Assignment1 k-Nearest Neighbors

Preprocessing data

Data Information

```
RangeIndex: 699 entries, 0 to 698
Data columns (total 11 columns):
        Column
 #
                                         Non-Null Count Dtype
        id
                                         699 non-null
                                                                     int64
 0
 1
        clump thickness 699 non-null
                                                                    int64
 2 size_uniformity 699 non-null int64
3 shape_uniformity 699 non-null int64
 4 marginal_adhesion 699 non-null int64
5 epithelial_size 699 non-null int64
6 bare_nucleoli 699 non-null object
7 bland_chromatin 699 non-null int64
8 normal_nucleoli 699 non-null int64
9 mitoses 699 non-null int64
10 class 699 non-null int64
dtypes: int64(10), object(1)
memory usage: 60.2+ KB
```

The bare_nucleoli column, initially of type object, was converted to numeric to address the discrepancy.

```
data['bare_nucleoli'] = pd.to_numeric(data['bare_nucleoli'],
errors='coerce')
```

Data Preprocessing Steps

Convert the classes to 0 (benign) and 1 (malignant) for using in the classifier

The class column originally contains values 2 (benign) and 4 (malignant). These were converted to 0 and 1 respectively for compatibility with the classifier.

```
data['class'] = data['class'].map({2: 0, 4: 1})
```

Fill in Missing values, if exist (try using Mode value)

```
data.fillna(data.mode().iloc[0],inplace=True)
```

Drop non-value added features

The id column was dropped because it does not provide meaningful information for classification.

```
data = data.drop(['id'], axis=1)
```

Standardization (Only feature)

Only the features were standardized. The target variable (class) was not standardized as it represents categorical data.

```
X = data.drop(columns=['class'])
y = data['class']

std = StandardScaler()
X_scaled = std.fit_transform(X)
```

Train-Test Split

The dataset was split into training and testing sets, with 80% of the data used for training and 20% for testing. A random_state of 1234 was set to ensure reproducibility.

```
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y,
test_size=0.2, random_state=1234)
```

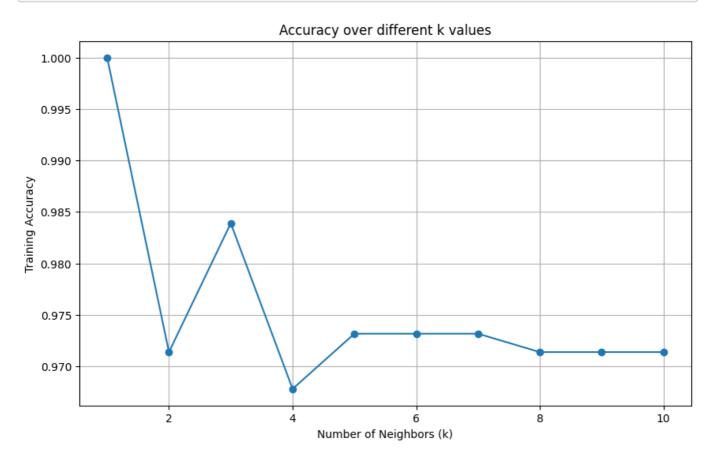
Tuning K

Looping k=1 to k=10 and plot the graph for finding the appropiate k

```
k_values = range(1, 11)
accuracies = []

for k in k_values:
    knn = KNeighborsClassifier(n_neighbors=k, metric='minkowski', p=2)
    knn.fit(X_train, y_train)
    y_pred_train = knn.predict(X_train)
    accuracy = knn.score(X_train, y_train)
    accuracies.append(accuracy)
```

```
plt.figure(figsize=(10, 6))
plt.plot(k_values, accuracies, marker='o', linestyle='-')
plt.title('Accuracy over different k values')
plt.xlabel('Number of Neighbors (k)')
plt.ylabel('Training Accuracy')
plt.grid()
plt.show()
```



Selecting K

The results indicated that the highest training accuracy was achieved with k = 1. However, this choice raises several concerns:

- Overfitting Risk: A k value of 1 can perfectly fit the training data but may not generalize well to new, unseen data, risking overfitting. Sensitivity to Noise: With k = 1, a single noisy data point can disproportionately affect predictions.
- As k increases, the model's generalization improves, but it may underfit the data if k becomes too large. Thus, the appropriate k value should balance bias and variance to ensure good generalization on unseen data. Typically, an odd value of k is preferred to avoid ties.

Given these considerations, I selected k = 3 because it is the second highest peak in accuracy. This value provides a better balance between performance and generalization, minimizing the risks associated with overfitting.

Train the Model by Selected K

```
selected_k = 3

final_model = KNeighborsClassifier(n_neighbors=selected_k,
metric='minkowski', p=2)
final_model.fit(X_train, y_train)
test_accuracy = final_model.score(X_test, y_test)
print(f"\nFinal test set accuracy with k={selected_k}:
{test_accuracy:.4f}")

y_pred = final_model.predict(X_test)
print("\nConfusion Matrix:")
print(confusion_matrix(y_test, y_pred))
print("\nClassification_Report:")
print(classification_report(y_test, y_pred))
```

Result

• Final Test Set Accuracy: The model achieved an accuracy of 0.9643 on the test set with K = 3. This indicates that approximately 96.43% of the predictions made by the model were correct.

Confusion Matrix: [[97 3] [2 38]] Classification Report:	Final test se	t accuracy	with $k = 3$: 0.9643	
Classification Report: precision		rix:			
precision recall f1-score support 0 0.98 0.97 0.97 100 1 0.93 0.95 0.94 40 accuracy 0.96 140	[2 38]]				
0 0.98 0.97 0.97 100 1 0.93 0.95 0.94 40 accuracy 0.96 140	Classificatio				
1 0.93 0.95 0.94 40 accuracy 0.96 140		precision	recall	f1-score	support
accuracy 0.96 140	0	0.98	0.97	0.97	100
,	1	0.93	0.95	0.94	40
macro avg 0.95 0.96 0.96 140	accuracy			0.96	140
macro avg 0133 0130 0130 110	macro avg	0.95	0.96	0.96	140
weighted avg 0.96 0.96 0.96 140	weighted avg	0.96	0.96	0.96	140

Extra: Finding the Best k for Test Data

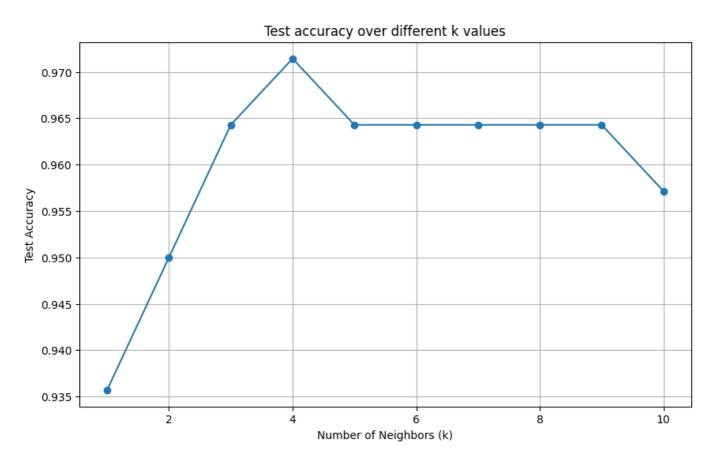
To further refine the model's performance, we evaluated the accuracy of the k-NN classifier across various k values specifically on the test dataset. This helps identify the optimal k that maximizes test accuracy.

```
test_accuracies = []
for k in k_values:
   final_model = KNeighborsClassifier(n_neighbors=k, metric='minkowski',
p=2)
   final_model.fit(X_train, y_train)
   test_accuracy = final_model.score(X_test, y_test)
   test_accuracies.append(test_accuracy)
print('Highest accuracy:', max(test_accuracies), ', with K =',
test_accuracies.index(max(test_accuracies)) + 1)
plt.figure(figsize=(10, 6))
plt.plot(k_values, test_accuracies, marker='o', linestyle='-')
plt.title('Test accuracy over different k values')
plt.xlabel('Number of Neighbors (k)')
plt.ylabel('Test Accuracy')
plt.grid()
plt.show()
```

Results

The evaluation of various k values revealed that the model achieved its highest accuracy at k=4, with a remarkable accuracy of 97.14%. This indicates that the k-NN classifier performed exceptionally well in distinguishing between benign and malignant cases.





While the accuracy at k=3 was also strong at 96.43%, the difference of approximately 0.71% between k=3 and k=4 suggests that the choice of k has a relatively modest impact on performance in this instance. This slight improvement highlights the importance of carefully tuning k to optimize model performance while balancing the risks of overfitting and underfitting.

In summary, although both k=3 and k=4 yielded high accuracies, selecting k=4 maximizes the model's predictive capability, ensuring robust performance on unseen data.