: 4.9,3.1,1.5,0.2,"Iris-setosa" where the error is in the fourth feature. The 38th sample: 4.9,3.6,1.4,0.1,"Iris-setosa" where the errors are in the second and third features.

2 Theory

In this lab demonstrate how to use machine learning based technique to identify the category of the biological data(flowers) using their features.

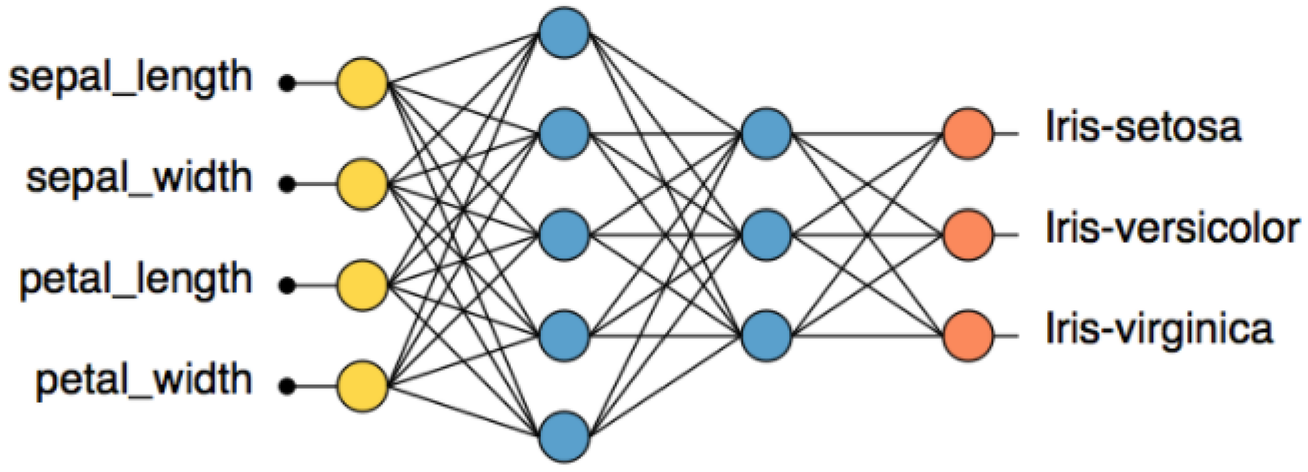


- Attribute Information (All in centimeters)
  - Sepal length
  - Sepal width
  - Petal length
  - Petal width
  - Flower class

```
Ex:   5.3,3.7,1.5,0.2,Iris-setosa
      5.0,3.3,1.4,0.2,Iris-setosa
      7.0,3.2,4.7,1.4,Iris-versicolor
      6.4,3.2,4.5,1.5,Iris-versicolor
      6.3,3.3,6.0,2.5,Iris-virginica
      5.8,2.7,5.1,1.9,Iris-virginica
```

3 Procedure

The neural network model were utilized to predict the category.



3.1 Load Data

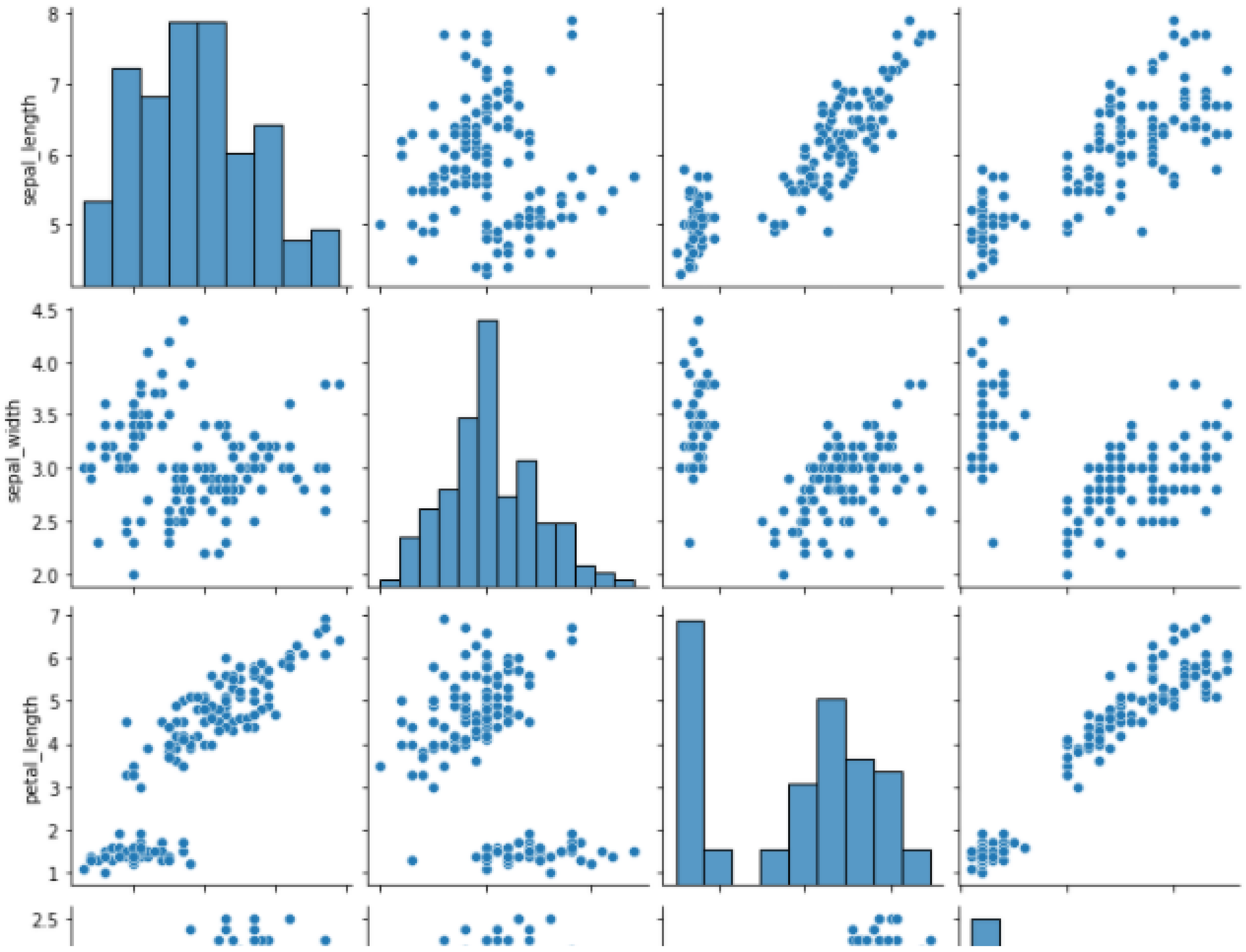
We download the iris data set and load our google colab as a data frame.It has 5 attributes and 4 of them are inputs and species name act as the output.

```
dataset = pd.read_csv('/content/drive/My Drive/Iris_data/iris.csv')
```

4 Analysis

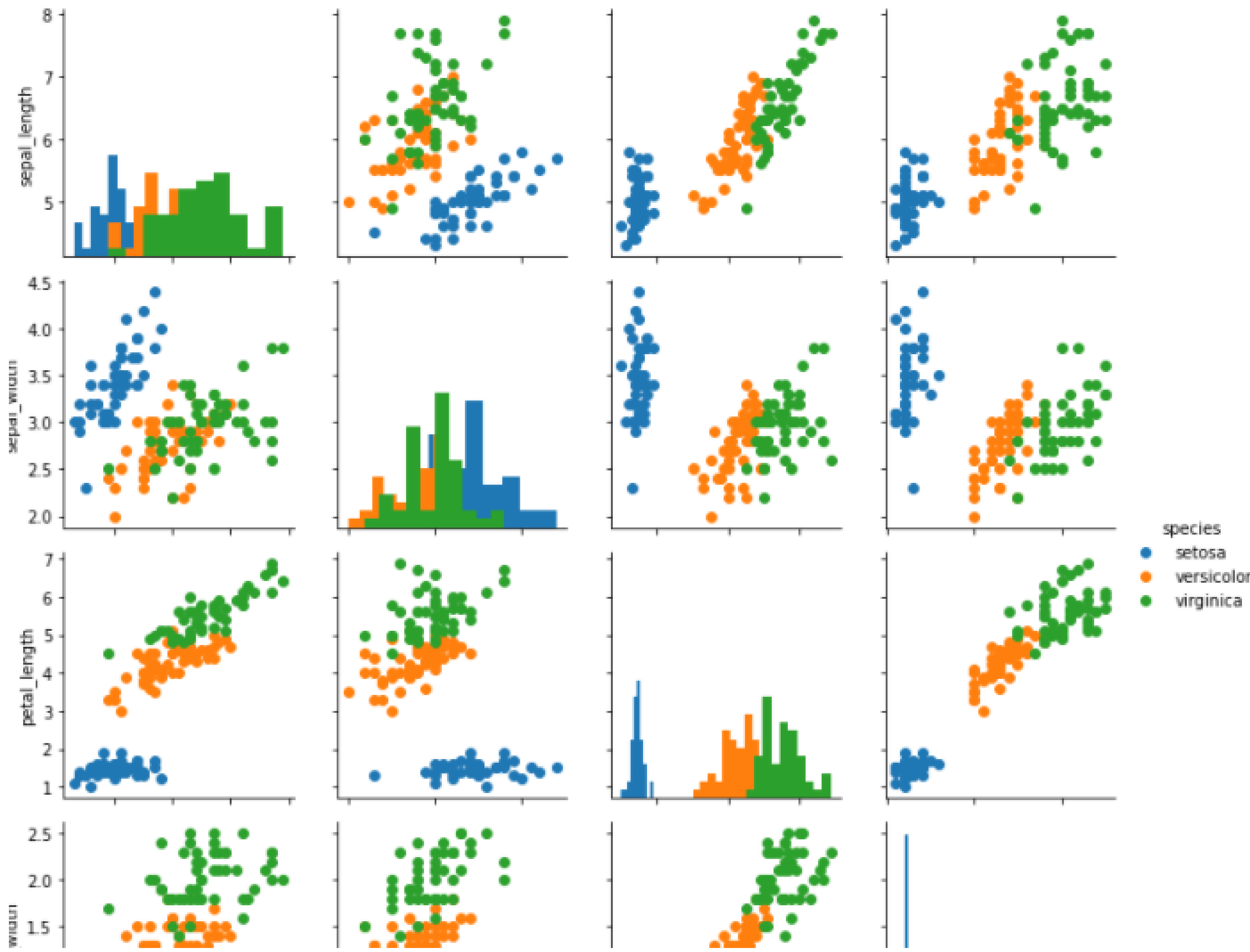
This Part will how to find the species category using the external measurements of the species.First,we Find the pairwise relationship of variables

```
g = sns.pairplot(dataset) # pairplot for each variables
```



We can use these pairwise plot to identify the relationships between variables.After that we execute the same plot for different species.

```
g = sns.PairGrid(dataset, hue="species") # pareplot for each 2 pair of varoab
g = g.map_diag(plt.hist)
g = g.map_offdiag(plt.scatter)
g = g.add_legend()
```



4.1 Inputs and outputs

In this part we separate our inputs and outputs and convert into a array.

```
target_data = dataset[['species']]              # all the data values without sp
input_data = dataset.drop(['species'], axis=1)
input_data = np.array(input_data)# convert list to an array
target_data = pd.get_dummies(target_data.species)# outputs
_, target_data = np.where(target_data==1)
```

```
X = input_data[r[:cut],:]
X_test = input_data[r[cut:],:]
Y = target_data[r[:cut]]
```

```
Y_test = target_data[r[cut:]]

def softmax(x):
    s1 = torch.exp(x - torch.max(x,1)[0][:,None])
    s = s1 / s1.sum(1)[:,None]
    return s

def cross_entropy(outputs, labels):
    return -torch.sum(softmax(outputs).log()[range(outputs.size()[0]), labels

def randn_trunc(s): #Truncated Normal Random Numbers
    mu = 0
    sigma = 0.1
    R = stats.truncnorm((-2*sigma - mu) / sigma, (2*sigma - mu) / sigma, loc=
    return R.rvs(s)
def acc(out,y):
    with torch.no_grad():
        return (torch.sum(torch.max(out,1)[1] == y).item())/y.shape[0]
def GPU(data):
    return torch.tensor(data, requires_grad=True, dtype=torch.float, device=t

def GPU_data(data):
    return torch.tensor(data, requires_grad=False, dtype=torch.float, device=
def get_batch(mode):
    b = c.b
    if mode == "train":
        r = np.random.randint(X.shape[0]-b)
        x = X[r:r+b,:]
        y = Y[r:r+b]
    elif mode == "test":
        r = np.random.randint(X_test.shape[0]-b)
        x = X_test[r:r+b,:]
        y = Y_test[r:r+b]
    return x,y
def gradient_step(w):

    for j in range(len(w)):

            w[j].data = w[j].data - c.h*w[j].grad.data

            w[j].grad.data.zero_()

def make_plots():

    acc_train = acc(model(x,w),y)
```

```
        xt,yt = get_batch('test')

        acc_test = acc(model(xt,w),yt)

        wb.log({"acc_train": acc_train, "acc_test": acc_test})

X = GPU_data(X)
Y = GPU_data(Y)
X_test = GPU_data(X_test)
Y_test = GPU_data(Y_test)
```