Malaria Cell Classification using Multi-Layer Perceptron

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1. Introduction:

We use the Multilayer perceptron(MLP) to classify 4 different cells, that are: "red blood cell", "ring", "schizont" and "trophozoite". Over the 7 days of the competition an average score of 7.55747E-01.

2. Thought process for training the models:

Day 1- Basic model, I did not make a lot of changes, I wanted to make sure that the model runs and that it correctly inputs the image path without errors.

Day 2- Corrupt model

Day 3- Corrupt model

Day 4- Manually running multiple iterations with sets of learning rate, number of neurons, number of epochs, batch size and dropout, this gave me a very small improvement on my machine, but the mean score dropped on the held out set.

I was only focussing on changing the 4 hyperparameters:

```
LR, N EPOCHS, BATCH SIZE, DROPOUT.
```

Day 5- Next I ran a Grid Search CV, which did not work, it gave an error for the sequential model. I attempted to emulate the process by using multiple for loops, but the process never ended and went into a forever loop.

```
LR = [0.1, 0.01, 0.001, 0.0001, 0.00001]
N = [100, 200, 300, 400, 500]
NN I = [128, 32, 32]
N = [100, 150, 250, 300]
BATCH SIZE = [54, 68, 81, 102, 108, 324, 512, 612]
DROPOUT = [0.1, 0.2, 0.3, 0.4, 0.5]
KI= ['uniform', 'normal', 'lecun normal']
ACT=['relu', 'elu', 'tanh', 'softmax', 'selu']
# %% ----- Data Prep
x, y = np.load("x_train.npy"), np.load("y_train.npy")
x train, x test, y train, y test = train test split(x, y, random state=SEED,
test size=0.2, stratify=y)
x train, x test = x train.reshape(len(x train), -1),
x test.reshape(len(x test), -1)
x train, x test = x train/255, x test/255
y train, y test = to categorical(y train, num classes=4),
to_categorical(y_test, num classes=4)
# %% ----- Training Prep
_____
#iterate:
df=pd.DataFrame()
l a=[]
nn a=[]
nn i a=[]
ne a=[]
b a=[]
da=[]
acc=[]
ck=[]
f1=[]
k a=[]
act a=[]
for 1 in LR:
  for nn in N NEURONS:
      for ne in N EPOCHS:
         for b in BATCH SIZE:
             for d in DROPOUT:
```

```
for k in KI:
                      for activ in ACT:
                         for nn i in NN I:
                             model = Sequential([
                                 Dense(nn, input dim=7500,
activation=activ, kernel initializer=k),
                                 Dense (nn i, activation=activ,
kernel initializer=k),
                                 Dense (4,
activation=activ, kernel initializer=k),
                                 BatchNormalization()
                             1)
                             model.compile(optimizer=Adam(lr=1),
loss="categorical crossentropy", metrics=["accuracy"])
                            # %% -----
Training Loop -----
                             model.fit(x train, y train, batch size=b,
epochs=ne, validation data=(x test, y test),
callbacks=[ModelCheckpoint("mlp grid.hdf5", monitor="val loss",
save best only=True)])
                             l a.append(1)
                             nn a.append(nn)
                             nn i a.append(nn i)
                             ne a.append(ne)
                             b a.append(b)
                             d a.append(d)
                             k a.append(k)
                             act a.append(activ)
                             acc.append(100 * model.evaluate(x test,
y test) [1])
ck.append(cohen kappa score(np.argmax(model.predict(x test), axis=1),
np.argmax(y test, axis=1)))
f1.append(f1 score(np.argmax(model.predict(x test), axis=1), np.argmax(y test,
axis=1), average='macro'))
df['learning rate']=l a
df['n neurons']=nn a
df['inner neuron']=nn i a
df['epochs']=ne a
df['batch']=b a
df['dropout']=d a
df['accuracy']=acc
df['cohens kappa']=ck
df['f1 score']=f1
```

```
df['Kernel activation']=k_a
df['activation']=act_a
print(df)
df.to csv(index=False)
```

Next, I attempted to look at various code changes that could improve the model.

I first attempted to modify the Adam optimizer. After looking into the documentation I realized that there were three hyper parameters, beta_1, beta_2, and epsilon. The model did not improve on changing the beta_1, beta_2 values, the default values(0.9, and 0.99) seemed to be the best values. Next I experimented on the epsilon values, according to an article(1), the value of epsilon should be set close to 1 for computer vision problems. This led to an extreme drop in the accuracy and therefore I discarded the idea.

Next, I attempted to increase the number of "steps per epoch", I quickly realized that as the batch size changes the value of steps per epoch is adjusted, therefore I discarded this idea too.

Then I started adding a kernel initializer, after experimenting with three initializers namely, glorot_uniform, he_uniform and lecun_uniform. I realized that the best kernel initializer was glorot uniform and improved the performance of the model.

After adding a few more layers to the sequential model, I began to modify the activation functions, tanh, sigmoid and relu were the activation functions that I was experimenting with initially. After reading the kears layer activation function documentation(2), I started experimenting selu, this activation function when added to the hidden layers caused a small increase in the mead score. So I used the selu activation function in the hidden layers.

Lastly I experimented with Batch Normalization, for most image classifications batch normalisation was used and after the activation function and the after adding the dropout rate, this significantly dropped the accuracy and so I discarded it.

Day 6- Did not submit a model as I did not create any model with an improvement

Day 7- Final Model

The final model includes,

```
LR = 0.0001
N EPOCHS = 150
```

```
BATCH_SIZE = 68
DROPOUT = 0.1
```

I used a loop function to find batch size values, as we want there to be no remainders.

```
for i in range(1,5508):
    if (5508%i) == 0:
        print(i)
```

Next I used a 4 layer sequential function,

```
model = Sequential()
model.add(Dense(128,
input_dim=7500,activation="relu",kernel_initializer=weight_init))
model.add(Dropout(DROPOUT, seed=SEED))
model.add(Dense(32, activation="selu",kernel_initializer=weight_init))
model.add(Dropout(DROPOUT, seed=SEED))
model.add(Dense(32, activation="selu",kernel_initializer=weight_init))
model.add(Dropout(DROPOUT, seed=SEED))
model.add(Dense(4,activation="softmax",kernel_initializer=weight_init))
```

In some of my initial models I set the last layer to 10,

```
model.add(Dense(10, activation="softmax", kernel initializer=weight init))
```

But the output of the MLP should only be 4 classes and therefore I changed the value in both number of classes and dense layer to 4.

```
y_train, y_test = to_categorical(y_train, num_classes=4),
to categorical(y test, num classes=4)
```

Although setting num_classes=10 and having 10 dense layers as the output layer does give a higher mean score, I do not believe it is the right approach and therefore I chose to change the values to 4.

Note: As I have only submitted 4 fully working models, I will add only those 4 folders, day 2,3 and 6 folders will be missing.

References:

- 1. https://machinelearningmastery.com/adam-optimization-algorithm-for-deep-learning/
- 2. https://keras.io/api/layers/activations/