

Ex No.10: *Applying Deep Learning Methods to Solve an application*

Problem Statement:

To develop a Deep Neural Network to predict cancer as malignant or benign.

Deep Learning

Deep learning is a subset of machine learning, which is essentially a neural network with three or more layers. These neural networks attempt to simulate the behaviour of the human brain—albeit far from matching its ability—allowing it to “learn” from large amounts of data. While a neural network with a single layer can still make approximate predictions, additional hidden layers can help to optimize and refine for accuracy.

Deep learning drives many artificial intelligence (AI) applications and services that improve automation, performing analytical and physical tasks without human intervention. Deep learning technology lies behind everyday products and services (such as digital assistants, voice-enabled TV remotes, and credit card fraud detection) as well as emerging technologies (such as self-driving cars).

Deep Neural Network to predict cancer as malignant or benign

Importing Dataset

```
In [ ]:
```

```
from sklearn.datasets import load_breast_cancer
dataset = load_breast_cancer()
```

```
In [ ]:
```

```
print(dataset.DESCR)
```

```
.. _breast_cancer_dataset:
```

```
Breast cancer wisconsin (diagnostic) dataset
```

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```

```
**Data Set Characteristics:**
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```
:Number of Instances: 569
```

```
:Number of Attributes: 30 numeric, predictive attributes and the class
```

```
:Attribute Information:
```

- radius (mean of distances from center to points on the perimeter)
- texture (standard deviation of gray-scale values)
- perimeter
- area
- smoothness (local variation in radius lengths)
- compactness (perimeter² / area - 1.0)
- concavity (severity of concave portions of the contour)
- concave points (number of concave portions of the contour)
- symmetry
- fractal dimension ("coastline approximation" - 1)

The mean, standard error, and "worst" or largest (mean of the three largest values) of these features were computed for each image, resulting in 30 features. For instance, field 3 is Mean Radius, field 13 is Radius SE, field 23 is Worst Radius.

- class:
 - WDBC-Malignant
 - WDBC-Benign

```
:Summary Statistics:
```

	Min	Max
radius (mean):	6.981	28.11
texture (mean):	9.71	39.28
perimeter (mean):	43.79	188.5
area (mean):	143.5	2501.0
smoothness (mean):	0.053	0.163
compactness (mean):	0.019	0.345
concavity (mean):	0.0	0.427
concave points (mean):	0.0	0.201
symmetry (mean):	0.106	0.304
fractal dimension (mean):	0.05	0.097
radius (standard error):	0.112	2.873
texture (standard error):	0.36	4.885
perimeter (standard error):	0.757	21.98
area (standard error):	6.802	542.2
smoothness (standard error):	0.002	0.031
compactness (standard error):	0.002	0.135
concavity (standard error):	0.0	0.396
concave points (standard error):	0.0	0.053

```

symmetry (standard error):      0.008  0.079
fractal dimension (standard error): 0.001  0.03
radius (worst):                 7.93   36.04
texture (worst):                12.02  49.54
perimeter (worst):              50.41  251.2
area (worst):                   185.2  4254.0
smoothness (worst):             0.071  0.223
compactness (worst):            0.027  1.058
concavity (worst):              0.0    1.252
concave points (worst):         0.0    0.291
symmetry (worst):               0.156  0.664
fractal dimension (worst):      0.055  0.208
=====

```

:Missing Attribute Values: None

:Class Distribution: 212 - Malignant, 357 - Benign

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:Donor: Nick Street

:Date: November, 1995

This is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.
<https://goo.gl/U2Uwz2>

Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image.

Separating plane described above was obtained using Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree Construction Via Linear Programming." Proceedings of the 4th Midwest Artificial Intelligence and Cognitive Science Society, pp. 97-101, 1992], a classification method which uses linear programming to construct a decision tree. Relevant features were selected using an exhaustive search in the space of 1-4 features and 1-3 separating planes.

The actual linear program used to obtain the separating plane in the 3-dimensional space is that described in:
 [K. P. Bennett and O. L. Mangasarian: "Robust Linear Programming Discrimination of Two Linearly Inseparable Sets", Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server:

```

ftp ftp.cs.wisc.edu
cd math-prog/cpo-dataset/machine-learn/WDBC/

```

.. topic:: References

- W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on Electronic Imaging: Science and Technology, volume 1905, pages 861-870, San Jose, CA, 1993.
- O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and prognosis via linear programming. Operations Research, 43(4), pages 570-577, July-August 1995.
- W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning techniques to diagnose breast cancer from fine-needle aspirates. Cancer Letters 77 (1994) 163-171.

In []:

```

features = dataset.data
target = dataset.target

```

In []:

```
print(features.shape)
```

```
(569, 30)
```

```
In [ ]:
```

```
print(target.shape)
```

```
(569,)
```

Splitting dataset into training set and test set

```
In [ ]:
```

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(features, target, test_size = 0.2)
```

```
In [ ]:
```

```
print(X_train.shape)
```

```
(455, 30)
```

```
In [ ]:
```

```
print(y_train.shape)
```

```
(455,)
```

```
In [ ]:
```

```
print(X_test.shape)
```

```
(114, 30)
```

```
In [ ]:
```

```
print(y_test.shape)
```

```
(114,)
```

```
In [ ]:
```

```
from keras.models import Sequential
from keras.layers import Dense
```

```
In [ ]:
```

```
model = Sequential()
model.add(Dense(32, input_dim = 30, activation = 'relu')) ## hidden layer 1
model.add(Dense(64, activation = 'relu')) ## hidden layer 2
model.add(Dense(1, activation = 'sigmoid'))
```

```
In [ ]:
```

```
model.compile(loss = 'binary_crossentropy', optimizer = 'adam', metrics = ['accuracy'])
```

```
In [ ]:
```

```
model.summary()
```

Model: "sequential_8"

Layer (type)	Output Shape	Param #
dense_24 (Dense)	(None, 32)	992
dense_25 (Dense)	(None, 64)	2112
dense_26 (Dense)	(None, 1)	65

```
Total params: 3,169
Trainable params: 3,169
Non-trainable params: 0
```

```
In [ ]:
```

```
model.fit(X_train, y_train, epochs = 10)
```

```
Epoch 1/10
15/15 [=====] - 0s 1ms/step - loss: 0.0297 - accuracy: 0.9890
Epoch 2/10
15/15 [=====] - 0s 1ms/step - loss: 0.0180 - accuracy: 0.9934
Epoch 3/10
15/15 [=====] - 0s 1ms/step - loss: 0.0173 - accuracy: 0.9956
Epoch 4/10
15/15 [=====] - 0s 1ms/step - loss: 0.0263 - accuracy: 0.9890
Epoch 5/10
15/15 [=====] - 0s 1ms/step - loss: 0.0257 - accuracy: 0.9890
Epoch 6/10
15/15 [=====] - 0s 1ms/step - loss: 0.0161 - accuracy: 0.9978
Epoch 7/10
15/15 [=====] - 0s 2ms/step - loss: 0.0172 - accuracy: 0.9934
Epoch 8/10
15/15 [=====] - 0s 1ms/step - loss: 0.0148 - accuracy: 0.9956
Epoch 9/10
15/15 [=====] - 0s 1ms/step - loss: 0.0145 - accuracy: 0.9956
Epoch 10/10
15/15 [=====] - 0s 2ms/step - loss: 0.0144 - accuracy: 0.9934
```

```
Out[ ]:
```

```
<keras.callbacks.History at 0x7fd5019442d0>
```

```
In [ ]:
```

```
scores = model.evaluate(X_test, y_test)
print(scores) ## returns loss and accuracy
```

```
4/4 [=====] - 0s 2ms/step - loss: 0.4843 - accuracy: 0.9386
[0.48427480459213257, 0.9385964870452881]
```

```
In [ ]:
```

```
predictions = model.predict(X_test)
label = []
for pred in predictions:
    if pred>=0.5:
        print("Malignant")
    else:
        print("Benign")
```

```
Malignant
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RESULT

A Deep Neural Network was successfully developed to determine cancer as malignant or benign.

In []: