Part 01 :

1. Consider this dataset from kaggle. (Download the dataset from following link : https://www.kaggle.com/shrutimechlearn/step-by-step-kmeans-explained-in-detail/data) and answer the following questions :

Importing the necessary lib

In [1]:
```
import warnings
warnings.filterwarnings('ignore')
```

In [2]:
```
import pandas as pd
import numpy as np
from sklearn.preprocessing import LabelEncoder
from sklearn.cluster import KMeans
from sklearn.decomposition import PCA
from sklearn.manifold import TSNE
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn import metrics
from sklearn.metrics import accuracy_score, classification_report
```

In [3]:
```
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
sns.set(style="whitegrid", color_codes=True, palette="dark" )
```

Load Dataset

In [4]:
```
mall_customers = pd.read_csv("Mall_Customers.csv")
```

Exploratory Data Analysis (EDA)

In [5]:
```
mall_customers.sample(10)
```

Out[5]:

	CustomerID	Genre	Age	Annual_Income_(k$)	Spending_Score
152	153	Female	44	78	20
61	62	Male	19	46	55
49	50	Female	31	40	42
196	197	Female	45	126	28
135	136	Female	29	73	88
77	78	Male	40	54	48
18	19	Male	52	23	29
78	79	Female	23	54	52
9	10	Female	30	19	72
33	34	Male	18	33	92

In [6]:
```
mall_customers.dtypes
```

Out[6]:
```
CustomerID             int64
Genre                 object
Age                    int64
Annual_Income_(k$)     int64
Spending_Score         int64
dtype: object
```

In [7]:
```
mall_customers.shape
```

Out[7]:
```
(200, 5)
```

In [8]:
```
duplicate_rows = mall_customers[mall_customers.duplicated()]

print("Duplicate Rows:")
duplicate_rows
```

```
Duplicate Rows:
```

Out[8]:

CustomerID	Genre	Age	Annual_Income_(k$)	Spending_Score

In [9]:
```
mall_customers.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 200 entries, 0 to 199
Data columns (total 5 columns):
 #   Column              Non-Null Count  Dtype 
---  ------              --------------  ----- 
 0   CustomerID          200 non-null    int64 
 1   Genre               200 non-null    object
 2   Age                 200 non-null    int64 
 3   Annual_Income_(k$)  200 non-null    int64 
 4   Spending_Score      200 non-null    int64 
dtypes: int64(4), object(1)
memory usage: 7.9+ KB
```

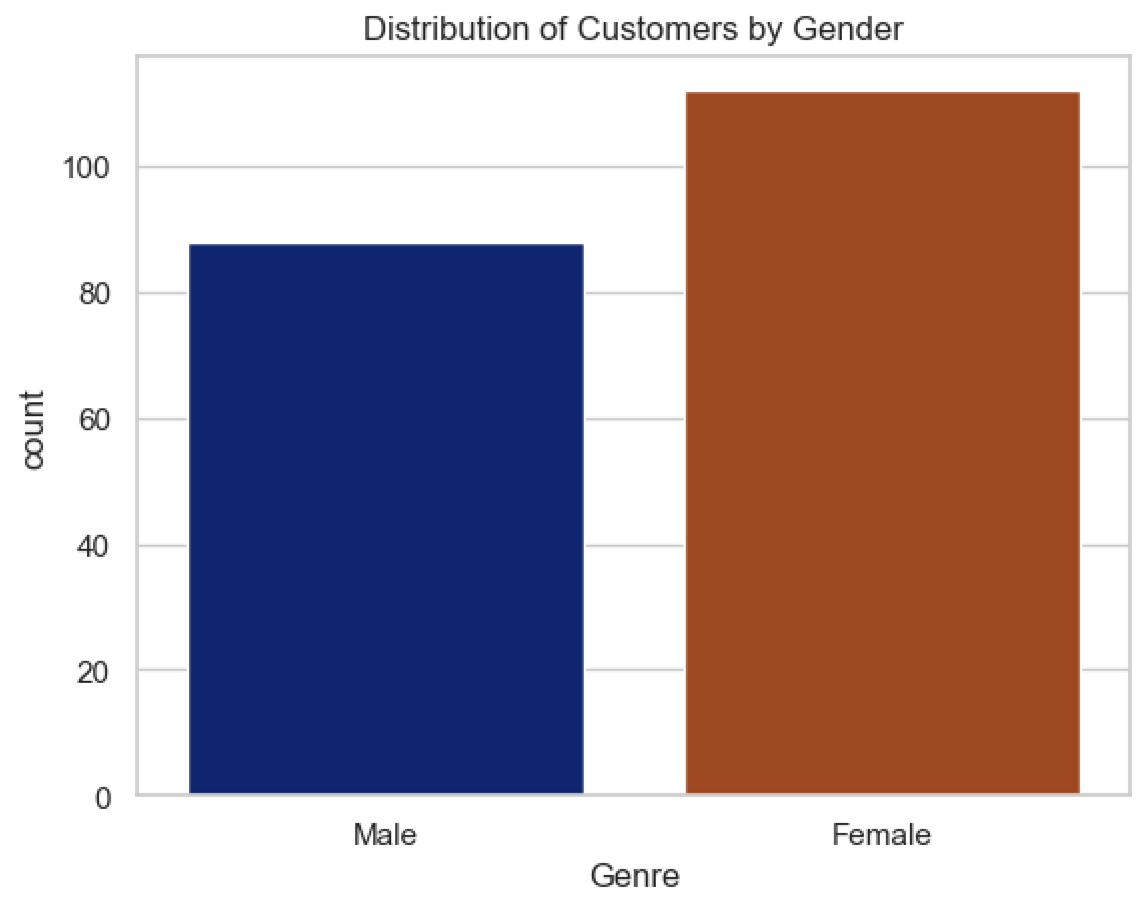
In [10]:
```
mall_customers.isnull().sum()
```

Out[10]:
```
CustomerID            0
Genre                 0
Age                   0
Annual_Income_(k$)    0
Spending_Score        0
dtype: int64
```

In [11]:
```
print(mall_customers.groupby('Genre').size())

sns.countplot(x='Genre', data=mall_customers)
plt.title("Distribution of Customers by Gender")
plt.show()
```

```
Genre
Female    112
Male       88
dtype: int64
```



In [12]:
```
mall_customers.describe().T
```

Out[12]:

	count	mean	std	min	25%	50%	75%	max
CustomerID	200.0	100.50	57.879185	1.0	50.75	100.5	150.25	200.0
Age	200.0	38.85	13.969007	18.0	28.75	36.0	49.00	70.0
Annual_Income_(k$)	200.0	60.56	26.264721	15.0	41.50	61.5	78.00	137.0
Spending_Score	200.0	50.20	25.823522	1.0	34.75	50.0	73.00	99.0

Checking skewness

In [13]:
```
numeric_skewness = mall_customers.select_dtypes(include=[np.number]).skew()
print("Skewness:")
print(numeric_skewness)
```

```
Skewness:
CustomerID            0.000000
Age                   0.485569
Annual_Income_(k$)    0.321843
Spending_Score       -0.047220
dtype: float64
```

Applying Label Encoding to "Genre" column.

In [14]:
```
mall_customers_encoded = mall_customers.copy()
label_encoder = LabelEncoder()
mall_customers_encoded['Genre'] = label_encoder.fit_transform(mall_customers_encoded['Genre'])
mall_customers_encoded
```

Out[14]:

	CustomerID	Genre	Age	Annual_Income_(k$)	Spending_Score
0	1	1	19	15	39
1	2	1	21	15	81
2	3	0	20	16	6
3	4	0	23	16	77
4	5	0	31	17	40
...	...	...	...	...	...
195	196	0	35	120	79
196	197	0	45	126	28
197	198	1	32	126	74
198	199	1	32	137	18
199	200	1	30	137	83

200 rows × 5 columns

1.1 Perform k-means clustering over this dataset using Manhattan distance as the distance-measure. (10 Points)

Def function for manhattan_distance measure

In [15]:
```
def manhattan_distance(point1, point2):
    """
    Calculate the Manhattan distance between two points.

    Parameters:
    - point1: Tuple or list representing the coordinates of the first point.
    - point2: Tuple or list representing the coordinates of the second point.

    Returns:
    - The Manhattan distance between the two points.
    """
    distance = sum(abs(x - y) for x, y in zip(point1, point2))
    return distance
```

k-means clustering with Manhattan distance

In [16]:
```
features = mall_customers[['Age', 'Annual_Income_(k$)', 'Spending_Score']].values

k = 5
kmeans = KMeans(n_clusters=k, init='k-means++', algorithm='elkan', n_init=10, random_state=34)

kmeans.fit(features)

cluster_centers = kmeans.cluster_centers_
cluster_labels = kmeans.labels_

manhattan_distances = manhattan_distance(features, cluster_centers)

print("Cluster Centers:")
cluster_centers_df = pd.DataFrame(cluster_centers, columns=['Age', 'Annual_Income_(k$)', 'Spending_Score'])
print(cluster_centers_df, '\n')
```

```
print("Manhattan Distances to Cluster Centers:", manhattan_distances)
```

```
Cluster Centers:
         Age  Annual_Income_(k$)  Spending_Score
0  43.282051           55.025641       49.692308
1  32.692308           86.538462       82.128205
2  25.521739           26.304348       78.565217
3  45.217391           26.304348       20.913043
4  40.324324           87.432432       18.189189

Manhattan Distances to Cluster Centers: [ 73.03781373 202.60523065 162.28349754]
```

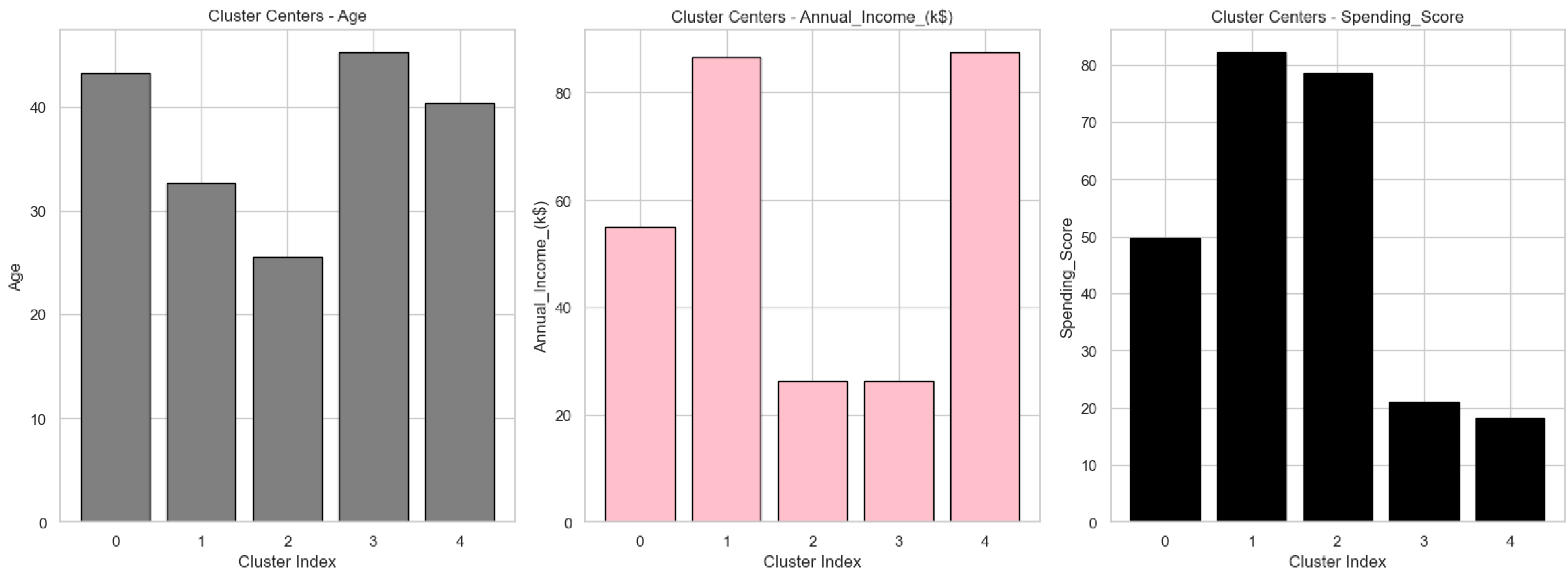
Visualization of Cluster Center output using histogram

In [17]:
```
plt.figure(figsize=(16, 6))

colors = ['gray', 'pink', 'black']

for i, feature in enumerate(cluster_centers_df.columns):
    plt.subplot(1, 3, i+1)
    plt.bar(range(len(cluster_centers_df)), cluster_centers_df[feature], color=colors[i], edgecolor = 'black')
    plt.xlabel('Cluster Index')
    plt.ylabel(feature)
    plt.title(f'Cluster Centers - {feature}')
    plt.xticks(range(len(cluster_centers_df)))
    plt.tight_layout()

plt.show()
```



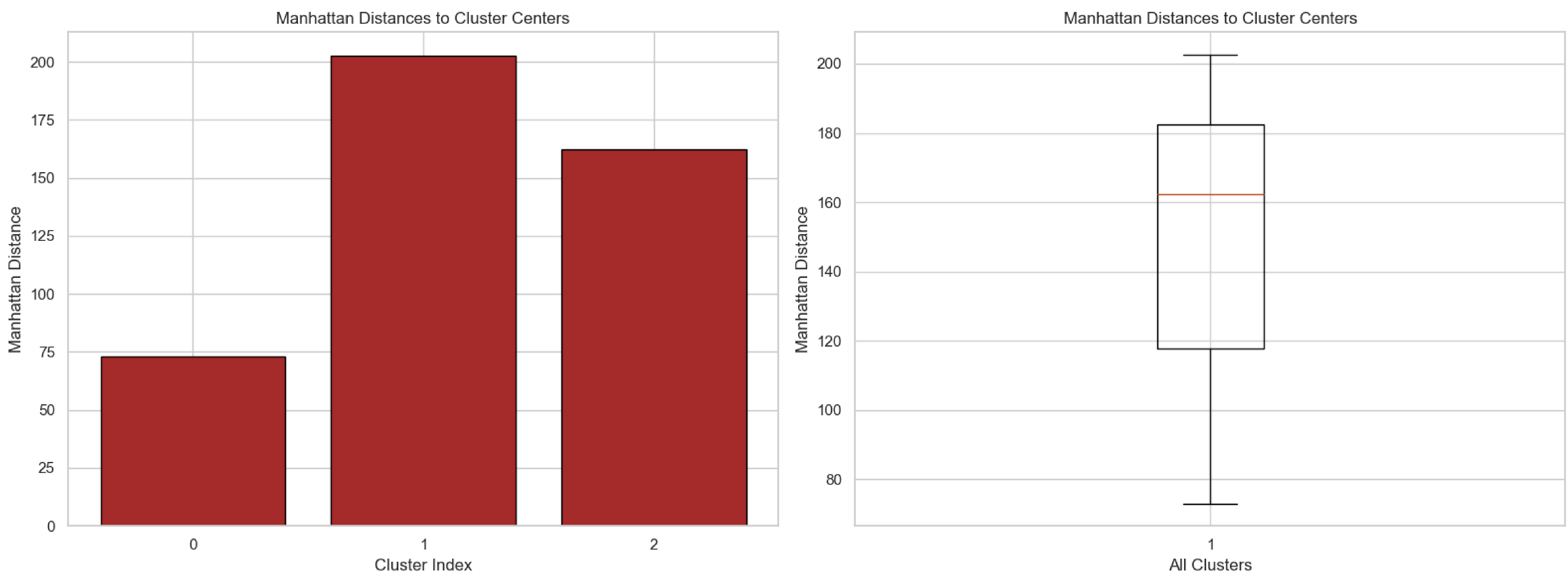
Visualization for Manhattan Distances to Cluster Centers uisng histogram and box-plot

In [101…
```
plt.figure(figsize=(16, 6))

plt.subplot(1, 2, 1)
plt.bar(range(len(manhattan_distances)), manhattan_distances, color='Brown', edgecolor = 'black')
plt.xlabel('Cluster Index')
plt.ylabel('Manhattan Distance')
plt.title('Manhattan Distances to Cluster Centers')
plt.xticks(range(len(manhattan_distances)))

plt.subplot(1, 2, 2)
plt.boxplot(manhattan_distances)
plt.xlabel('All Clusters')
plt.ylabel('Manhattan Distance')
plt.title('Manhattan Distances to Cluster Centers')

plt.tight_layout()
plt.show()
```



Visualization of the clusters to check if they have a distinct distinction in the feature space.

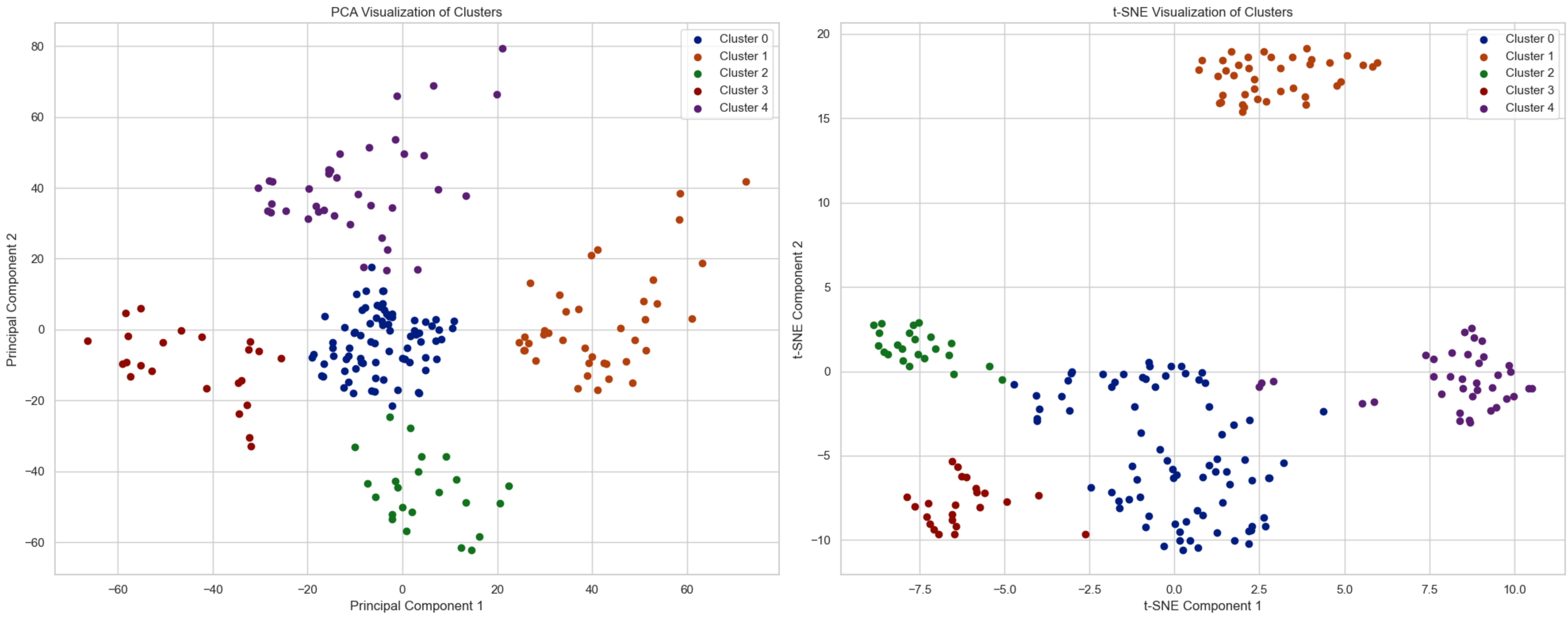
In [96]:
```
pca = PCA(n_components=2)
data_pca = pca.fit_transform(features)

tsne = TSNE(n_components=2, random_state=42)
data_tsne = tsne.fit_transform(features)

plt.figure(figsize=(20, 8))
plt.subplot(1, 2, 1)
for label in set(cluster_labels):
    plt.scatter(data_pca[cluster_labels == label, 0], data_pca[cluster_labels == label, 1], label=f'Cluster {label}')
plt.title('PCA Visualization of Clusters')
plt.xlabel('Principal Component 1')
```

```
plt.ylabel('Principal Component 2')
plt.legend()

plt.subplot(1, 2, 2)
for label in set(cluster_labels):
    plt.scatter(data_tsne[cluster_labels == label, 0], data_tsne[cluster_labels == label, 1], label=f'Cluster {label}')
plt.title('t-SNE Visualization of Clusters')
plt.xlabel('t-SNE Component 1')
plt.ylabel('t-SNE Component 2')
plt.legend()
plt.tight_layout()
plt.show()
```



The above output, displays the scatter plot for both PCA and t-SNE to identify clusters within the data.

The clusters appear to be distinct and well-separated in the feature space, implying that the data points within each cluster are similar to one another while differentiating from data points in other clusters. This is a good indicator since it shows that the clustering algorithm successfully grouped comparable data points together.

1.2 After performing k-means clustering, extract the groups or clusters and add a separate column in your dataset as ‘Labels’ and fill it with cluster number assigned by k-means algorithm. (5 Points)

Adding the 'Lables' columns to Dataset.

In [20]:
```
mall_customers_with_labels = pd.DataFrame(mall_customers_encoded, columns=mall_customers_encoded.columns)
mall_customers_with_labels['Labels'] = cluster_labels
mall_customers_with_labels
```

Out[20]:

	CustomerID	Genre	Age	Annual_Income_(k$)	Spending_Score	Labels
0	1	1	19	15	39	3
1	2	1	21	15	81	2
2	3	0	20	16	6	3
3	4	0	23	16	77	2
4	5	0	31	17	40	3
...	...	...	...	...	...	...
195	196	0	35	120	79	1
196	197	0	45	126	28	4
197	198	1	32	126	74	1
198	199	1	32	137	18	4
199	200	1	30	137	83	1

200 rows × 6 columns

In [21]:
```
print(mall_customers_with_labels.groupby('Labels').size())
```

```
Labels
0    78
1    39
2    23
3    23
4    37
dtype: int64
```

1.3 Now, you should be ready with your labeled dataset. Perform standard classification task using logistic regression, decision trees, random forest, and Naive Bayes algorithm. (25 Points)

In [22]:
```
X = mall_customers_with_labels.drop(columns=['Labels'])
y = mall_customers_with_labels['Labels']

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.4, random_state=98, stratify=y)

classifiers = {
    "Logistic Regression": LogisticRegression(),
    "Decision Tree": DecisionTreeClassifier(),
    "Random Forest": RandomForestClassifier(),
    "Naive Bayes": GaussianNB()
}


classifiers_accuracys = {}
for name, clf in classifiers.items():

    clf.fit(X_train, y_train)

    y_pred = clf.predict(X_test)

    accuracy = accuracy_score(y_test, y_pred)

    classifiers_accuracys[name] = accuracy
```

```python
for name, accuracy in classifiers_accuracys.items():
    print(f"{name}: Accuracy - {(accuracy)*100} %")
```

```
Logistic Regression: Accuracy - 88.75 %
Decision Tree: Accuracy - 96.25 %
Random Forest: Accuracy - 100.0 %
Naive Bayes: Accuracy - 98.75 %
```

In [53]:
```python
sorted_classifiers_accuracys = sorted(classifiers_accuracys.items(), key=lambda x: x[1], reverse=True)

for name, accuracy in sorted_classifiers_accuracys:
    print(f"{name}: {round(accuracy, 4)*100} %")
```

```
Random Forest: 100.0 %
Naive Bayes: 98.75 %
Decision Tree: 96.25 %
Logistic Regression: 88.75 %
```

1. **Classification Results**:

- Random Forest: Accuracy - 100.0%
- Naive Bayes: Accuracy - 98.75%
- Decision Tree: Accuracy - 96.25%
- Logistic Regression: Accuracy - 89.75%

All classification algorithms achieved high accuracies, indicating that they were able to successfully classify the data points into their respective clusters.

1.4 Compare the performance of these various supervised learning algorithm and comment on the homogeneity of clusters, like is the clusters or groups are making sense or not ? (10 Points)

1. **Homogeneity of Clusters**:

- The classification algorithms' high accuracy ratings indicate that the clusters are somewhat homogeneous.
- High Accuracy: A high accuracy score implies that the supervised learning algorithms accurately classified the data points into their appropriate classes with high confidence. This implies that the data points within each class are largely uniform and distinguishable from those in other classes.
    - Impact on Cluster Homogeneity: While the accuracy of supervised learning methods does not directly assess cluster homogeneity, it does indirectly indicate cluster separation and coherence. Higher accuracy indicates that the clusters or groupings identified by the clustering algorithm make sense and are internally consistent.
- Potential Insights: If the supervised learning algorithms perform well, it means that the clusters identified by the clustering algorithm are significant and represent separate groups in the data. In contrast, low accuracy may signal that the clusters are less uniform and require more refinement.

In conclusion, the high accuracy ratings obtained from the supervised learning methods indicate that the clusters produced by the clustering algorithm are most likely meaningful and internally homogeneous. Otherwise, if classification performance is low or inconsistent, it suggests that the clusters might not be well-separated or meaningful.

Part 02 :

2. Consider the breast_cancer dataset given in the sklearn library and answer the following questions.

Importing the necessary lib

In [24]:
```python
from sklearn.datasets import load_breast_cancer
from sklearn.preprocessing import StandardScaler
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis as LDA
```

2.1 Import the breast_cancer dataset from sklearn.datasets library. (5 Points)

In [25]:
```python
breast_cancer = load_breast_cancer()
```

Convert to pandas DataFrame

In [26]:
```python
breast_cancer_df = pd.DataFrame(breast_cancer.data, columns=breast_cancer.feature_names)
breast_cancer_df['target'] = breast_cancer.target
```

Exploratory Data Analysis (EDA)

In [27]:
```python
pd.set_option('display.max_columns', None)
breast_cancer_df.sample(10)
```

Out[27]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension
128	15.100	16.39	99.58	674.5	0.11500	0.18070	0.11380	0.08534	0.2001	0.06467
486	14.640	16.85	94.21	666.0	0.08641	0.06698	0.05192	0.02791	0.1409	0.05355
369	22.010	21.90	147.20	1482.0	0.10630	0.19540	0.24480	0.15010	0.1824	0.06140
18	19.810	22.15	130.00	1260.0	0.09831	0.10270	0.14790	0.09498	0.1582	0.05395
117	14.870	16.67	98.64	682.5	0.11620	0.16490	0.16900	0.08923	0.2157	0.06768
441	17.270	25.42	112.40	928.8	0.08331	0.11090	0.12040	0.05736	0.1467	0.05407
551	11.130	22.44	71.49	378.4	0.09566	0.08194	0.04824	0.02257	0.2030	0.06552
41	10.950	21.35	71.90	371.1	0.12270	0.12180	0.10440	0.05669	0.1895	0.06870
359	9.436	18.32	59.82	278.6	0.10090	0.05956	0.02710	0.01406	0.1506	0.06959
287	12.890	13.12	81.89	515.9	0.06955	0.03729	0.02260	0.01171	0.1337	0.05581

	radius error	texture error	perimeter error	area error	smoothness error	compactness error	concavity error	concave points error	symmetry error	frac dimens er
128	0.4309	1.0680	2.796	39.84	0.009006	0.041850	0.03204	0.022580	0.02353	0.0049
486	0.2204	1.0060	1.471	19.98	0.003535	0.013930	0.01800	0.006144	0.01254	0.001
369	1.0080	0.6999	7.561	130.20	0.003978	0.028210	0.03576	0.014710	0.01518	0.0037
18	0.7582	1.0170	5.865	112.40	0.006494	0.018930	0.03391	0.015210	0.01356	0.0019
117	0.4266	0.9489	2.989	41.18	0.006985	0.025630	0.03011	0.012710	0.01602	0.0038
441	0.5100	1.6790	3.283	58.38	0.008109	0.043080	0.04942	0.017420	0.01594	0.0037
551	0.2800	1.4670	1.994	17.85	0.003495	0.030510	0.03445	0.010240	0.02912	0.0047
41	0.2366	1.4280	1.822	16.97	0.008064	0.017640	0.02595	0.010370	0.01357	0.0030
359	0.5079	1.2470	3.267	30.48	0.006836	0.008982	0.02348	0.006565	0.01942	0.002
287	0.1532	0.4690	1.115	12.68	0.004731	0.013450	0.01652	0.005905	0.01619	0.0020

In [28]:
```python
breast_cancer_df.dtypes
```

Out[28]:
```
mean radius                float64
mean texture               float64
mean perimeter             float64
mean area                  float64
mean smoothness            float64
mean compactness           float64
mean concavity             float64
mean concave points        float64
mean symmetry              float64
mean fractal dimension     float64
radius error               float64
texture error              float64
perimeter error            float64
area error                 float64
smoothness error           float64
compactness error          float64
concavity error            float64
concave points error       float64
symmetry error             float64
fractal dimension error    float64
worst radius               float64
worst texture              float64
worst perimeter            float64
worst area                 float64
worst smoothness           float64
worst compactness          float64
worst concavity            float64
worst concave points       float64
worst symmetry             float64
worst fractal dimension    float64
target                       int64
dtype: object
```

In [29]:
```
breast_cancer_df.shape
```

Out[29]:
```
(569, 31)
```

In [30]:
```
duplicate_rows = breast_cancer_df[breast_cancer_df.duplicated()]

if not duplicate_rows.empty:
    print("Duplicate rows found. Details:")
    print(duplicate_rows)
else:
    print("No duplicate rows found.")
```

```
No duplicate rows found.
```

In [31]:
```
breast_cancer_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   mean radius              569 non-null    float64
 1   mean texture             569 non-null    float64
 2   mean perimeter           569 non-null    float64
 3   mean area                569 non-null    float64
 4   mean smoothness          569 non-null    float64
 5   mean compactness         569 non-null    float64
 6   mean concavity           569 non-null    float64
 7   mean concave points      569 non-null    float64
 8   mean symmetry            569 non-null    float64
 9   mean fractal dimension   569 non-null    float64
 10  radius error             569 non-null    float64
 11  texture error            569 non-null    float64
 12  perimeter error          569 non-null    float64
 13  area error               569 non-null    float64
 14  smoothness error         569 non-null    float64
 15  compactness error        569 non-null    float64
 16  concavity error          569 non-null    float64
 17  concave points error     569 non-null    float64
 18  symmetry error           569 non-null    float64
 19  fractal dimension error  569 non-null    float64
 20  worst radius             569 non-null    float64
 21  worst texture            569 non-null    float64
 22  worst perimeter          569 non-null    float64
 23  worst area               569 non-null    float64
 24  worst smoothness         569 non-null    float64
 25  worst compactness        569 non-null    float64
 26  worst concavity          569 non-null    float64
 27  worst concave points     569 non-null    float64
 28  worst symmetry           569 non-null    float64
 29  worst fractal dimension  569 non-null    float64
 30  target                   569 non-null    int64  
dtypes: float64(30), int64(1)
memory usage: 137.9 KB
```

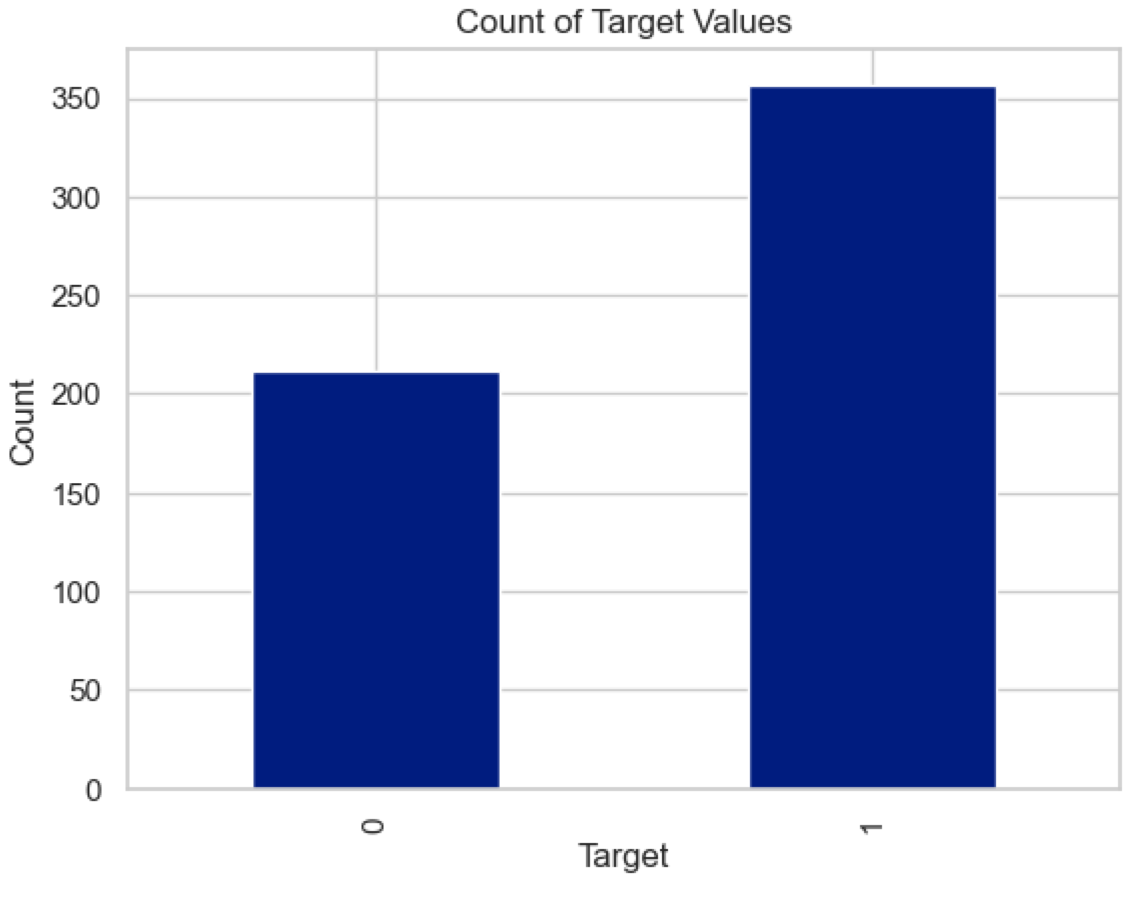
In [32]:
```
null_counts = breast_cancer_df.isnull().sum()
if null_counts.any():
    print("Null values present. Details:")
    print(null_counts)
else:
    print("No null values present.")
```

```
No null values present.
```

In [33]:
```
target_counts = breast_cancer_df.groupby('target').size()

target_counts.plot(kind='bar', title='Count of Target Values', xlabel='Target', ylabel='Count')

plt.show()
```



In [34]:
```
breast_cancer_df.describe().T
```

Out[34]:

	count	mean	std	min	25%	50%	75%	max
mean radius	569.0	14.127292	3.524049	6.981000	11.700000	13.370000	15.780000	28.11000
mean texture	569.0	19.289649	4.301036	9.710000	16.170000	18.840000	21.800000	39.28000
mean perimeter	569.0	91.969033	24.298981	43.790000	75.170000	86.240000	104.100000	188.50000
mean area	569.0	654.889104	351.914129	143.500000	420.300000	551.100000	782.700000	2501.00000
mean smoothness	569.0	0.096360	0.014064	0.052630	0.086370	0.095870	0.105300	0.16340
mean compactness	569.0	0.104341	0.052813	0.019380	0.064920	0.092630	0.130400	0.34540
mean concavity	569.0	0.088799	0.079720	0.000000	0.029560	0.061540	0.130700	0.42680
mean concave points	569.0	0.048919	0.038803	0.000000	0.020310	0.033500	0.074000	0.20120
mean symmetry	569.0	0.181162	0.027414	0.106000	0.161900	0.179200	0.195700	0.30400
mean fractal dimension	569.0	0.062798	0.007060	0.049960	0.057700	0.061540	0.066120	0.09744
radius error	569.0	0.405172	0.277313	0.111500	0.232400	0.324200	0.478900	2.87300
texture error	569.0	1.216853	0.551648	0.360200	0.833900	1.108000	1.474000	4.88500
perimeter error	569.0	2.866059	2.021855	0.757000	1.606000	2.287000	3.357000	21.98000
area error	569.0	40.337079	45.491006	6.802000	17.850000	24.530000	45.190000	542.20000
smoothness error	569.0	0.007041	0.003003	0.001713	0.005169	0.006380	0.008146	0.03113
compactness error	569.0	0.025478	0.017908	0.002252	0.013080	0.020450	0.032450	0.13540
concavity error	569.0	0.031894	0.030186	0.000000	0.015090	0.025890	0.042050	0.39600
concave points error	569.0	0.011796	0.006170	0.000000	0.007638	0.010930	0.014710	0.05279
symmetry error	569.0	0.020542	0.008266	0.007882	0.015160	0.018730	0.023480	0.07895
fractal dimension error	569.0	0.003795	0.002646	0.000895	0.002248	0.003187	0.004558	0.02984
worst radius	569.0	16.269190	4.833242	7.930000	13.010000	14.970000	18.790000	36.04000
worst texture	569.0	25.677223	6.146258	12.020000	21.080000	25.410000	29.720000	49.54000
worst perimeter	569.0	107.261213	33.602542	50.410000	84.110000	97.660000	125.400000	251.20000
worst area	569.0	880.583128	569.356993	185.200000	515.300000	686.500000	1084.000000	4254.00000
worst smoothness	569.0	0.132369	0.022832	0.071170	0.116600	0.131300	0.146000	0.22260
worst compactness	569.0	0.254265	0.157336	0.027290	0.147200	0.211900	0.339100	1.05800
worst concavity	569.0	0.272188	0.208624	0.000000	0.114500	0.226700	0.382900	1.25200
worst concave points	569.0	0.114606	0.065732	0.000000	0.064930	0.099930	0.161400	0.29100
worst symmetry	569.0	0.290076	0.061867	0.156500	0.250400	0.282200	0.317900	0.66380
worst fractal dimension	569.0	0.083946	0.018061	0.055040	0.071460	0.080040	0.092080	0.20750
target	569.0	0.627417	0.483918	0.000000	0.000000	1.000000	1.000000	1.00000

Checking skewness

In [35]:

```
numeric_skewness = breast_cancer_df.select_dtypes(include=[np.number]).skew()
print("Skewness:")
print(numeric_skewness)
```

```
Skewness:
mean radius                0.942380
mean texture               0.650450
mean perimeter             0.990650
mean area                  1.645732
mean smoothness            0.456324
mean compactness           1.190123
mean concavity             1.401180
mean concave points        1.171180
mean symmetry              0.725609
mean fractal dimension     1.304489
radius error               3.088612
texture error              1.646444
perimeter error            3.443615
area error                 5.447186
smoothness error           2.314450
compactness error          1.902221
concavity error            5.110463
concave points error       1.444678
symmetry error             2.195133
fractal dimension error    3.923969
worst radius               1.103115
worst texture              0.498321
worst perimeter            1.128164
worst area                 1.859373
worst smoothness           0.415426
worst compactness          1.473555
worst concavity            1.150237
worst concave points       0.492616
worst symmetry             1.433928
worst fractal dimension    1.662579
target                    -0.528461
dtype: float64
```

Handling the skewness

In [36]:

```
breast_cancer_new = breast_cancer_df.copy()
skew_threshold = 0.75

skewed_features = numeric_skewness[abs(numeric_skewness) > skew_threshold].index

breast_cancer_new[skewed_features] = np.log1p(breast_cancer_df[skewed_features])
print("Skewness after applying the log1p :\n")
breast_cancer_new.skew()
```

```
Skewness after applying the log1p :
```

Out[36]:
```
mean radius                0.348744
mean texture               0.650450
mean perimeter             0.328800
mean area                  0.287328
mean smoothness            0.456324
mean compactness           1.043195
mean concavity             1.206982
mean concave points        1.083180
mean symmetry              0.725609
mean fractal dimension     1.272294
radius error               1.713417
texture error              0.629526
perimeter error            1.025375
area error                 0.847298
smoothness error           2.283394
compactness error          1.816278
concavity error            4.231738
concave points error       1.399869
symmetry error             2.135874
fractal dimension error    3.874373
worst radius               0.506347
worst texture              0.498321
worst perimeter            0.462758
worst area                 0.457614
worst smoothness           0.415426
worst compactness          1.048729
worst concavity            0.717939
worst concave points       0.492616
worst symmetry             1.152984
worst fractal dimension    1.558559
target                    -0.528461
dtype: float64
```

Histogram for all columns of Dataframe

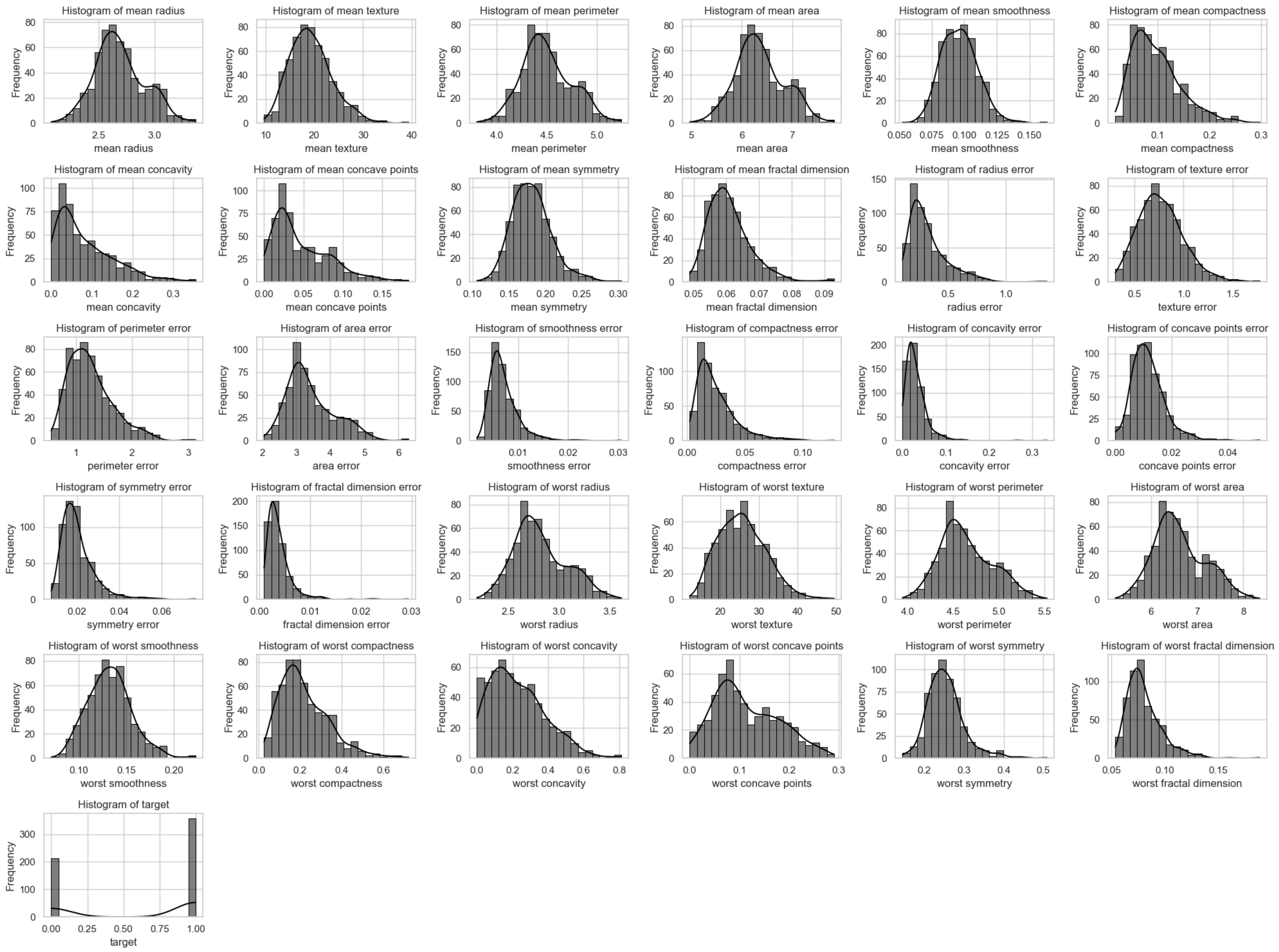
In [37]:
```python
num_rows = 6
num_cols = 6

fig, axes = plt.subplots(num_rows, num_cols, figsize=(20, 15))

for i, column in enumerate(breast_cancer_new.columns):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row][col]
    sns.histplot(breast_cancer_new[column], kde=True ,bins=20, color='black', edgecolor='black', ax=ax)
    ax.set_xlabel(column)
    ax.set_ylabel('Frequency')
    ax.set_title(f'Histogram of {column}')
    ax.grid(True)

for i in range(len(breast_cancer_new.columns), num_rows * num_cols):
    row = i // num_cols
    col = i % num_cols
    fig.delaxes(axes[row][col])

plt.tight_layout()
plt.show()
```



Box-plot

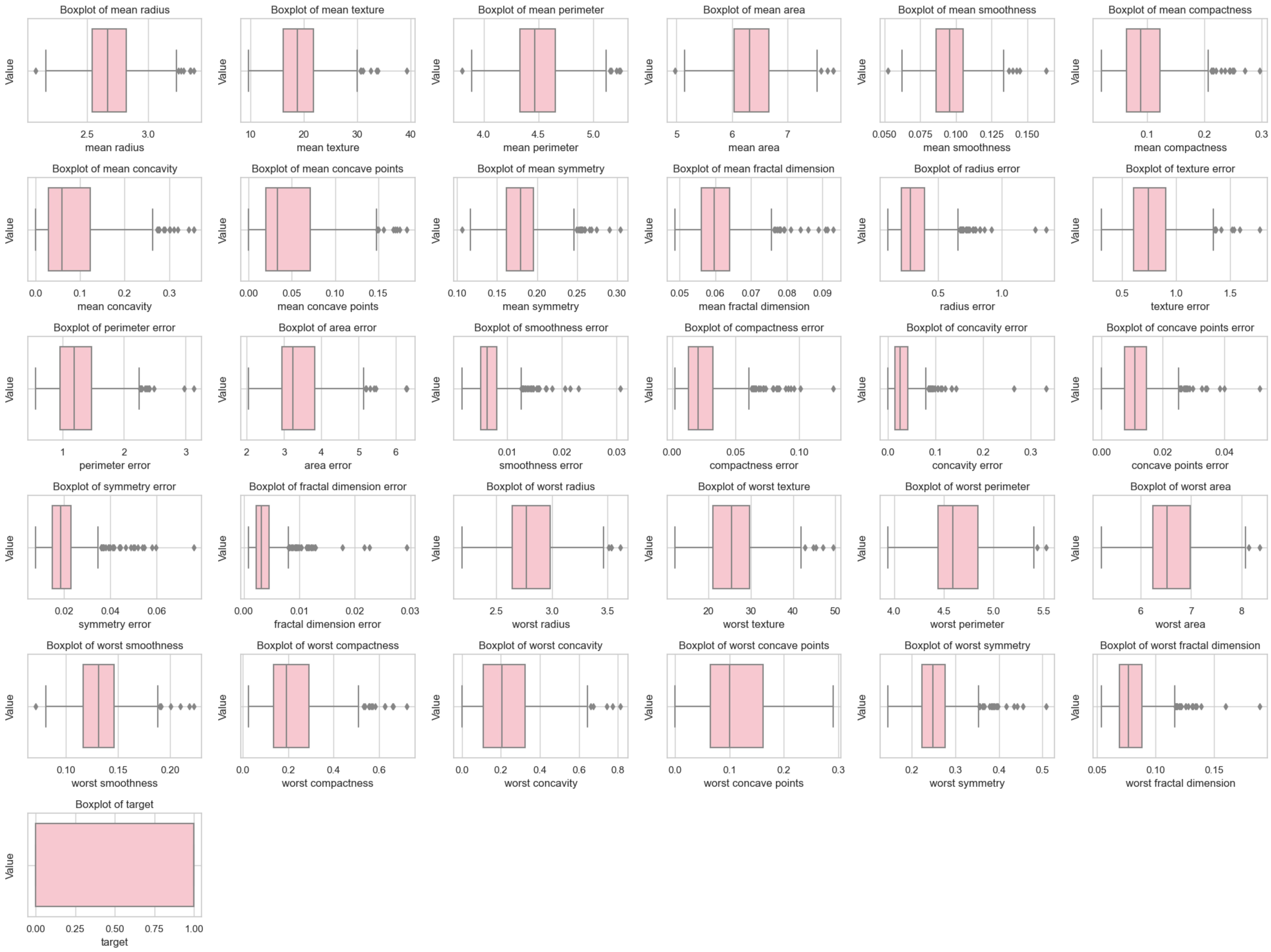
In [86]:
```python
num_rows = 6
num_cols = 6

fig, axes = plt.subplots(num_rows, num_cols, figsize=(20, 15))
```

```
for i, column in enumerate(breast_cancer_new.columns):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row][col]
    sns.boxplot(x=breast_cancer_new[column], color='pink', ax=ax)
    ax.set_xlabel(column)
    ax.set_ylabel('Value')
    ax.set_title(f'Boxplot of {column}')
    ax.grid(True)

for i in range(len(breast_cancer_new.columns), num_rows * num_cols):
    row = i // num_cols
    col = i % num_cols
    fig.delaxes(axes[row][col])

plt.tight_layout()
plt.show()
```



Outliers detection using quantile method

In [39]:
```
Q1 = breast_cancer_new.quantile(0.25)
Q3 = breast_cancer_new.quantile(0.75)

IQR = Q3 - Q1

threshold = 1.5

outliers = (breast_cancer_new < (Q1 - threshold * IQR)) | (breast_cancer_new > (Q3 + threshold * IQR))

outliers_count = outliers.sum()
total_outliers1 = outliers_count.sum()
print("\nTotal number of outliers:", total_outliers1, '\n')
```

```
Total number of outliers: 388
```

Removing outliers using quantile method

In [40]:
```
quantile_data = breast_cancer_new[~outliers.any(axis=1)]

print("Shape before removing outliers:", breast_cancer_new.shape)
print("Shape after removing outliers:", quantile_data.shape)

Q2 = quantile_data.quantile(0.25)
Q4 = quantile_data.quantile(0.75)

IQR = Q4 - Q2

threshold = 1.5

outliers2 = (quantile_data < (Q2 - threshold * IQR)) | (quantile_data > (Q4 + threshold * IQR))

print("Outliers:")
outliers_count2 = outliers2.sum()
total_outliers = outliers_count2.sum()
print("\nTotal number of outliers after performing the outlier removel:", total_outliers)
```

```
Shape before removing outliers: (569, 31)
Shape after removing outliers: (433, 31)
Outliers:

Total number of outliers after performing the outlier removel: 122
```

In [41]:
```
print("Date Loss after removing the outliers : ", ((569-433)/569)*100, '%')
```

```
Date Loss after removing the outliers :  23.901581722319857 %
```

Box-plot after removing the outliers

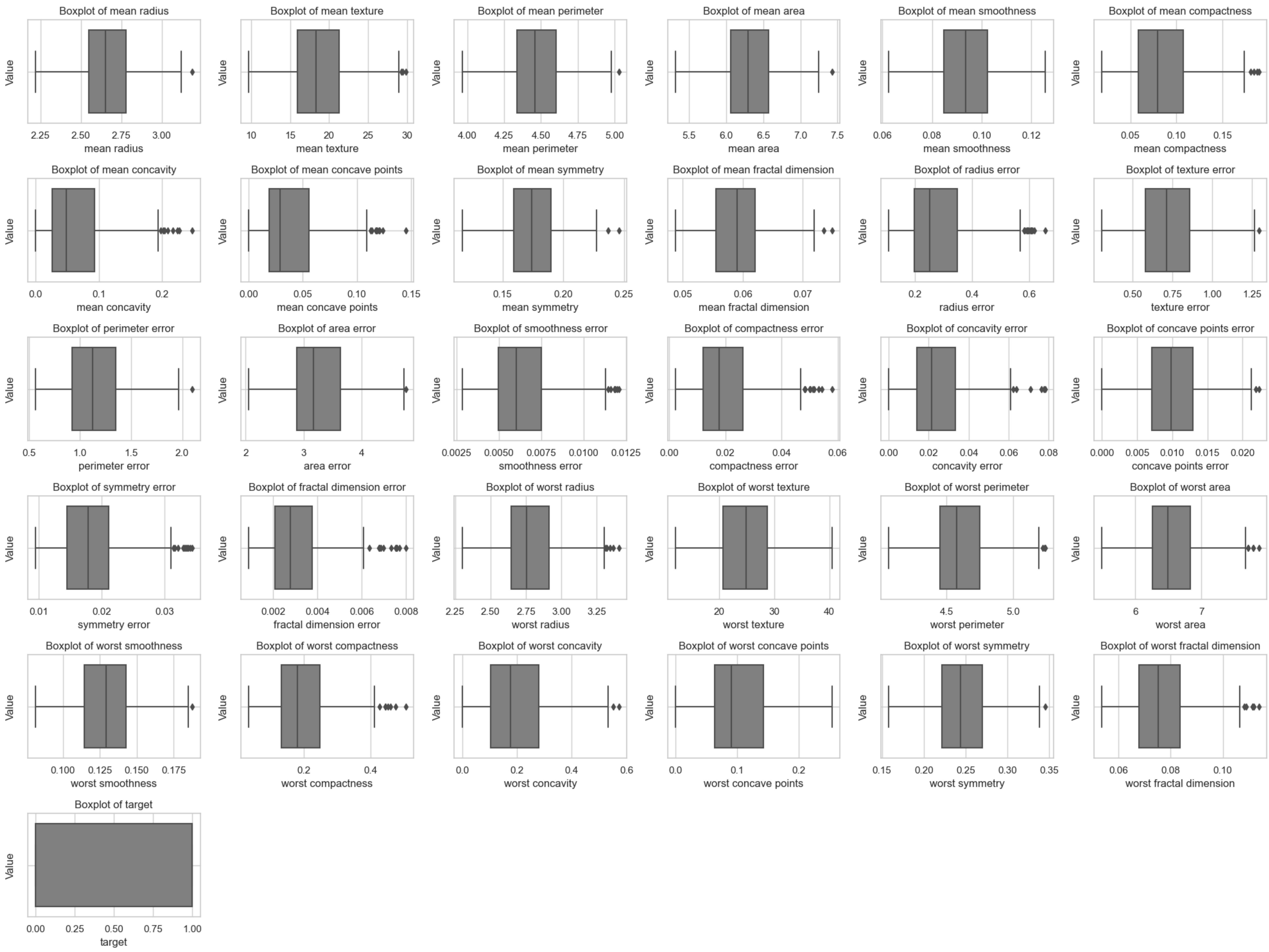
In [80]:
```python
num_rows = 6
num_cols = 6

fig, axes = plt.subplots(num_rows, num_cols, figsize=(20, 15))

for i, column in enumerate(quantile_data.columns):
    row = i // num_cols
    col = i % num_cols
    ax = axes[row][col]
    sns.boxplot(x=quantile_data[column], color='gray', ax=ax)
    ax.set_xlabel(column)
    ax.set_ylabel('Value')
    ax.set_title(f'Boxplot of {column}')
    ax.grid(True)

for i in range(len(quantile_data.columns), num_rows * num_cols):
    row = i // num_cols
    col = i % num_cols
    fig.delaxes(axes[row][col])

plt.tight_layout()
plt.show()
```



Define X and Y

In [43]:
```python
X = quantile_data.drop(['target'], axis=1)
Y = quantile_data['target']

X = pd.get_dummies(X)
X
```

Out[43]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	radius error	texture error	perimeter error	area error	smoothness error	compactness error	concavity error	concave points error	symm
1	3.071303	17.77	4.897093	7.190676	0.08474	0.075701	0.083330	0.067818	0.1812	0.055122	0.434053	0.550373	1.481150	4.318554	0.005211	0.012995	0.018429	0.013311	0.01
2	3.029650	21.25	4.875197	7.093405	0.10960	0.148334	0.180153	0.120357	0.2069	0.058259	0.557098	0.580482	1.720084	4.554193	0.006131	0.039278	0.037604	0.020371	0.02
4	3.058237	14.34	4.913390	7.168580	0.10030	0.124692	0.180653	0.099212	0.1809	0.057165	0.563722	0.577343	1.862218	4.558498	0.011424	0.024312	0.055321	0.018675	0.01
6	2.957511	19.98	4.792479	6.947937	0.09463	0.103459	0.106789	0.071390	0.1794	0.055832	0.369285	0.572786	1.430311	4.005695	0.004305	0.013725	0.022290	0.010336	0.01
7	2.688528	20.83	4.513055	6.361130	0.11890	0.152292	0.089530	0.058127	0.2196	0.071865	0.459638	0.865839	1.580215	3.950474	0.008766	0.029840	0.024576	0.014376	0.01
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
555	2.423917	27.61	4.199755	5.775793	0.09030	0.073789	0.058259	0.027012	0.1593	0.059466	0.198769	1.175265	0.890768	2.738256	0.011978	0.026992	0.046922	0.017064	0.01
558	2.746630	22.68	4.578724	6.489357	0.08473	0.124869	0.097943	0.036679	0.1454	0.059655	0.203267	0.745740	1.170623	3.022374	0.004233	0.045346	0.063707	0.015932	0.01
560	2.711378	27.15	4.525911	6.399260	0.09929	0.106700	0.043653	0.042140	0.1537	0.059881	0.310788	0.913086	1.357895	3.428813	0.007230	0.026428	0.020498	0.016129	0.02
565	3.050694	28.25	4.884316	7.140453	0.09780	0.098396	0.134531	0.093408	0.1752	0.053854	0.568434	1.242135	1.825033	4.605570	0.005752	0.023941	0.038740	0.016641	0.01
566	2.867899	28.08	4.694096	6.755885	0.08455	0.097399	0.088478	0.051662	0.1590	0.054943	0.375968	0.729961	1.487270	3.902982	0.005886	0.036631	0.046215	0.015450	0.01

433 rows × 30 columns

Applying Standard Scaler

In [44]:
```
scaler = StandardScaler()
X_scaled = pd.DataFrame(scaler.fit_transform(X), columns=X.columns)
print("\nScaled DataFrame using StandardScaler:")
X_scaled
```

```
Scaled DataFrame using StandardScaler:
```

Out[44]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	radius error	texture error	perimeter error	area error	smoothness error	compactness error	concavity error	concave points error
0	2.092937	-0.244628	1.982150	2.089041	-0.754191	-0.289086	0.380612	1.002205	0.294948	-0.891428	1.246656	-0.889997	1.019126	1.736042	-0.589733	-0.669121	-0.423463	0.738427
1	1.870551	0.639468	1.877112	1.849882	1.333734	1.871704	2.315526	2.851326	1.501153	-0.207284	2.277146	-0.739206	1.785724	2.133038	-0.121606	1.816986	0.885998	2.456474
2	2.023178	-1.116021	2.060327	2.034714	0.552652	1.168386	2.325537	2.107108	0.280867	-0.446078	2.332615	-0.754926	2.241746	2.140292	2.572491	0.401331	2.095909	2.043623
3	1.485397	0.316824	1.480303	1.492224	0.076444	0.536692	0.849435	1.127937	0.210466	-0.736689	0.704238	-0.777751	0.856015	1.208947	-1.051196	-0.600054	-0.159821	0.014563
4	0.049287	0.532767	0.139868	0.049454	2.114817	1.989453	0.504518	0.661166	2.097216	2.759851	1.460927	0.689908	1.336967	1.115911	1.219657	0.924245	-0.003723	0.997628
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
428	-1.363473	2.255229	-1.363071	-1.389701	-0.287221	-0.345957	-0.120391	-0.433931	-0.732909	0.055910	-0.723810	2.239561	-0.875058	-0.926398	2.854194	0.654864	1.522310	1.651603
429	0.359496	1.002760	0.454889	0.364723	-0.755031	1.173637	0.672648	-0.093700	-1.385292	0.097006	-0.686136	0.088430	0.022830	-0.447724	-1.087685	2.390929	2.668576	1.376333
430	0.171286	2.138366	0.201538	0.143204	0.467825	0.633108	-0.412284	0.098480	-0.995739	0.146310	0.214334	0.926526	0.623674	0.237031	0.437557	0.601448	-0.282147	1.424229
431	1.982902	2.417821	1.920856	1.965559	0.342684	0.386089	1.403821	1.902864	0.013343	-1.168167	2.372080	2.574460	2.122441	2.219598	-0.314372	0.366244	0.963563	1.548712
432	1.006955	2.374633	1.008348	1.020031	-0.770148	0.356416	0.483494	0.433627	-0.746989	-0.930646	0.760203	0.009408	1.038762	1.035898	-0.246567	1.566554	1.474074	1.258950

433 rows × 30 columns

2.2 Perform PCA (2 components) and LDA (1 components) over the dataset. (20 Points)

Perform PCA

In [45]:
```
pca = PCA(n_components=2)
X_pca = pca.fit_transform(X_scaled)

print("Explained variance ratio (PCA) components:")
print("PCA Component 1:", pca.explained_variance_ratio_[0])
print("PCA Component 2:", pca.explained_variance_ratio_[1])
```

```
Explained variance ratio (PCA) components:
PCA Component 1: 0.45393920463471377
PCA Component 2: 0.17305258074751867
```

In [46]:
```
print(f"Variance explained by the first 2 components: {sum(pca.explained_variance_ratio_[:2])}")
```

```
Variance explained by the first 2 components: 0.6269917853822324
```

Perform LDA

In [47]:
```
lda = LDA(n_components=1)
X_lda = lda.fit_transform(X_scaled, Y)

print("Explained variance ratio (LDA):", lda.explained_variance_ratio_[0])
```

```
Explained variance ratio (LDA): 1.0
```

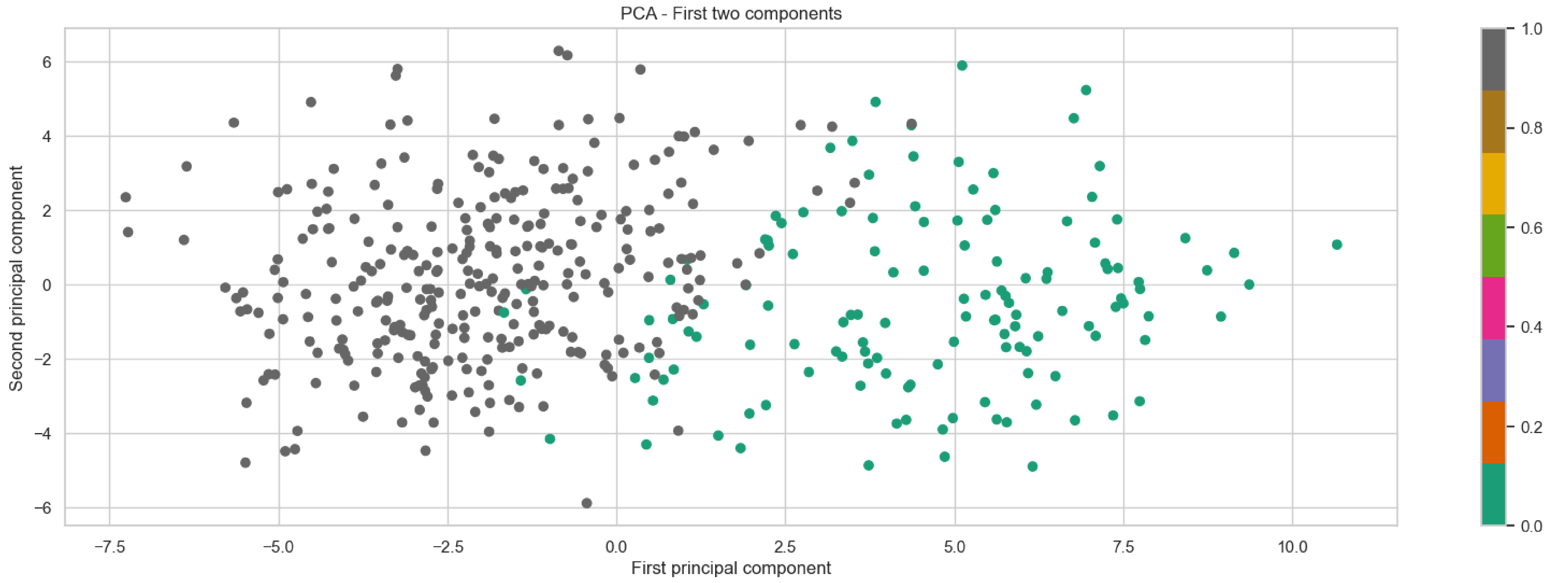
2.3 Visualise the components and see if its able to segregate the class label in breast_cancer dataset. (10 Points)

Scatter Plot for the PCA (2 components)

In [70]:
```
plt.figure(figsize=(20, 6))
plt.scatter(X_pca[:, 0], X_pca[:, 1], c=Y, cmap='Dark2')
plt.xlabel('First principal component')
plt.ylabel('Second principal component')
plt.title('PCA - First two components')
plt.colorbar()
```

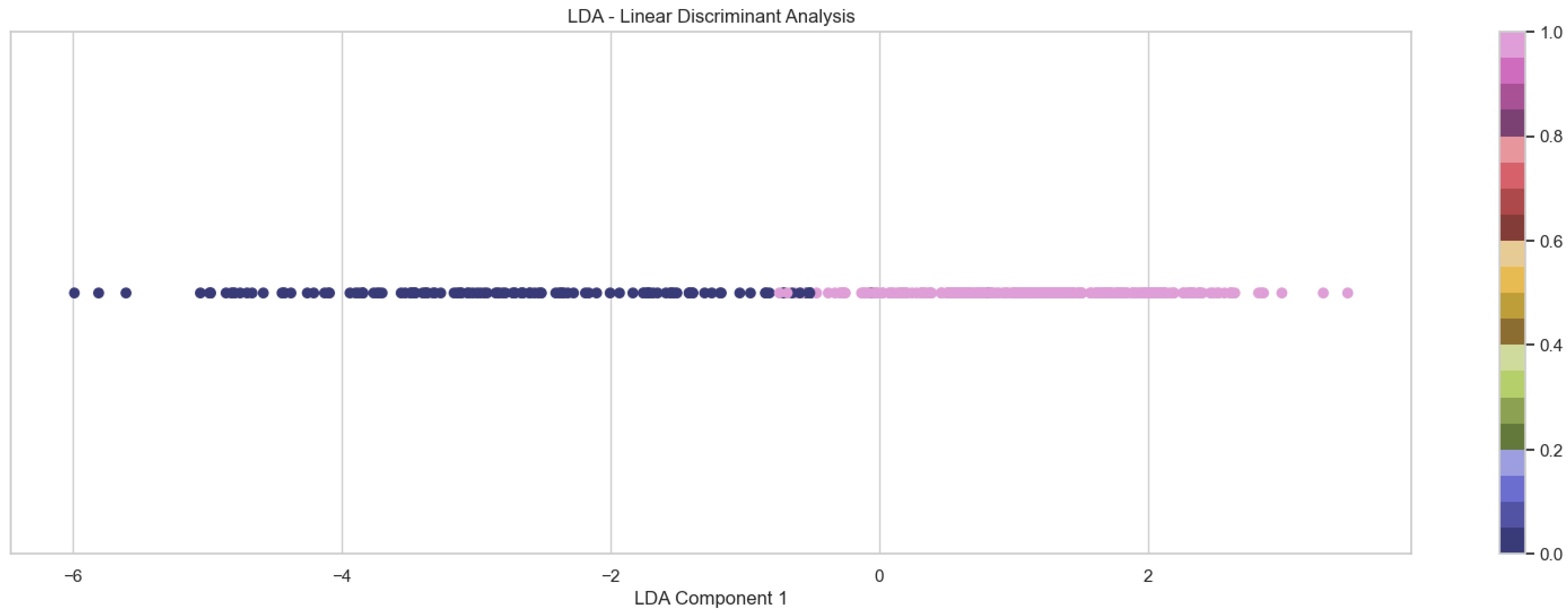
Out[70]:

```
<matplotlib.colorbar.Colorbar at 0x281f009d0>
```



Scatter Plot for LDA (1 components)

In [79]:
```
plt.figure(figsize=(20, 6))
plt.scatter(X_lda, [0] * len(X_lda), c=Y, cmap='tab20b')
plt.yticks([])
plt.xlabel('LDA Component 1')
plt.title('LDA - Linear Discriminant Analysis')
plt.colorbar()
plt.show()
```



2.4 What is the maximum variance explained by both the components in PCA and LDA. (10 Points)

Maximum variance explained by components in PCA

In [50]:
```
max_variance_pca = np.max(pca.explained_variance_ratio_)
print("Maximum variance explained by PCA components:", max_variance_pca)
```

```
Maximum variance explained by PCA components: 0.45393920463471377
```

Maximum variance explained by component in LDA

In [51]:
```
variance_lda = lda.explained_variance_ratio_[0]
print("Variance explained by the LDA component:", variance_lda)
```

```
Variance explained by the LDA component: 1.0
```

2.5 Comment on the working of PCA and LDA and which one is better for breast_cancer dataset. (5 Points)

Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA) are two common dimensionality reduction approaches in machine learning and statistics, but they provide different functions and operate in different ways.

PCA (Principal Component Analysis):

1. Purpose:
   - PCA is mostly used for unsupervised dimension reduction and feature extraction.
   - PCA seeks to identify the directions (principal components) that maximize variance in the data. It does not take into account class labels.
   - PCA is an unsupervised technique, which means it does not employ class information during the computation.
   - It is useful for lowering the dimensionality of the feature space while preserving as much variance as possible. This makes it appropriate for tasks where maintaining the overall structure of the data is critical.
2. Working:
   - PCA identifies orthogonal axes (principal components) in the feature space, with the first principal component capturing the most variation, the second principal component capturing the second most variance, and so on. Each primary component is a linear combination of the original attributes.
3. Objective:
   - The goal of PCA is to project data onto a lower-dimensional subspace while retaining as much original variation as possible.

LDA (Linear Discriminant Analysis):

1. Purpose:
   - LDA aims to find the directions that maximize the separation between multiple classes in the data.
   - LDA is a supervised technique as it takes class labels into account during computation.
   - It's particularly useful for classification tasks, as it tries to find the feature subspace that optimally separates different classes.
2. Working:
   - LDA aims to maximise the ratio of between-class to within-class variation. It projects the data onto a lower-dimensional space in such a way that the distances between the means of various classes are increased while the variations within each class are reduced.
3. Objective:
   - The goal of LDA is to identify the linear combinations of features that best distinguish the classes in the dataset.

Which one is better for the breast_cancer dataset:

- For the breast_cancer dataset, which is a classification problem, LDA may be more appropriate. This is because LDA directly models class differences and seeks to identify the feature subspace that maximizes class separation. Because the dataset includes class labels, LDA can use this information to identify the most discriminative features.

- If computing economy is an issue, PCA can also be used for visualization or to reduce the dimensionality of a dataset.

- Finally, the decision between PCA and LDA is determined by the precise analytic aims and the type of the dataset.

  1. If classification is the goal and maximum class separation is important, LDA may be preferable.
  2. If the goal is dimensionality reduction or visualization, PCA.