Pima Indians - diabetes prediction

Neural Network for binary classification

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In [30]:
```
# Import necessary libraries
from keras.models import Sequential
from keras.layers import Dense
from keras.layers import Dropout
from keras.constraints import maxnorm
from keras.models import model_from_json
from keras import optimizers
import numpy as np
from sklearn.metrics import classification_report, confusion_matrix
import os

# set random seed for reproducibility
np.random.seed(7)

# change the operating system directory
os.chdir("/Users/karimaidrissi/Desktop/DSSA 5104 DL/week13")
# load pima indians dataset
dataset = np.loadtxt("pima-indians-diabetes.csv", delimiter=",")

# splitting Pima-Indians-diabetes dataset into observed features(input)
 and targets variable(output)
X = dataset[:,0:8] #input
Y = dataset[:,8] #output
```

PART I : SET UP DROPOUT

Dropout rate and Validation_split equal to 10%

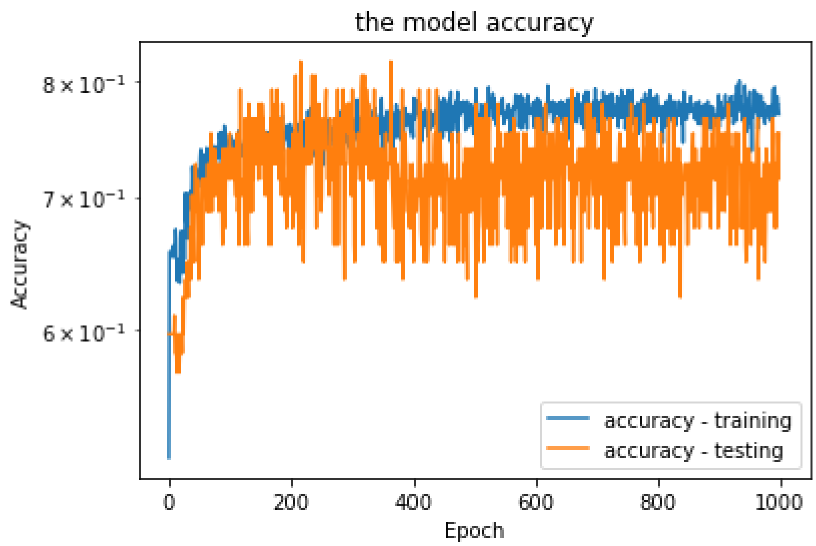
In [31]:
```
######################################
##### Architecture of the model ######
#####################################

# create a binary classification model
model = Sequential()
# Dropout used in Neural Network to reduce overfitting and improve gener
alization error
# Adding Dropout layer between 8 inputs(or visible layer) and 10 first h
idden layer
# Dropout rate is set to 10% means that one in 10 inputs will be randoml
y excluded from each update cycle
model.add(Dropout(0.1,input_shape=(8,)))
# Adding relu function to the first 10 hidden layers, also a constraint
 is imposed on the weights of hidden layers
# ensuring that the maximum norm of the weights doesn not exceed a value
of 3
model.add(Dense(10,  kernel_initializer='normal', activation='relu',kern
el_constraint=maxnorm(3)))
# Adding the second hidden layer with a constraint doesn't exceed 3 also
adding normal distribution for intializing the weights
model.add(Dense(8,  kernel_initializer='normal', activation='relu',kerne
l_constraint=maxnorm(3)))
# Adding the last output layer with the activation function sigmoid
model.add(Dense(1, kernel_initializer='normal', activation='sigmoid'))

# compiling the model with binary_crossentropy for loss function, Adam
 as optimizer default and the accuracy for out metrics.
model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['ac
curacy'])

# train the model by passing features and target variable with 1000 iter
ations
# setting validation_split to separate 10% of the training data into a v
alidation dataset that can be used to evaluate our model
history=model.fit(X,Y,validation_split=0.10,epochs=1000,verbose=0)

# Evaluate the model
scores = model.evaluate(X, Y)
Y_predict = model.predict(X)

print("\n%s: %.2f%%" % (model.metrics_names[1], scores[1]*100))

##########################################
######## Save Model to disk #############
#########################################

# Save the model structure as json format
model_json = model.to_json()
with open('model.json', 'w') as json_file:
    json_file.write(model_json)
# Save weights and biases to HD5 file
model.save_weights('model.h5')

print('==================')
print('Saved model to disk')
```

```
print('===================')

# create confusion matrix details
rounded = [round(i[0]) for i in Y_predict]
y_pred = np.array(rounded,dtype='int64')
print('Confusion Matrix')
print('================')
CM = confusion_matrix(Y, y_pred)
print('True negatives: ',CM[0,0])
print('False negatives: ',CM[1,0])
print('False positives: ',CM[0,1])
print('True positives: ',CM[1,1])
```

```
768/768 [==============================] - 0s 29us/step

accuracy: 78.78%
===================
Saved model to disk
===================
Confusion Matrix
================
True negatives:  460
False negatives:  123
False positives:  40
True positives:  145
```

- In my working directory the network weights is saved in json format
- the accuracy of our model is 78.78%
- The confusion matrix can be interpreted as follows out of 768 observations in Pima-Indians-Diabetes dataset, 605 observation were correctly predicted while 163 were incorrectly predicted
- We can also calculate the accuracy by adding True negatives and True positive then divide the sum by the total number of observations: 605/768= 0.7878 which gives 78.78%

In [32]:
```
# Plotting the accuracy of training and testing our model
import matplotlib.pyplot as plt # importing matplotlib library
accuracy_training = history.history['accuracy']
loss = history.history['loss']
accuracy_testing = history.history['val_accuracy']
#plt.semilogy(loss,label='loss')
plt.semilogy(accuracy_training,label='accuracy - training')
plt.semilogy(accuracy_testing,label='accuracy - testing')
plt.xlabel('Epoch' )
plt.ylabel('Accuracy')
plt.title('the model accuracy')
plt.legend()
plt.show()
```



- Overall, the accuracy model on training and testing dataset shows that the model has better performance on the training dataset than testing.
- We can see clearly that the testing accuracy increases to certain points up to 400 epochs then begin to degrade, this's possibly a sign of overfitting

Adjusting the Dropout and validation_split to 20%

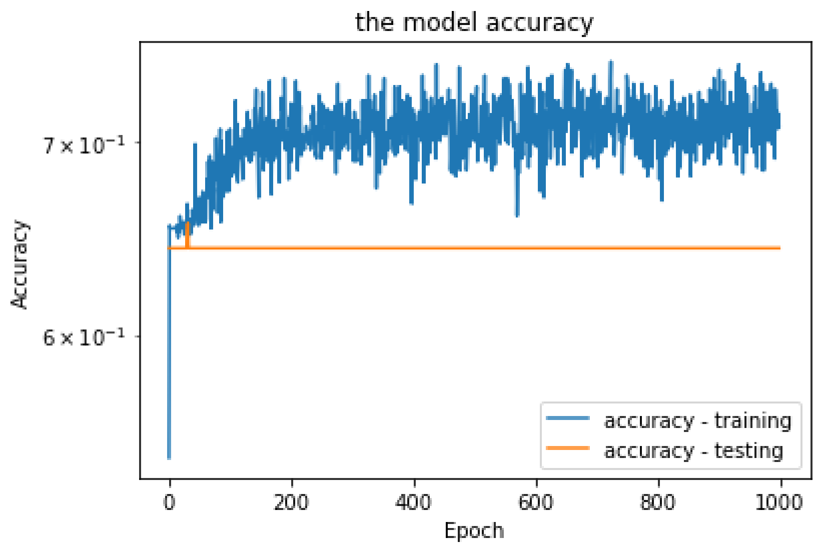
In [33]:
```
#######################################
##### Architecture of the model ######
######################################

# create a binary classification model
model = Sequential()
# Dropout used in Neural Network to reduce overfitting and improve gener
alization error
# Adding Dropout layer between 8 inputs(or visible layer) and 10 first h
idden layer
# Dropout rate is set to 20% means that one in 5 inputs will be randomly
excluded from each update cycle
model.add(Dropout(0.5,input_shape=(8,)))
# Adding relu function to the first 10 hidden layers, also a constraint
 is imposed on the weights of hidden layers
# ensuring that the maximum norm of the weights doesn not exceed a value
of 3
model.add(Dense(10,  kernel_initializer='normal', activation='relu',kern
el_constraint=maxnorm(3)))
# Adding the second hidden layer with a constraint doesn't exceed 3 also
adding normal distribution for intializing the weights
model.add(Dense(8,  kernel_initializer='normal', activation='relu',kerne
l_constraint=maxnorm(3)))
# Adding the last output layer with the activation function sigmoid
model.add(Dense(1, kernel_initializer='normal', activation='sigmoid'))

# compiling the model with binary_crossentropy for loss function, Adam
 as optimizer default and the accuracy for out metrics.
model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['ac
curacy'])

# train the model by passing features and target variable with 1000 iter
ations
# setting validation_split to separate 20% of the training data into a v
alidation dataset that can be used to evaluate our model
history=model.fit(X,Y,validation_split=0.20,epochs=1000,verbose=0)

# Evaluate the model
scores = model.evaluate(X, Y)
Y_predict = model.predict(X)

print("\n%s: %.2f%%" % (model.metrics_names[1], scores[1]*100))

##########################################
######## Save Model to disk #############
#########################################

# Save the model structure as json format
model_json = model.to_json()
with open('model.json', 'w') as json_file:
    json_file.write(model_json)
# Save weights and biases to HD5 file
model.save_weights('model.h5')

print('==================')
print('Saved model to disk')
```

```
print('===================')

# create confusion matrix details
rounded = [round(i[0]) for i in Y_predict]
y_pred = np.array(rounded,dtype='int64')
print('Confusion Matrix')
print('================')
CM = confusion_matrix(Y, y_pred)
print('True negatives: ',CM[0,0])
print('False negatives: ',CM[1,0])
print('False positives: ',CM[0,1])
print('True positives: ',CM[1,1])
```

```
768/768 [==============================] - 0s 24us/step

accuracy: 65.10%
===================
Saved model to disk
===================
Confusion Matrix
================
True negatives:  500
False negatives:  268
False positives:  0
True positives:  0
```

- In my working directory the network weights is saved in json format
- the accuracy of our model is 65.10%
- The confusion matrix can be interpreted as follows out of 768 observations in Pima-Indians-Diabetes dataset, 500 observation were correctly predicted while 268 were incorrectly predicted
- We can also calculate the accuracy by adding True negatives and True positive then divide the sum by the total number of observations: 500/768= 0.6510 which gives 65.10%

In [34]:
```
# Plotting the accuracy of training and testing our model
import matplotlib.pyplot as plt # importing matplotlib library
accuracy_training = history.history['accuracy']
loss = history.history['loss']
accuracy_testing = history.history['val_accuracy']
#plt.semilogy(loss,label='loss')
plt.semilogy(accuracy_training,label='accuracy - training')
plt.semilogy(accuracy_testing,label='accuracy - testing')
plt.xlabel('Epoch' )
plt.ylabel('Accuracy')
plt.title('the model accuracy')
plt.legend()
plt.show()
```



- The accuracy model on training and testing dataset shows that the model has better performance on the training dataset than testing which means that the model is overfitted

Adjusting the Dropout and validation_split to 30%

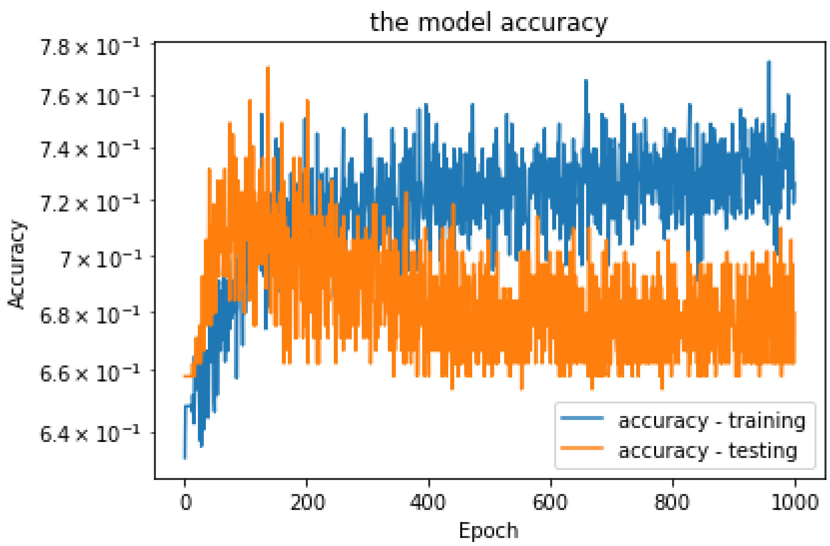
In [35]:
```
#######################################
##### Architecture of the model ######
######################################

# create a binary classification model
model = Sequential()
# Dropout used in Neural Network to reduce overfitting and improve gener
alization error
# Adding Dropout layer between 8 inputs(or visible layer) and 10 first h
idden layer
# Dropout rate is set to 30% means that three in 10 inputs will be rando
mly excluded from each update cycle
model.add(Dropout(0.3,input_shape=(8,)))
# Adding relu function to the first 10 hidden layers, also a constraint
 is imposed on the weights of hidden layers
# ensuring that the maximum norm of the weights doesn not exceed a value
of 3
model.add(Dense(10,  kernel_initializer='normal', activation='relu',kern
el_constraint=maxnorm(3)))
# Adding the second hidden layer with a constraint doesn't exceed 3 also
adding normal distribution for intializing the weights
model.add(Dense(8,  kernel_initializer='normal', activation='relu',kerne
l_constraint=maxnorm(3)))
# Adding the last output layer with the activation function sigmoid
model.add(Dense(1, kernel_initializer='normal', activation='sigmoid'))

# compiling the model with binary_crossentropy for loss function, Adam
 as optimizer default and the accuracy for out metrics.
model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['ac
curacy'])

# train the model by passing features and target variable with 1000 iter
ations
# setting validation_split to separate 30% of the training data into a v
alidation dataset that can be used to evaluate our model
history=model.fit(X,Y,validation_split=0.30,epochs=1000,verbose=0)

# Evaluate the model
scores = model.evaluate(X, Y)
Y_predict = model.predict(X)

print("\n%s: %.2f%%" % (model.metrics_names[1], scores[1]*100))

#########################################
######## Save Model to disk ############
#########################################

# Save the model structure as json format
model_json = model.to_json()
with open('model.json', 'w') as json_file:
    json_file.write(model_json)
# Save weights and biases to HD5 file
model.save_weights('model.h5')

print('==================')
print('Saved model to disk')
```

```
print('===================')

# create confusion matrix details
rounded = [round(i[0]) for i in Y_predict]
y_pred = np.array(rounded,dtype='int64')
print('Confusion Matrix')
print('================')
CM = confusion_matrix(Y, y_pred)
print('True negatives: ',CM[0,0])
print('False negatives: ',CM[1,0])
print('False positives: ',CM[0,1])
print('True positives: ',CM[1,1])
```

```
768/768 [==============================] - 0s 26us/step

accuracy: 67.58%
===================
Saved model to disk
===================
Confusion Matrix
================
True negatives:  499
False negatives:  248
False positives:  1
True positives:  20
```

- In my working directory the network weights is saved in json format
- the accuracy of our model is 67.58%
- The confusion matrix can be interpreted as follows out of 768 observations in Pima-Indians-Diabetes dataset, 519 observation were correctly predicted while 249 were incorrectly predicted
- We can also calculate the accuracy by adding True negatives and True positive then divide the sum by the total number of observations: 519/768= 0.6758 which gives 67.58%

In [36]:
```
# Plotting the accuracy of training and testing our model
import matplotlib.pyplot as plt # importing matplotlib library
accuracy_training = history.history['accuracy']
loss = history.history['loss']
accuracy_testing = history.history['val_accuracy']
#plt.semilogy(loss,label='loss')
plt.semilogy(accuracy_training,label='accuracy - training')
plt.semilogy(accuracy_testing,label='accuracy - testing')
plt.xlabel('Epoch' )
plt.ylabel('Accuracy')
plt.title('the model accuracy')
plt.legend()
plt.show()
```



- Overall, Dropout layers is an effective way to prevent or decrease overfitting in our model

PART II : SET UP CHECKPOINTING

Dropout rate and Validation_split equal to 10%

In [38]:
```
from keras.callbacks import ModelCheckpoint

#######################################
##### Architecture of the model ######
######################################

# create a binary classification model
model = Sequential()
# Dropout used in Neural Network to reduce overfitting and improve gener
alization error
# Adding Dropout layer between 8 inputs(or visible layer) and 10 first h
idden layer
# Dropout rate is set to 10% means that one in 10 inputs will be randoml
y excluded from each update cycle
model.add(Dropout(0.1,input_shape=(8,)))
# Adding relu function to the first 10 hidden layers, also a constraint
 is imposed on the weights of hidden layers
# ensuring that the maximum norm of the weights doesn not exceed a value
of 3
model.add(Dense(10,  kernel_initializer='normal', activation='relu',kern
el_constraint=maxnorm(3)))
# Adding the second hidden layer with a constraint doesn't exceed 3 also
adding normal distribution for intializing the weights
model.add(Dense(8,  kernel_initializer='normal', activation='relu',kerne
l_constraint=maxnorm(3)))
# Adding the last output layer with the activation function sigmoid
model.add(Dense(1, kernel_initializer='normal', activation='sigmoid'))

# compiling the model with binary_crossentropy for loss function, Adam
 as optimizer default and the accuracy for out metrics.
model.compile(loss='binary_crossentropy', optimizer='adam', metrics=['ac
curacy'])


##########################################
######## Save Model to disk ############
#########################################

# Save model structure as json format
print('===================')
print('Saving model to disk')
print('===================')
model_json = model.to_json()
with open('model.json', 'w') as json_file:
    json_file.write(model_json)


##########################################
######## Set up Checkpointing ###########
#########################################

# Checkpointing is an approach where a snapshot of the state of the syst
em is taken in case of the system failure or if there's any problem
# the good use of checkpointing is to output the model weights each time
an improvement is observed during training
```

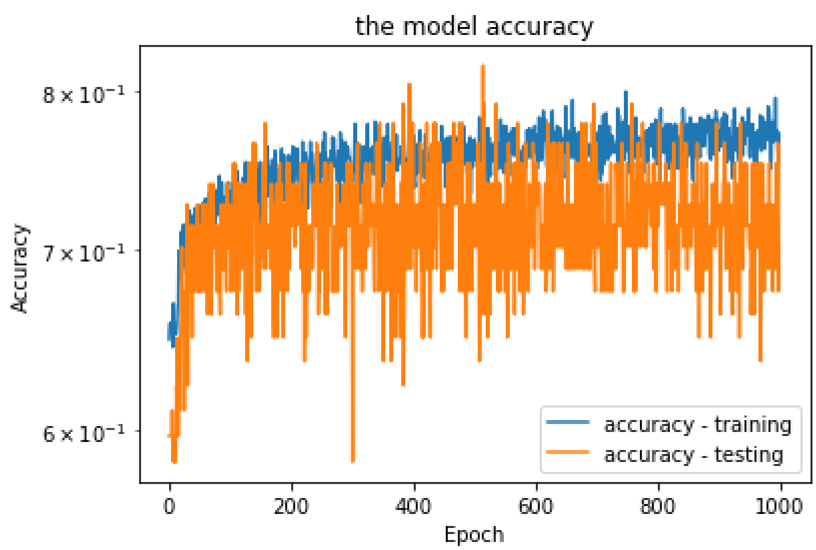
```
filepath = 'weights.best.hdh5' # weights are stored in a hdh5 file
checkpoint = ModelCheckpoint(filepath,monitor='val_acc',verbose=1,save_b
est_only=True,mode='max')
callbacks_list = [checkpoint]

# train the model by passing features and target variable with 1000 iter
ations
# setting validation_split to separate 10% of the training data into a v
alidation dataset that can be used to evaluate our model
history=model.fit(X,Y,validation_split=0.1,epochs=1000,verbose=0,callbac
ks=callbacks_list)

# Evaluate the model
scores = model.evaluate(X, Y)
Y_predict = model.predict(X)

print("\n%s: %.2f%%" % (model.metrics_names[1], scores[1]*100))


# create confusion matrix details
rounded = [round(i[0]) for i in Y_predict]
y_pred = np.array(rounded,dtype='int64')
print('Confusion Matrix')
print('================')
CM = confusion_matrix(Y, y_pred)
print('True negatives: ',CM[0,0])
print('False negatives: ',CM[1,0])
print('False positives: ',CM[0,1])
print('True positives: ',CM[1,1])
```

```
===================
Saving model to disk
===================

/Users/karimaidrissi/opt/anaconda3/lib/python3.7/site-packages/keras/ca
llbacks/callbacks.py:707: RuntimeWarning: Can save best model only with
val_acc available, skipping.
  'skipping.' % (self.monitor), RuntimeWarning)

768/768 [==============================] - 0s 27us/step

accuracy: 74.87%
Confusion Matrix
================
True negatives:  491
False negatives:  184
False positives:  9
True positives:  84
```

- In my working directory the network weights is saved in jason and h5 format
- the accuracy of our model is 74.87%
- The confusion matrix can be interpreted as follows out of 768 observations in Pima-Indians-Diabetes dataset, 575 observation were correctly predicted while 193 were incorrectly predicted
- We can also calculate the accuracy by adding True negatives and True positive then divide the sum by the total number of observations: 575/768= 0.7487 which gives 74.87%

Plotting the accuracy of the model

In [41]:
```
accuracy_training = history.history['accuracy']
loss = history.history['loss']
accuracy_testing = history.history['val_accuracy']
plt.semilogy(accuracy_training,label='accuracy - training')
plt.semilogy(accuracy_testing,label='accuracy - testing')
plt.xlabel('Epoch' )
plt.ylabel('Accuracy')
plt.title("the model accuracy")
plt.legend()
plt.show()
```



- the model accuracy on training and testing dataset shows that the model has better performance on the training dataset than testing, we can decrease overfitting by setting another Dropout.
- when I was reading an article about overfitting, I found that early stopping is another helpful technique to stop training when a monitored quantity stopped improving in the model

In [ ]: