

ASSIGNMENT 2

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```
In [8]: import pandas as pd

#import the data
train_data = pd.read_csv('./data_train.csv')
test_data = pd.read_csv('./data_test.csv')
output_data = pd.read_csv('./Copy of actual.csv')

#manipulating the data
train_data.drop(train_data.columns[0], axis=1, inplace=True)
test_data.drop(test_data.columns[0],axis=1,inplace=True)

num_columns_train = len(train_data.columns)
num_columns_test = len(test_data.columns)

for i in range(1,num_columns_train-1,2):
    train_data[train_data.columns[i]]=train_data[train_data.columns[i+1]]

for i in range(1,num_columns_test-1,2):
    test_data[test_data.columns[i]]=test_data[test_data.columns[i+1]]

train_data.drop(train_data.columns[2::2], axis=1, inplace=True)
test_data.drop(test_data.columns[2::2], axis=1, inplace=True)

train_data=train_data.T
test_data=test_data.T

train_data.reset_index(inplace=True)
train_data.columns=train_data.iloc[0]
train_data=train_data[1:]
train_data = train_data.rename(columns={'Gene Accession Number': 'patient'})

test_data.reset_index(inplace=True)
test_data.columns=test_data.iloc[0]
test_data=test_data[1:]
test_data = test_data.rename(columns={'Gene Accession Number': 'patient'})

train_data['patient'] = train_data['patient'].astype('int64')
test_data['patient'] = test_data['patient'].astype('int64')

trainD=pd.merge(train_data,output_data,on='patient',how='inner')
testD=pd.merge(test_data,output_data,on='patient',how='inner')

# The final data set has each patient as a sample data(rows) and each gene
# column represent the target value (cancer)
print("Train data: \n")
print(trainD)
print("Test data: \n")
print(testD)
```

Train data:

	patient	AFFX-BioB-5_at	AFFX-BioB-M_at	AFFX-BioB-3_at	AFFX-BioC-5_at
\					
0	1	A	A	A	A
1	2	A	A	A	A
2	3	A	A	A	A
3	4	A	A	A	A
4	5	A	A	A	A
5	6	A	A	A	A
6	7	A	A	A	A
7	8	A	A	A	A
8	9	A	A	A	A
9	10	A	A	A	M
10	11	A	A	A	A
11	12	A	A	A	A
12	13	A	A	A	A
13	14	A	A	A	M
14	15	A	A	A	A
15	16	A	A	A	A
16	17	A	A	A	A
17	18	A	A	A	A
18	19	A	A	A	A
19	20	A	A	A	A
20	21	A	A	A	A
21	22	A	A	A	A
22	23	A	A	A	A
23	24	A	A	A	A
24	25	A	A	A	A
25	26	A	A	A	A
26	27	A	A	A	A
27	34	A	A	A	A
28	35	A	A	A	A
29	36	A	A	A	A
30	37	A	A	A	A
31	38	A	A	A	P
32	28	A	A	A	A
33	29	A	A	A	A
34	30	A	A	A	A
35	31	A	A	A	P
36	32	A	A	A	A
37	33	A	A	A	A

	AFFX-BioC-3_at	AFFX-BioDn-5_at	AFFX-BioDn-3_at	AFFX-CreX-5_at	\
0	A	A	A	A	
1	A	A	A	A	
2	A	A	A	A	
3	A	A	A	A	
4	A	A	A	A	
5	A	A	A	A	
6	A	A	A	A	
7	A	A	A	A	
8	A	A	A	A	
9	A	A	A	A	
10	A	A	A	A	
11	A	A	A	A	
12	A	A	A	A	
13	A	A	A	A	
14	A	A	A	A	
15	A	A	A	A	
16	A	A	A	A	

17	A	A	A	A
18	A	A	A	A
19	A	A	A	A
20	A	A	A	A
21	A	A	A	A
22	A	A	A	A
23	A	A	A	A
24	A	A	A	A
25	A	A	A	A
26	A	A	A	A
27	A	A	A	A
28	A	A	A	A
29	A	A	A	A
30	A	A	A	A
31	A	A	A	A
32	A	A	A	A
33	A	A	A	A
34	A	A	A	A
35	A	A	A	A
36	A	A	A	A
37	A	A	A	A

	AFFX-CreX-3_at	... U58516_at	U73738_at	X06956_at	X16699_at	X83863_at
\						
0	A	...	A	A	P	A
1	A	...	A	A	A	A
2	A	...	A	A	A	A
3	A	...	A	A	A	A
4	A	...	A	A	P	A
5	A	...	A	A	A	A
6	A	...	A	A	A	A
7	A	...	A	A	A	A
8	A	...	A	A	A	A
9	A	...	P	A	A	A
10	A	...	A	A	A	A
11	A	...	A	A	A	A
12	A	...	A	A	P	A
13	A	...	A	A	A	A
14	A	...	P	A	P	A
15	A	...	A	A	A	A
16	A	...	A	A	A	A
17	A	...	A	A	P	A
18	A	...	A	A	P	A
19	A	...	A	A	A	A
20	A	...	P	A	A	A
21	A	...	A	A	P	A
22	A	...	A	A	A	A
23	A	...	A	A	A	A
24	A	...	A	A	P	A
25	A	...	A	A	P	A
26	A	...	A	A	A	A
27	A	...	A	A	A	A
28	A	...	A	A	A	A
29	A	...	A	A	P	A
30	A	...	A	A	A	A
31	A	...	A	A	A	A
32	A	...	A	A	P	A
33	A	...	A	A	P	A
34	A	...	A	A	P	A
35	A	...	A	A	A	A
36	A	...	A	A	A	A

```

37          A    ...          A          A          A          A          A
      Z17240_at L49218_f_at M71243_f_at Z78285_f_at cancer
0          A          A          A          A          ALL
1          A          A          A          A          ALL
2          P          A          A          A          ALL
3          A          A          A          A          ALL
4          A          A          A          A          ALL
5          A          A          A          A          ALL
6          A          A          P          A          ALL
7          P          A          P          A          ALL
8          A          P          A          A          ALL
9          P          A          M          A          ALL
10         A          A          A          A          ALL
11         A          A          A          A          ALL
12         A          A          A          A          ALL
13         A          A          A          A          ALL
14         A          A          A          A          ALL
15         P          A          P          A          ALL
16         P          A          A          A          ALL
17         P          A          A          A          ALL
18         A          A          A          A          ALL
19         A          A          P          A          ALL
20         A          A          A          A          ALL
21         A          A          M          A          ALL
22         A          A          M          A          ALL
23         A          A          A          A          ALL
24         A          A          P          A          ALL
25         P          A          A          A          ALL
26         A          A          A          A          ALL
27         A          A          M          A          AML
28         A          A          P          A          AML
29         A          A          A          A          AML
30         A          A          P          A          AML
31         A          A          P          A          AML
32         A          A          P          A          AML
33         A          A          P          A          AML
34         A          A          A          A          AML
35         A          A          A          A          AML
36         A          A          A          A          AML
37         A          A          P          A          AML

```

[38 rows x 7131 columns]

Test data:

```

      patient AFFX-BioB-5_at AFFX-BioB-M_at AFFX-BioB-3_at AFFX-BioC-5_at
\
0      39          A          A          A          A
1      40          A          A          A          A
2      42          A          A          A          A
3      47          A          A          A          A
4      48          A          A          A          A
5      49          A          A          A          A
6      41          A          A          A          A
7      43          A          A          A          A
8      44          A          A          A          A
9      45          A          A          A          A
10     46          A          A          A          A
11     70          A          A          A          A
12     71          A          A          A          A
13     72          A          A          A          A

```

14	68	A	A	A	A
15	69	A	A	A	A
16	67	A	A	A	A
17	55	A	A	A	A
18	56	A	A	A	A
19	59	A	A	A	A
20	52	A	A	A	A
21	53	A	A	A	A
22	51	A	A	A	A
23	50	A	A	A	A
24	54	A	A	A	P
25	57	A	A	A	A
26	58	A	A	A	A
27	60	A	A	A	A
28	61	A	A	A	A
29	65	A	A	A	A
30	66	A	A	A	A
31	63	A	A	A	A
32	64	A	A	A	A
33	62	A	A	A	A

	AFFX-BioC-3_at	AFFX-BioDn-5_at	AFFX-BioDn-3_at	AFFX-CreX-5_at	\
0	A	A	A	A	
1	A	A	A	A	
2	A	A	A	A	
3	A	A	A	A	
4	A	A	A	A	
5	A	A	A	A	
6	A	A	A	A	
7	A	A	A	A	
8	A	A	A	A	
9	A	A	A	A	
10	A	A	A	A	
11	A	A	A	A	
12	A	A	A	A	
13	A	A	A	A	
14	A	A	A	A	
15	A	A	A	A	
16	A	A	A	A	
17	A	A	A	A	
18	A	A	A	A	
19	A	A	A	A	
20	A	A	A	A	
21	A	A	A	A	
22	A	A	A	A	
23	A	A	A	A	
24	A	A	A	A	
25	A	A	A	A	
26	A	A	A	A	
27	A	A	A	A	
28	A	A	A	A	
29	A	A	A	A	
30	A	A	A	A	
31	A	A	A	A	
32	A	A	A	A	
33	A	A	A	A	

	AFFX-CreX-3_at	...	U58516_at	U73738_at	X06956_at	X16699_at	X83863_at
\							
0	A	...	A	A	A	A	A
1	A	...	A	A	P	A	A

2	A	...	A	A	P	A	P
3	A	...	A	A	A	A	A
4	A	...	A	A	P	A	A
5	A	...	A	A	A	A	A
6	A	...	P	A	A	A	A
7	A	...	A	A	P	A	A
8	A	...	P	A	P	A	A
9	A	...	A	A	A	A	A
10	A	...	P	A	A	A	A
11	A	...	A	A	A	A	A
12	A	...	A	A	P	A	A
13	A	...	A	A	P	A	A
14	A	...	A	A	P	A	A
15	A	...	A	A	P	A	A
16	A	...	A	A	A	A	A
17	A	...	A	A	A	A	A
18	A	...	A	A	P	A	A
19	A	...	A	A	P	A	A
20	A	...	A	A	A	A	A
21	A	...	A	A	A	A	A
22	A	...	A	A	A	A	A
23	A	...	A	A	A	A	A
24	A	...	A	A	A	A	A
25	A	...	A	A	A	A	A
26	A	...	A	A	A	A	A
27	A	...	A	A	A	A	A
28	A	...	A	A	A	A	A
29	A	...	A	A	P	A	A
30	A	...	A	A	P	A	A
31	A	...	A	A	P	A	A
32	A	...	A	A	A	A	A
33	A	...	A	A	P	A	A

	Z17240_at	L49218_f_at	M71243_f_at	Z78285_f_at	cancer
0	A	A	A	A	ALL
1	A	A	A	A	ALL
2	A	A	P	A	ALL
3	A	A	P	A	ALL
4	A	A	A	A	ALL
5	A	A	A	A	ALL
6	A	A	A	A	ALL
7	A	A	P	A	ALL
8	A	A	A	A	ALL
9	A	A	A	A	ALL
10	A	A	A	A	ALL
11	A	A	P	P	ALL
12	A	A	A	A	ALL
13	P	A	A	A	ALL
14	A	A	A	A	ALL
15	A	A	A	A	ALL
16	A	A	A	A	ALL
17	A	A	A	A	ALL
18	A	A	P	A	ALL
19	A	A	A	A	ALL
20	A	A	A	A	AML
21	P	A	A	A	AML
22	A	A	P	A	AML
23	A	A	P	A	AML
24	A	A	A	A	AML
25	A	A	A	A	AML
26	P	A	A	A	AML

27	A	A	M	A	AML
28	A	A	A	A	AML
29	A	A	A	A	AML
30	A	A	P	A	AML
31	A	A	A	A	AML
32	A	A	A	A	AML
33	A	A	A	A	AML

[34 rows x 7131 columns]


```

In [2]: #encoding the data values to make it processable to train the models
import pandas as pd
from sklearn.preprocessing import LabelEncoder

# Split the data into features (X) and target Labels (y)
X_train = trainD.drop(['patient', 'cancer'], axis=1)
y_train = trainD['cancer']

X_test = testD.drop(['patient', 'cancer'], axis=1)
y_test = testD['cancer']

# Initialize the LabelEncoder
encoder = LabelEncoder()

# Concatenate X_train and X_test to ensure all categories are seen
combined_data = pd.concat([X_train, X_test], axis=0)

# Apply Label encoding to combined_data
for column in combined_data.columns:
    combined_data[column] = encoder.fit_transform(combined_data[column])

# Split the encoded data back into X_train_encoded and X_test_encoded
X_train_encoded = combined_data.iloc[:len(X_train)]
X_test_encoded = combined_data.iloc[len(X_train):]

# Print X_train_encoded
print("X_train_encoded:\n")
print(X_train_encoded)

# Print X_test_encoded
print("\nX_test_encoded:\n")
print(X_test_encoded)

```

```

37      0      0      0      0
      AFFX-BioC-3_at AFFX-BioDn-5_at AFFX-BioDn-3_at AFFX-CreX-5_at
\
0      0      0      0      0
1      0      0      0      0
2      0      0      0      0
3      0      0      0      0
4      0      0      0      0
5      0      0      0      0
6      0      0      0      0
7      0      0      0      0
8      0      0      0      0
9      0      0      0      0
10     0      0      0      0
11     0      0      0      0
12     0      0      0      0
13     0      0      0      0
14     0      0      0      0
15     0      0      0      0

```

```
In [4]: #SVM model
from sklearn.preprocessing import StandardScaler
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score, precision_score, recall_score,

# Define a list of kernel names
kernels = ['linear', 'rbf', 'poly', 'sigmoid']

for kernel in kernels:
    # Create an SVM model with the specified kernel
    model = SVC(kernel=kernel)

    # Scale the features
    scaler = StandardScaler()
    X_train_scaled = scaler.fit_transform(X_train_encoded)
    X_test_scaled = scaler.transform(X_test_encoded)

    # Train the model
    model.fit(X_train_scaled, y_train)

    # Make predictions on the test data
    y_pred = model.predict(X_test_scaled)

    # Evaluate the model
    accuracy = accuracy_score(y_test, y_pred)
    precision = precision_score(y_test, y_pred, pos_label='ALL')
    recall = recall_score(y_test, y_pred, pos_label='ALL')
    f1 = f1_score(y_test, y_pred, pos_label='ALL')
    confusion = confusion_matrix(y_test, y_pred)

    # Print the evaluation metrics
    print(f"SVM Model with {kernel} kernel")
    print(f"Accuracy: {accuracy}")
    print(f"Precision: {precision}")
    print(f"Recall: {recall}")
    print(f"F1 Score: {f1}")
    print(f"Confusion Matrix:\n{confusion}\n")
```

```
SVM Model with linear kernel
Accuracy: 0.9117647058823529
Precision: 0.8695652173913043
Recall: 1.0
F1 Score: 0.9302325581395349
Confusion Matrix:
[[20  0]
 [ 3 11]]
```

```
SVM Model with rbf kernel
Accuracy: 0.5882352941176471
Precision: 0.5882352941176471
Recall: 1.0
F1 Score: 0.7407407407407407
Confusion Matrix:
[[20  0]
 [14  0]]
```

```
SVM Model with poly kernel
Accuracy: 0.5882352941176471
Precision: 0.5882352941176471
Recall: 1.0
F1 Score: 0.7407407407407407
Confusion Matrix:
[[20  0]
 [14  0]]
```

```
SVM Model with sigmoid kernel
Accuracy: 0.8529411764705882
Precision: 0.8
Recall: 1.0
F1 Score: 0.8888888888888889
Confusion Matrix:
[[20  0]
 [ 5  9]]
```

```
In [5]: #Random Forest
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, precision_score, recall_score,

# Create a Random Forest model
rf_model = RandomForestClassifier(n_estimators=100, random_state=42)

# Train the model
rf_model.fit(X_train_encoded, y_train)

# Make predictions on the test data
y_pred_rf = rf_model.predict(X_test_encoded)

# Evaluate the model
accuracy_rf = accuracy_score(y_test, y_pred_rf)
precision_rf = precision_score(y_test, y_pred_rf, pos_label='ALL')
recall_rf = recall_score(y_test, y_pred_rf, pos_label='ALL')
f1_rf = f1_score(y_test, y_pred_rf, pos_label='ALL')
confusion_rf = confusion_matrix(y_test, y_pred_rf)

# Print the evaluation metrics
print("Random Forest Model")
print(f"Accuracy: {accuracy_rf}")
print(f"Precision: {precision_rf}")
print(f"Recall: {recall_rf}")
print(f"F1 Score: {f1_rf}")
print(f"Confusion Matrix:\n{confusion_rf}\n")
```

```
Random Forest Model
Accuracy: 0.8823529411764706
Precision: 0.8333333333333334
Recall: 1.0
F1 Score: 0.9090909090909091
Confusion Matrix:
[[20  0]
 [ 4 10]]
```

```
In [7]: #Neural Network
from sklearn.neural_network import MLPClassifier
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score, precision_score, recall_score,
from sklearn.model_selection import GridSearchCV

# Create a Neural Network model
nn_model = MLPClassifier()

# Define the hyperparameter grid to search through
param_grid = {
    'hidden_layer_sizes': [(100, 50), (50, 25), (200, 100), (150, 75)],
    'alpha': [0.0001, 0.001, 0.01],
    'max_iter': [500, 1000, 1500],
    'solver': ['adam', 'lbfgs'],
    'learning_rate_init': [0.001, 0.01, 0.1]
}

# Create a grid search object
grid_search = GridSearchCV(estimator=nn_model, param_grid=param_grid, cv=5,

# Scale the features
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train_encoded)
X_test_scaled = scaler.transform(X_test_encoded)

# Perform the grid search
grid_search.fit(X_train_scaled, y_train)

# Get the best model and its hyperparameters
best_model = grid_search.best_estimator_
best_params = grid_search.best_params_

# Make predictions on the test data with the best model
y_pred_nn = best_model.predict(X_test_scaled)

# Evaluate the best model
accuracy_nn = accuracy_score(y_test, y_pred_nn)
precision_nn = precision_score(y_test, y_pred_nn, pos_label='ALL')
recall_nn = recall_score(y_test, y_pred_nn, pos_label='ALL')
f1_nn = f1_score(y_test, y_pred_nn, pos_label='ALL')
confusion_nn = confusion_matrix(y_test, y_pred_nn)

# Print the evaluation metrics and best hyperparameters
print("Neural Network Model with Hyperparameter Tuning")
print(f"Best Hyperparameters: {best_params}")
print(f"Accuracy: {accuracy_nn}")
print(f"Precision: {precision_nn}")
print(f"Recall: {recall_nn}")
print(f"F1 Score: {f1_nn}")
print(f"Confusion Matrix:\n{confusion_nn}\n")
```

Neural Network Model with Hyperparameter Tuning

Best Hyperparameters: {'alpha': 0.001, 'hidden_layer_sizes': (200, 100),
'learning_rate_init': 0.01, 'max_iter': 1000, 'solver': 'lbfgs'}

Accuracy: 0.9117647058823529

Precision: 0.9047619047619048

Recall: 0.95

F1 Score: 0.9268292682926829

Confusion Matrix:

```
[[19  1]
 [ 2 12]]
```