Exploratory Data Analysis – Breast Cancer Coimbra Dataset

This notebook performs exploratory data analysis (EDA) on the **Breast Cancer Coimbra** dataset.

- Goal: Explore clinical / metabolic features and their relationship with breast cancer status.
- Target variable: `Classification`
  - 0 = Healthy / Control
  - 1 = Patient / Malignant

This analysis includes:

1. Data loading and basic checks
2. Univariate analysis (distributions & summary statistics)
3. Bivariate analysis (feature vs target)
4. Correlation analysis
5. Outlier inspection
6. Scaling exploration
7. Simple feature-importance measures

More details and interpretations will be noted on later sections at where the corrisponding data was been extracted. A final summery is noted at the end as well.

In [1]:
```
#import lib
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from scipy import stats
from sklearn.feature_selection import mutual_info_classif, f_classif
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
```

1. Dataset Overview

Shape & Columns

- **Rows:** 4,000
- **Feature columns:** Age, BMI, Glucose, Insulin, HOMA, Leptin, Adiponectin, Resistin, MCP.1
- **Target:** `Classification` (0 or 1)

Data Types

All 9 features are numerical (`int64` or `float64`) and fully non-null.
No missing values were detected in any column.

Class Distribution

Class	Count	Proportion
0 – Healthy	1784	44.6%
1 – Patient	2216	55.4%

The dataset shows a **slight class imbalance**, with more patient samples than healthy ones.

A count plot confirms this visually.

In [5]:
```
#Load data
# Update the path if needed
df = pd.read_csv(r'D:\learning UCSD\ece143\Group_Project\breast_cancer_coimbra_c
print("Shape:", df.shape)
```

```
Shape: (4000, 10)
```

In [4]:
```
print("DataFrame Info:")
print(df.info())
print("\nSummary statistics:")
display(df.describe().T)

print("\nMissing values per column:")
print(df.isna().sum())
```

```
DataFrame Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4000 entries, 0 to 3999
Data columns (total 10 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   Age             4000 non-null   int64  
 1   BMI             4000 non-null   float64
 2   Glucose         4000 non-null   int64  
 3   Insulin         4000 non-null   float64
 4   HOMA            4000 non-null   float64
 5   Leptin          4000 non-null   float64
 6   Adiponectin     4000 non-null   float64
 7   Resistin        4000 non-null   float64
 8   MCP.1           4000 non-null   float64
 9   Classification  4000 non-null   int64  
dtypes: float64(7), int64(3)
memory usage: 312.6 KB
None

Summary statistics:
```

	count	mean	std	min	25%	50%	
Age	4000.0	56.210750	17.809650	32.000000	39.000000	56.000000	
BMI	4000.0	27.422280	4.413884	20.690751	23.079053	27.558485	
Glucose	4000.0	113.876500	25.837795	76.000000	76.000000	131.000000	1
Insulin	4000.0	8.654001	6.435160	2.821000	4.421750	5.818000	
HOMA	4000.0	2.024332	1.625638	0.590033	0.970090	1.373842	
Leptin	4000.0	25.137737	15.096446	6.831900	12.712750	19.805050	
Adiponectin	4000.0	9.364896	4.674244	3.192272	5.580210	8.286938	
Resistin	4000.0	13.053667	7.454424	4.190320	7.022095	10.692780	
MCP.1	4000.0	512.183456	253.279015	137.488000	299.665000	482.308000	6
Classification	4000.0	0.554000	0.497138	0.000000	0.000000	1.000000	

```
Missing values per column:
Age               0
BMI               0
Glucose           0
Insulin           0
HOMA              0
Leptin            0
Adiponectin       0
Resistin          0
MCP.1             0
Classification    0
dtype: int64
```

In [10]:
```python
TARGET_COL = "Classification"
feature_cols = [col for col in df.columns if col != TARGET_COL]

print("Target column:", TARGET_COL)
print("Feature columns:", feature_cols)


class_counts = df[TARGET_COL].value_counts().sort_index()
print("\nClass distribution:")
print(class_counts)

class_proportions = class_counts / len(df)
print("\nClass proportions:")
print(class_proportions)
```

```
Target column: Classification
Feature columns: ['Age', 'BMI', 'Glucose', 'Insulin', 'HOMA', 'Leptin', 'Adiponec
tin', 'Resistin', 'MCP.1']

Class distribution:
Classification
0    1784
1    2216
Name: count, dtype: int64

Class proportions:
Classification
0    0.446
1    0.554
Name: count, dtype: float64
```

2. Univariate Feature Distributions

Histograms and KDE curves were generated for each feature.

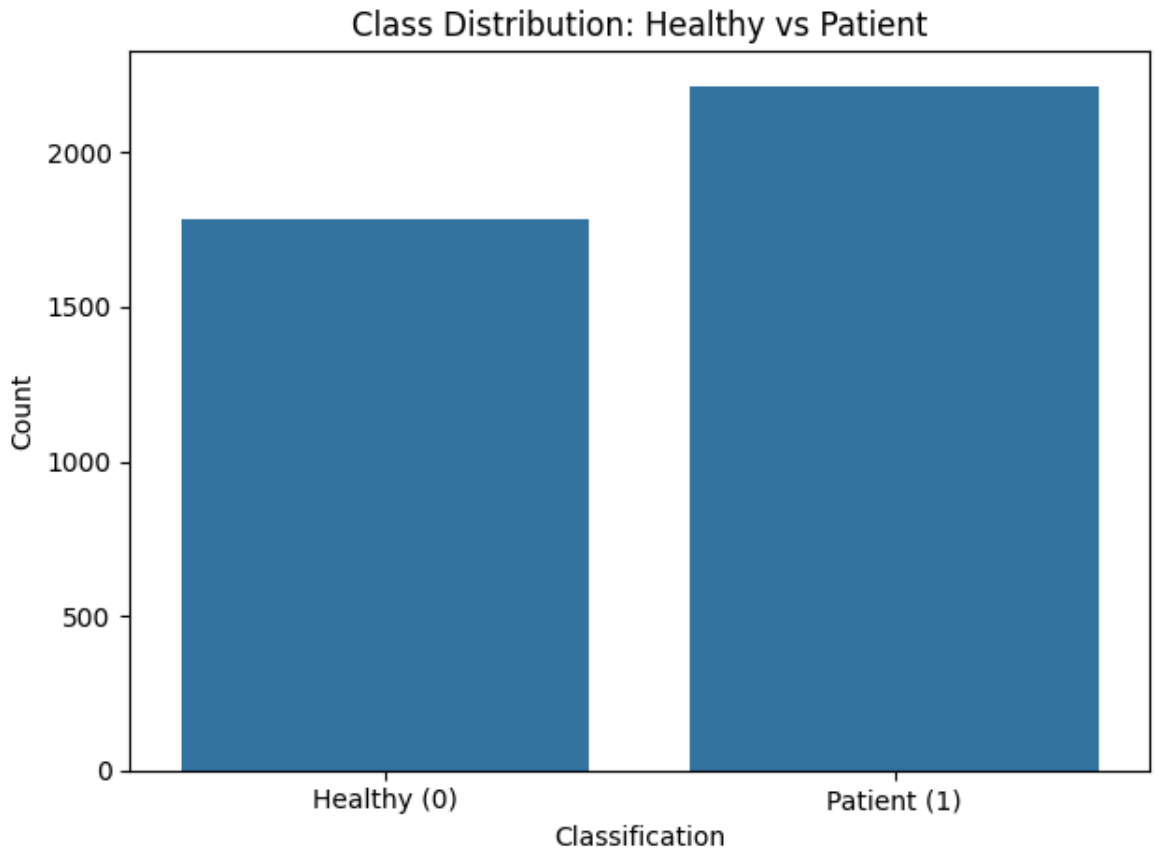
Key Observations

- **Age:** Broad distribution centered around ~56 years.
- **BMI:** Range ~21–36, mild multimodality.
- **Glucose:** Clearly **bimodal** with peaks around 76 and 131 mg/dL.
- **Insulin, HOMA, Resistin:** Strong **right skew** with long tails.
- **Leptin and Adiponectin:** Mild right skew.

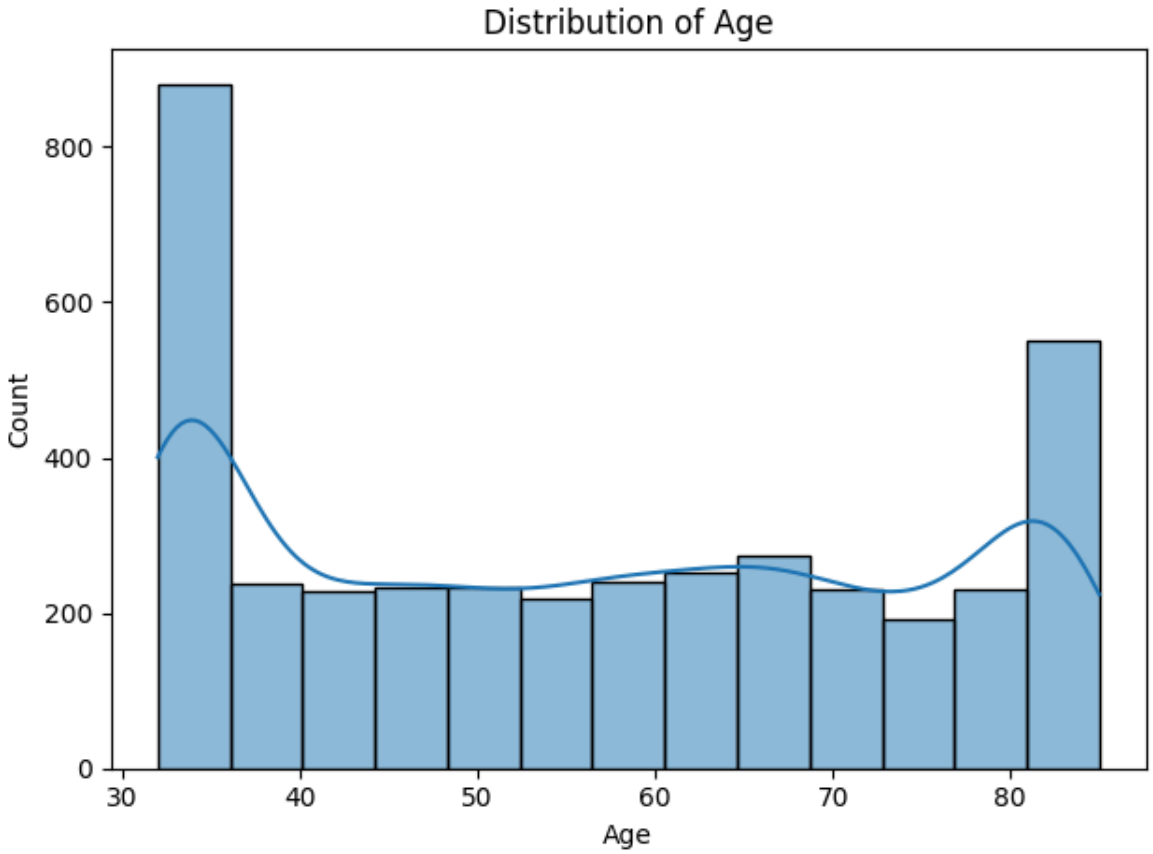
Interpretation

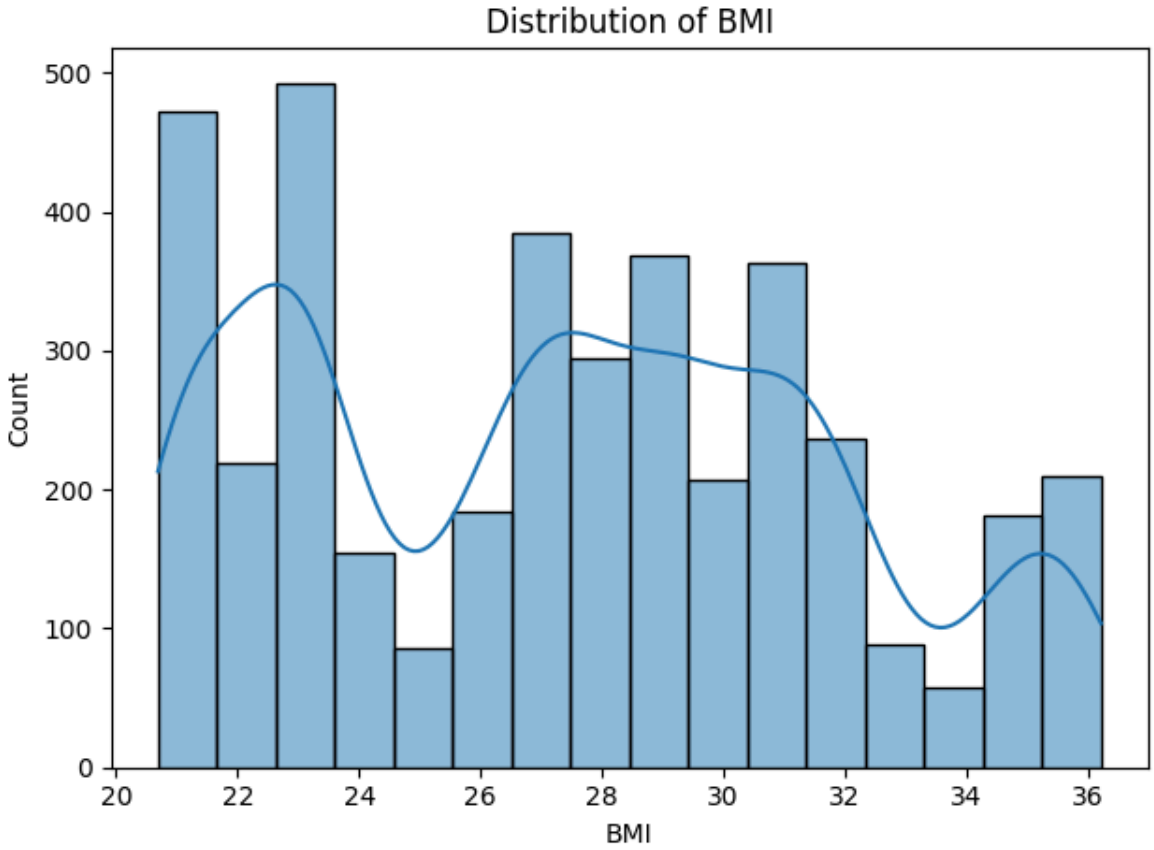
Several metabolic markers show skewed distributions, suggesting that **log-transforms or robust scaling** may help stabilize variance in modeling.

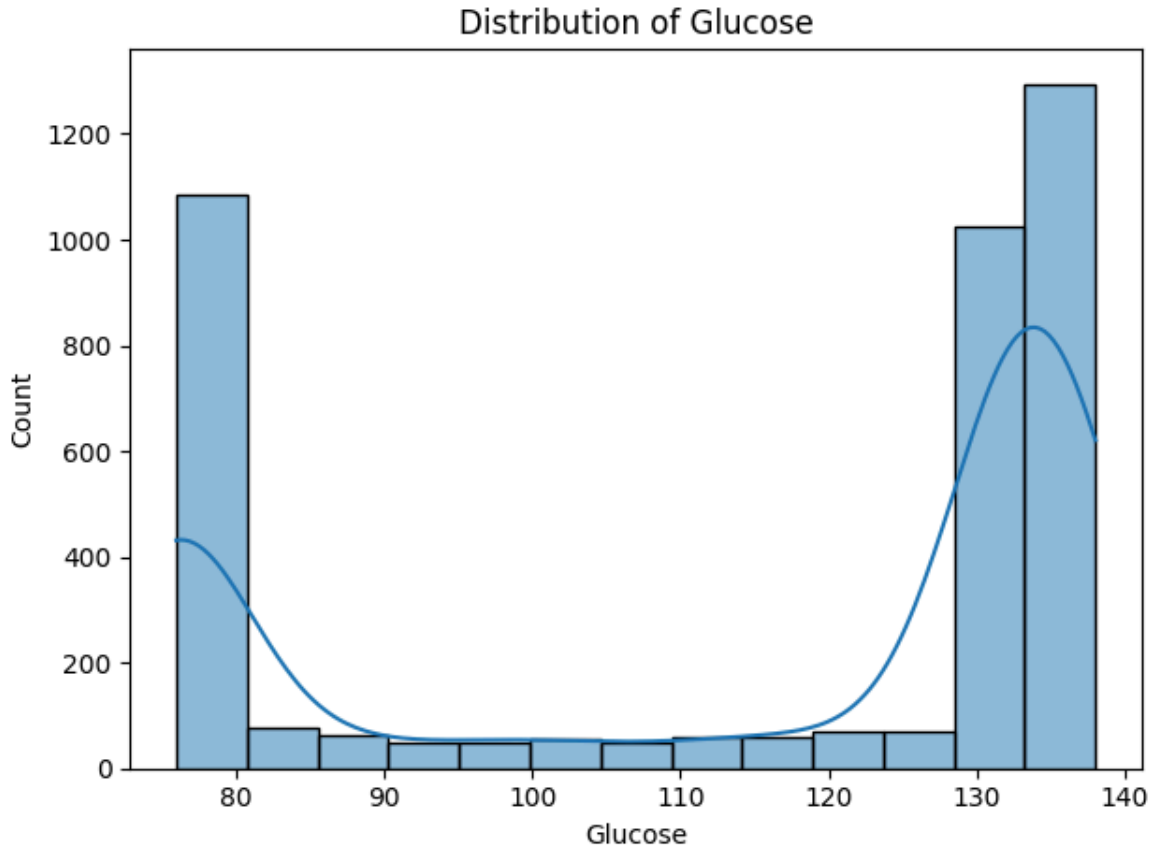
In [30]:
```
fig, ax = plt.subplots()
sns.countplot(x=TARGET_COL, data=df, ax=ax)
ax.set_xticks([0, 1])
ax.set_xticklabels(["Healthy (0)", "Patient (1)"])
ax.set_title("Class Distribution: Healthy vs Patient")
ax.set_xlabel("Classification")
ax.set_ylabel("Count")
plt.tight_layout()
plt.show()
```

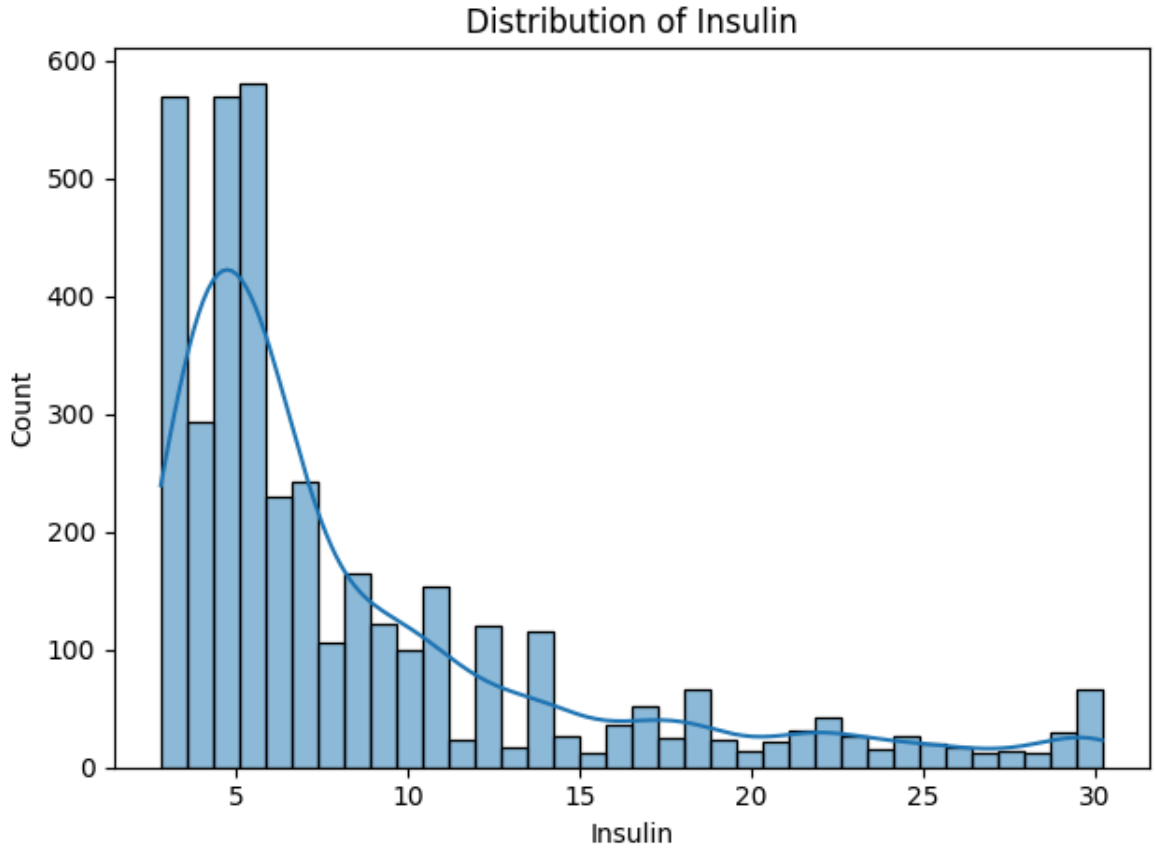


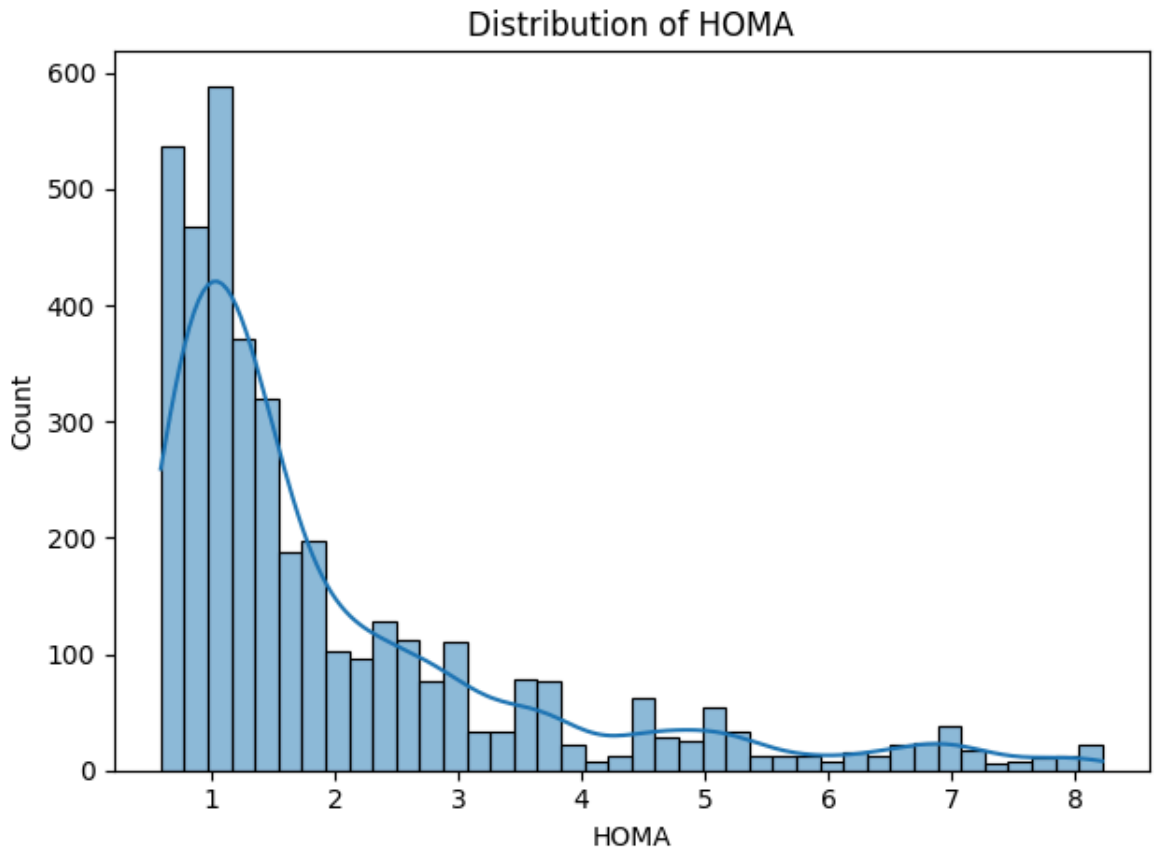
In [12]:
```
# Histograms/KDE (overall)
for col in feature_cols:
    fig, ax = plt.subplots()
    sns.histplot(df[col], kde=True, ax=ax)
    ax.set_title(f"Distribution of {col}")
    plt.tight_layout()
    plt.show()
```

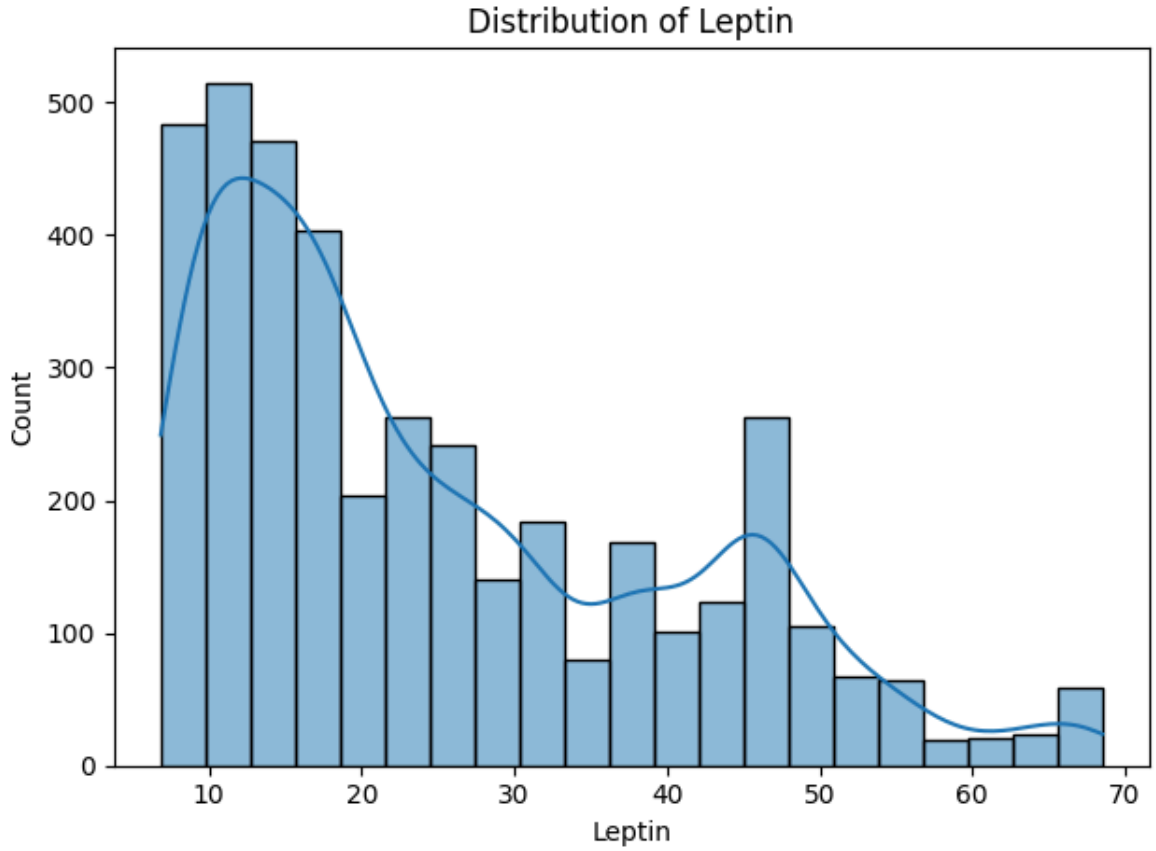

Distribution of Age
Count
Age
0
200
400
600
800
30
40
50
60
70
80

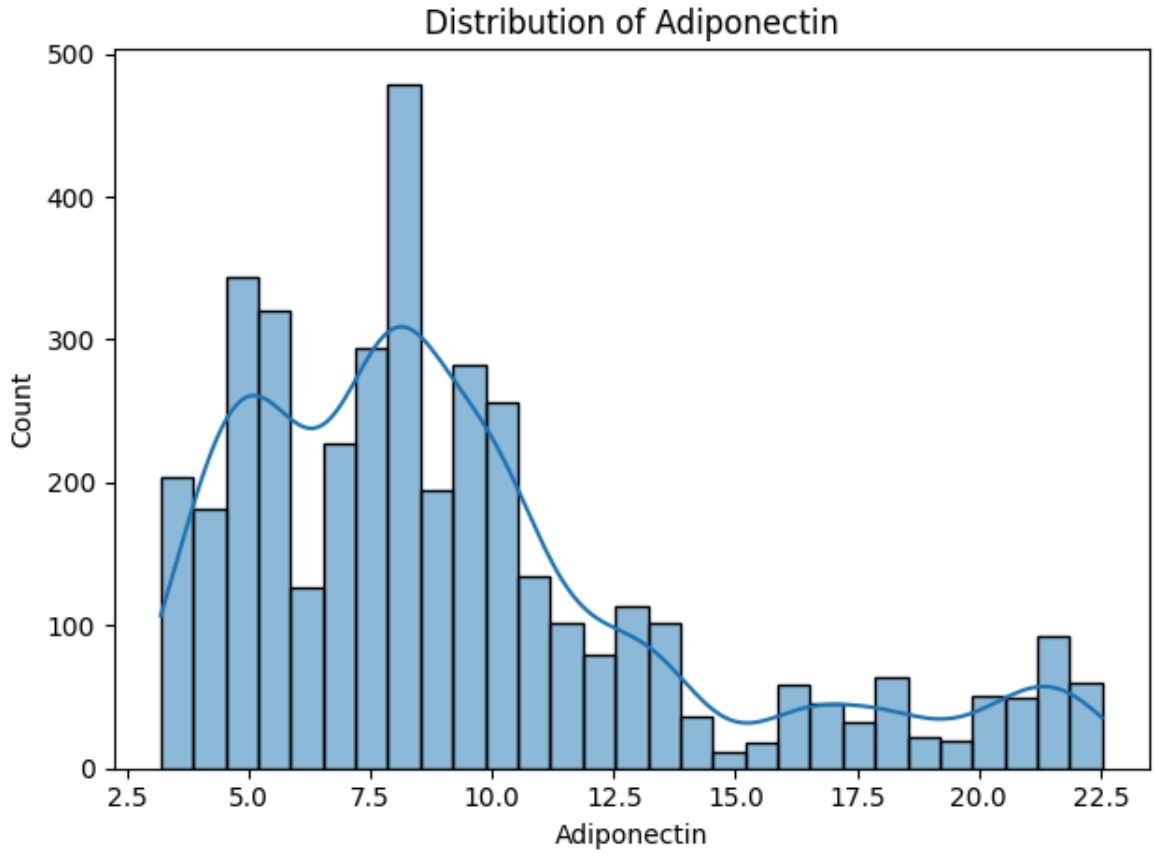

Distribution of BMI
Count
BMI
0
100
200
300
400
500
20
22
24
26
28
30
32
34
36

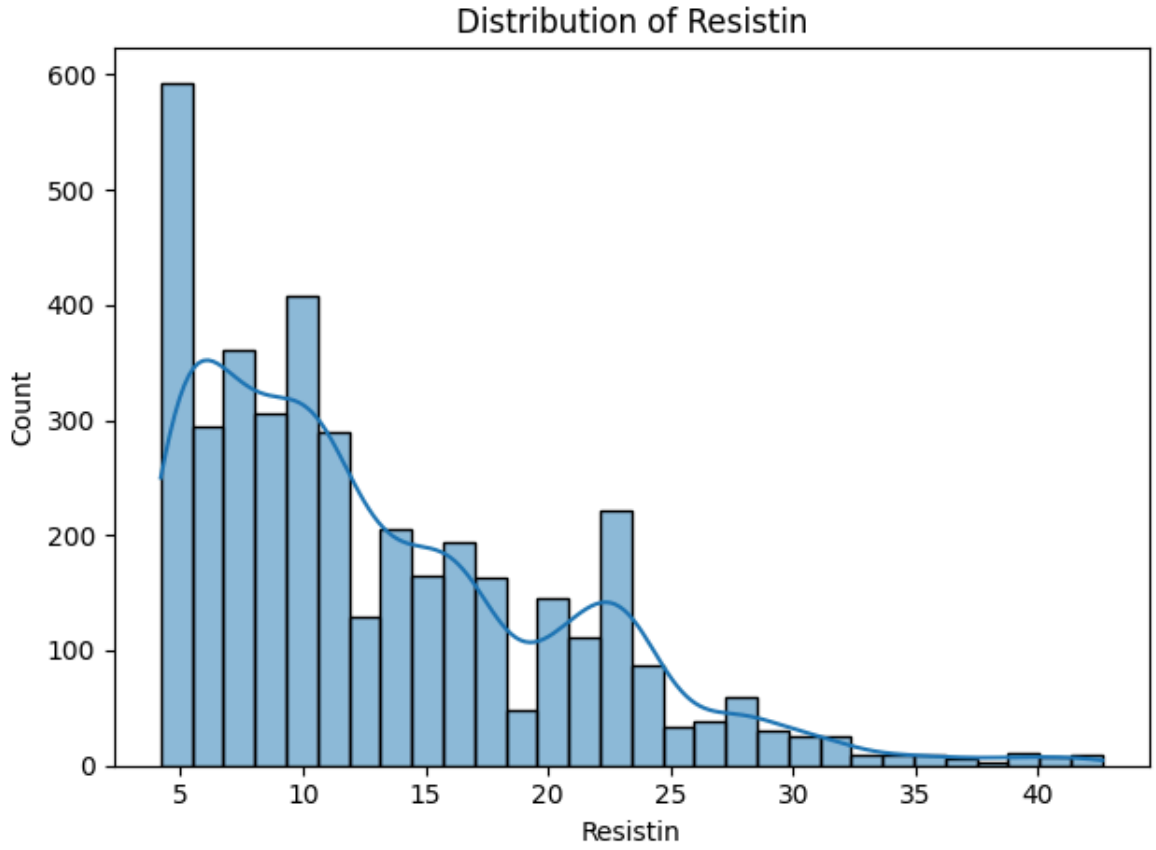

Distribution of Glucose
Count
Glucose
0
200
400
600
800
1000
1200
80
90
100
110
120
130
140

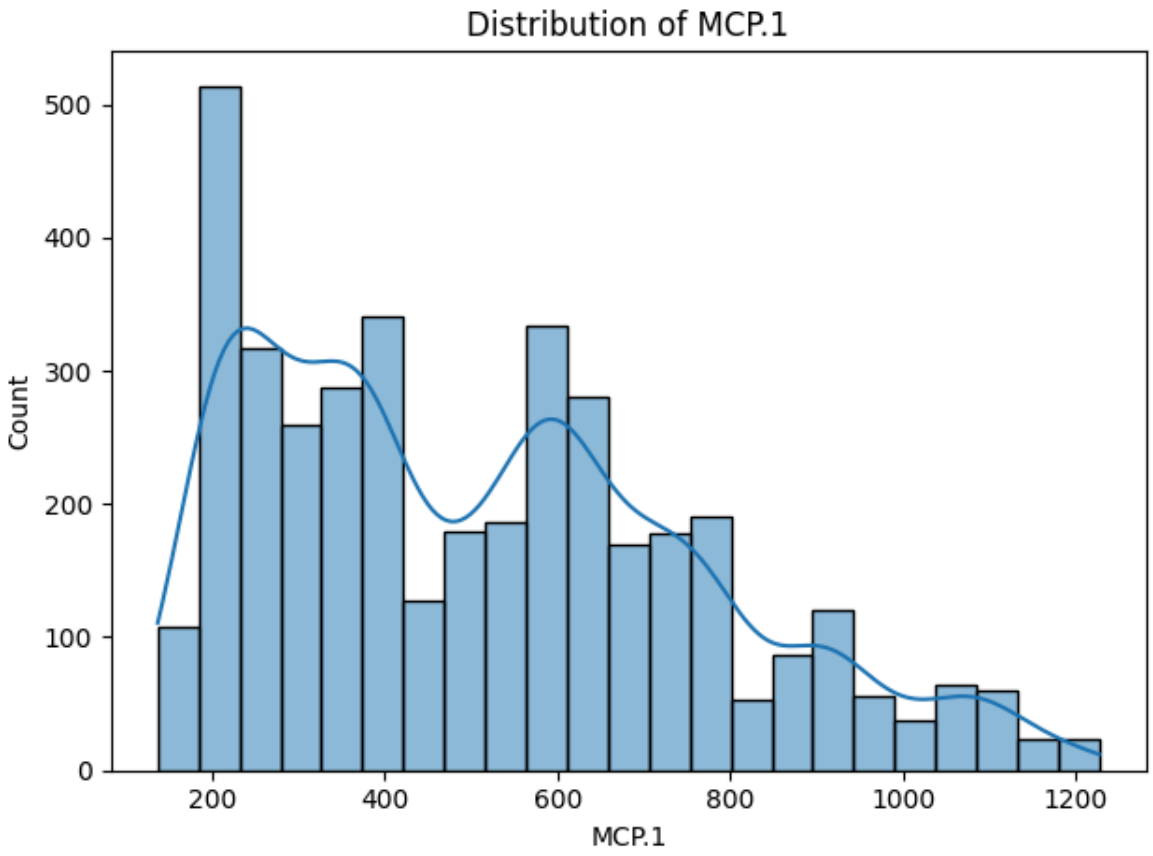

Distribution of Insulin
Count
Insulin
0
100
200
300
400
500
600
5
10
15
20
25
30


Distribution of HOMA
Count
HOMA
0
100
200
300
400
500
600
1
2
3
4
5
6
7
8


Distribution of Leptin
Count
Leptin
0
100
200
300
400
500
10
20
30
40
50
60
70


Distribution of Adiponectin
Count
Adiponectin
0
100
200
300
400
500
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5


Distribution of Resistin
Count
Resistin
0
100
200
300
400
500
600
5
10
15
20
25
30
35
40



3. Distributions by Class (Healthy vs Patient)

Overlaid histograms show how each feature differs between healthy and patient groups.

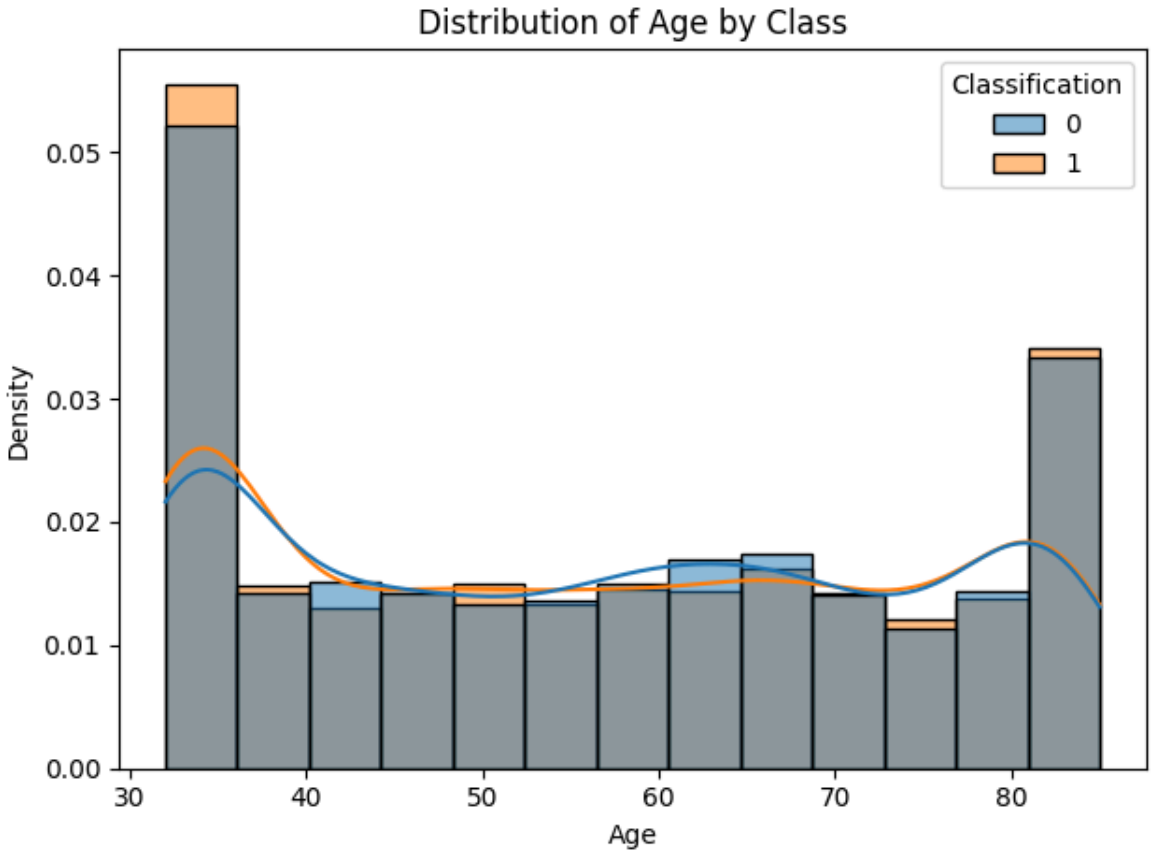
Key Observations

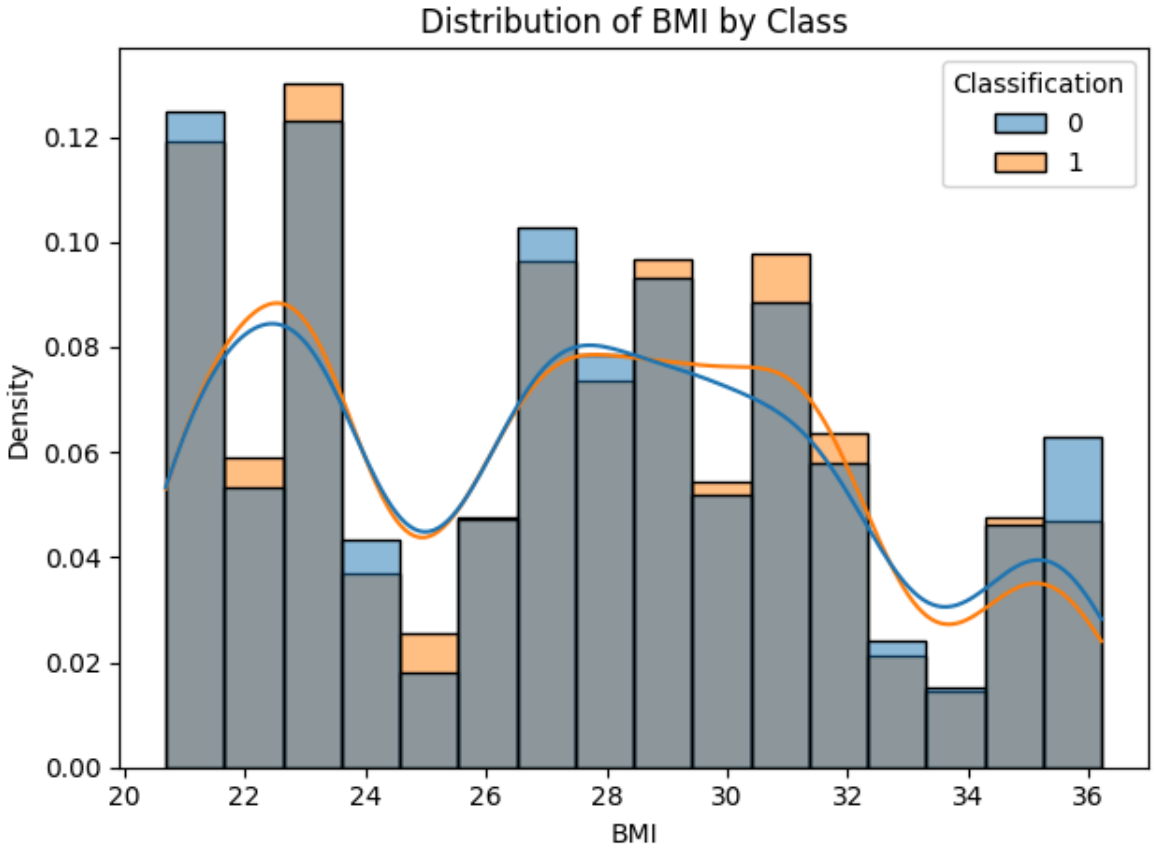
- Most features show **substantial overlap** between classes.
- **Insulin**, **HOMA**, and **Resistin** show slightly higher values for patients, but not strongly separated.
- **Glucose** distributions are similar in shape for both groups.

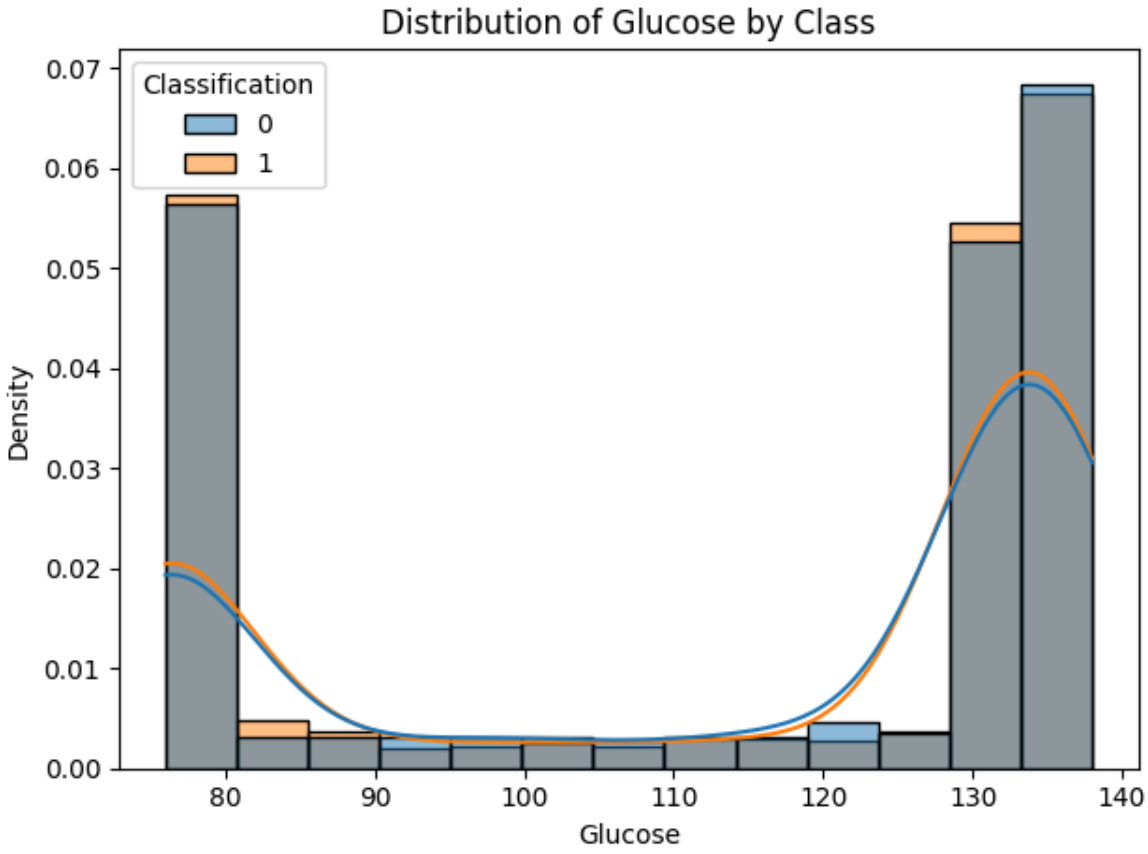
Conclusion

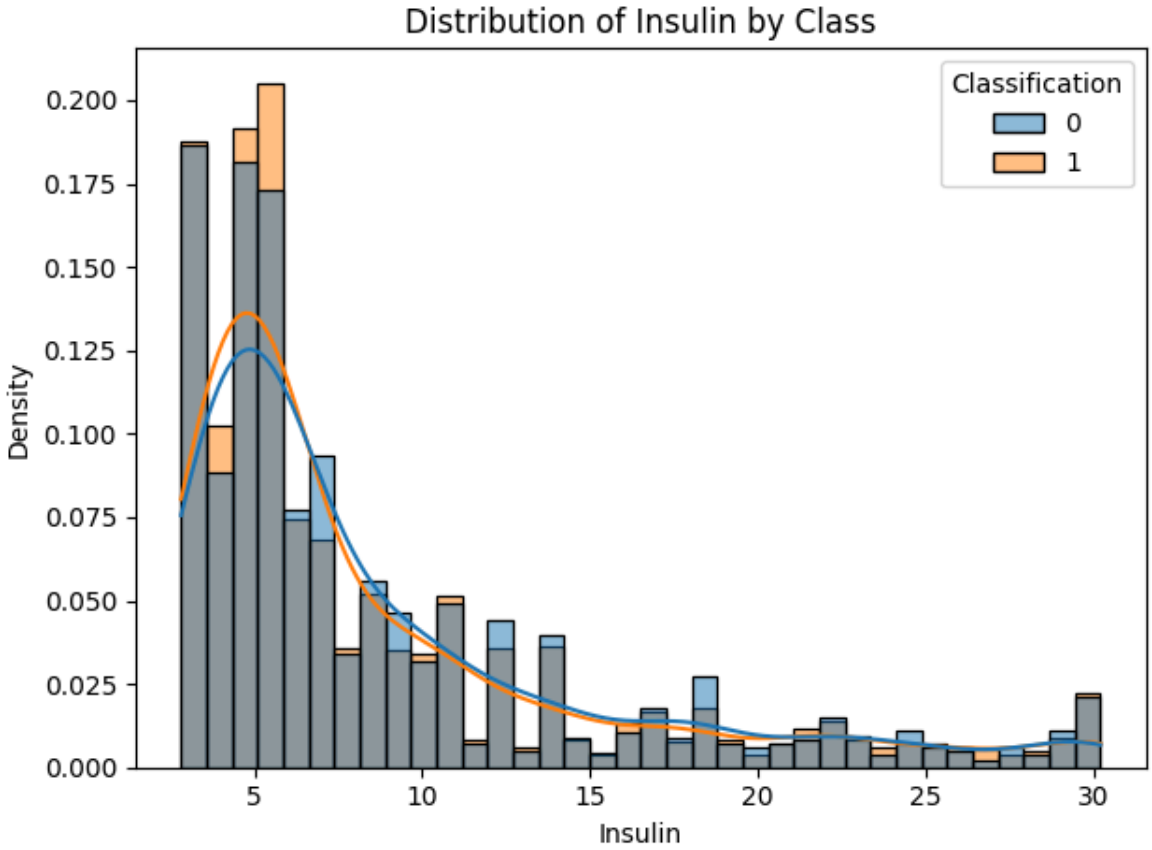
No single metabolic feature exhibits strong class-separation.
This suggests the need for **multivariate** and **nonlinear** modeling strategies.

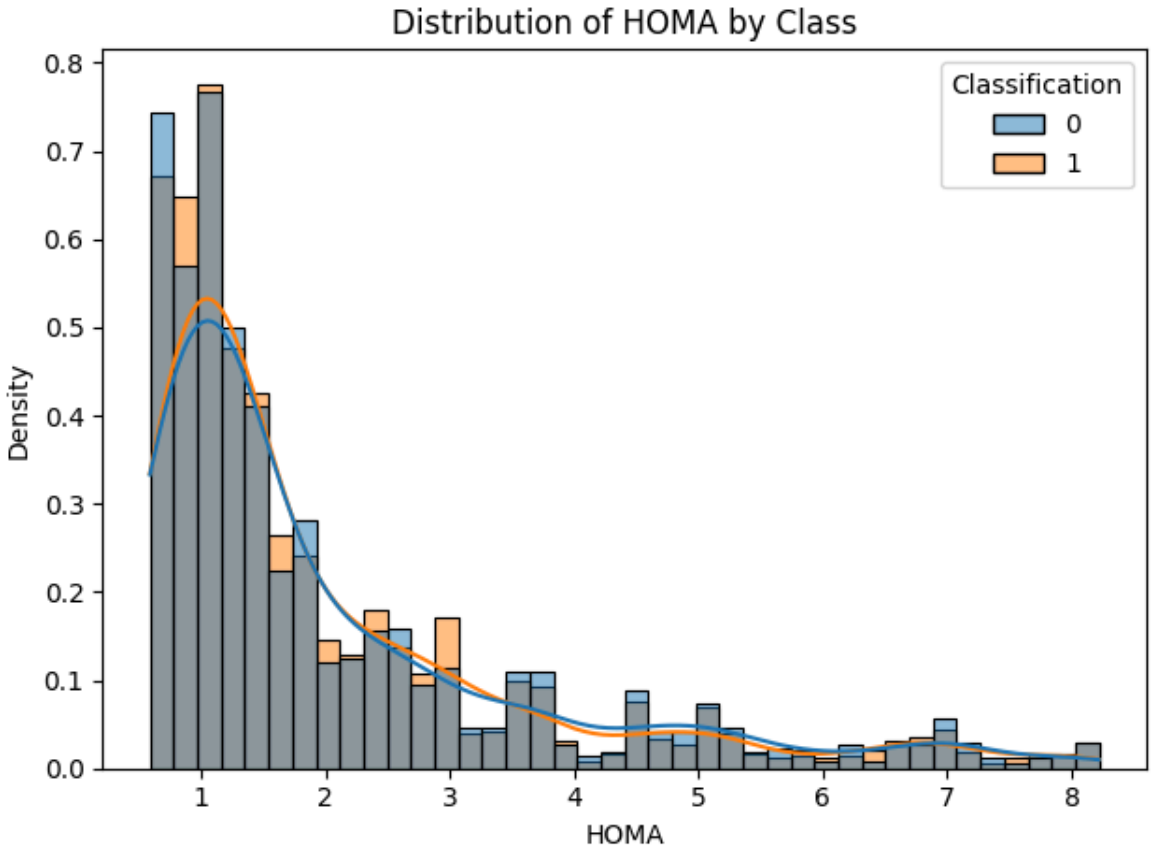
In [13]:
```
# Histograms by class (overlaid)
for col in feature_cols:
    fig, ax = plt.subplots()
    sns.histplot(data=df, x=col, hue=TARGET_COL, kde=True, stat="density", commo
    ax.set_title(f"Distribution of {col} by Class")
    ax.set_xlabel(col)
    plt.tight_layout()
    plt.show()
```

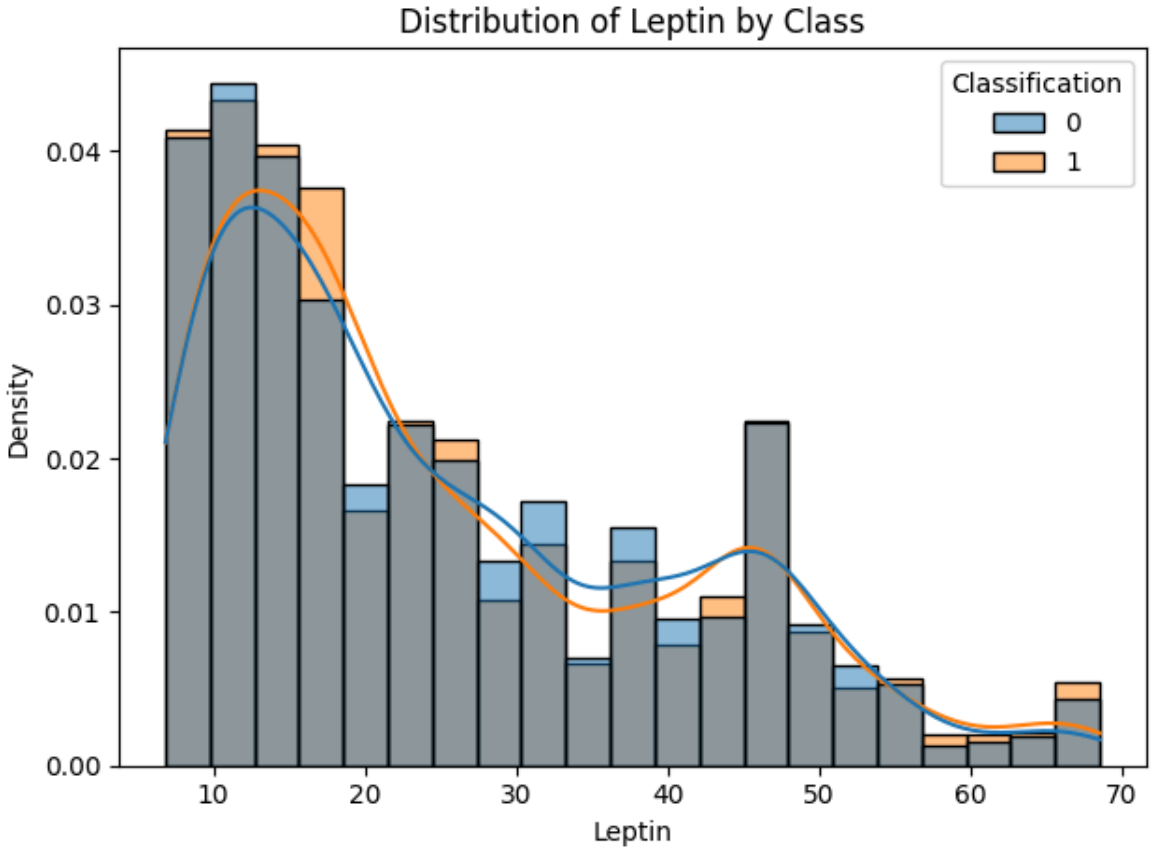

Distribution of Age by Class
Classification
0
1
Density
0.00
0.01
0.02
0.03
0.04
0.05
30
40
50
60
70
80
Age

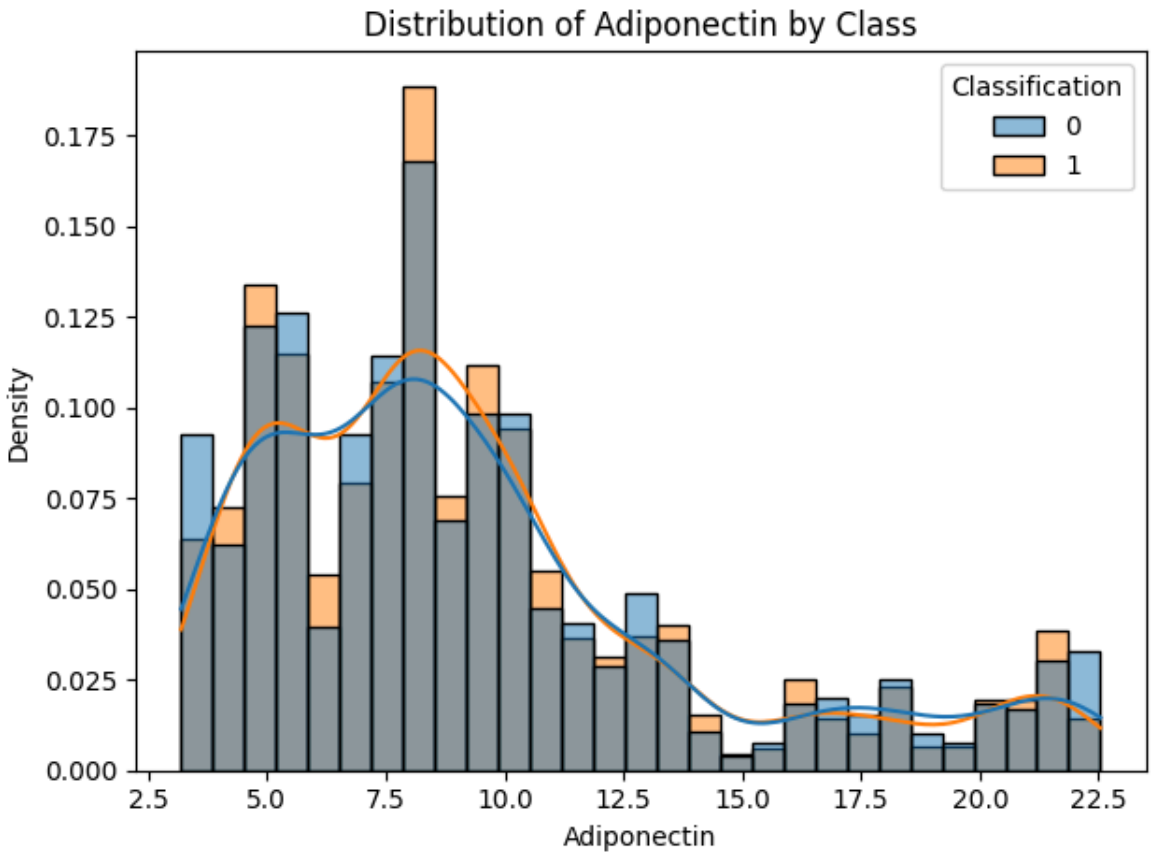

Distribution of BMI by Class
Classification
0
1
Density
0.00
0.02
0.04
0.06
0.08
0.10
0.12
20
22
24
26
28
30
32
34
36
BMI

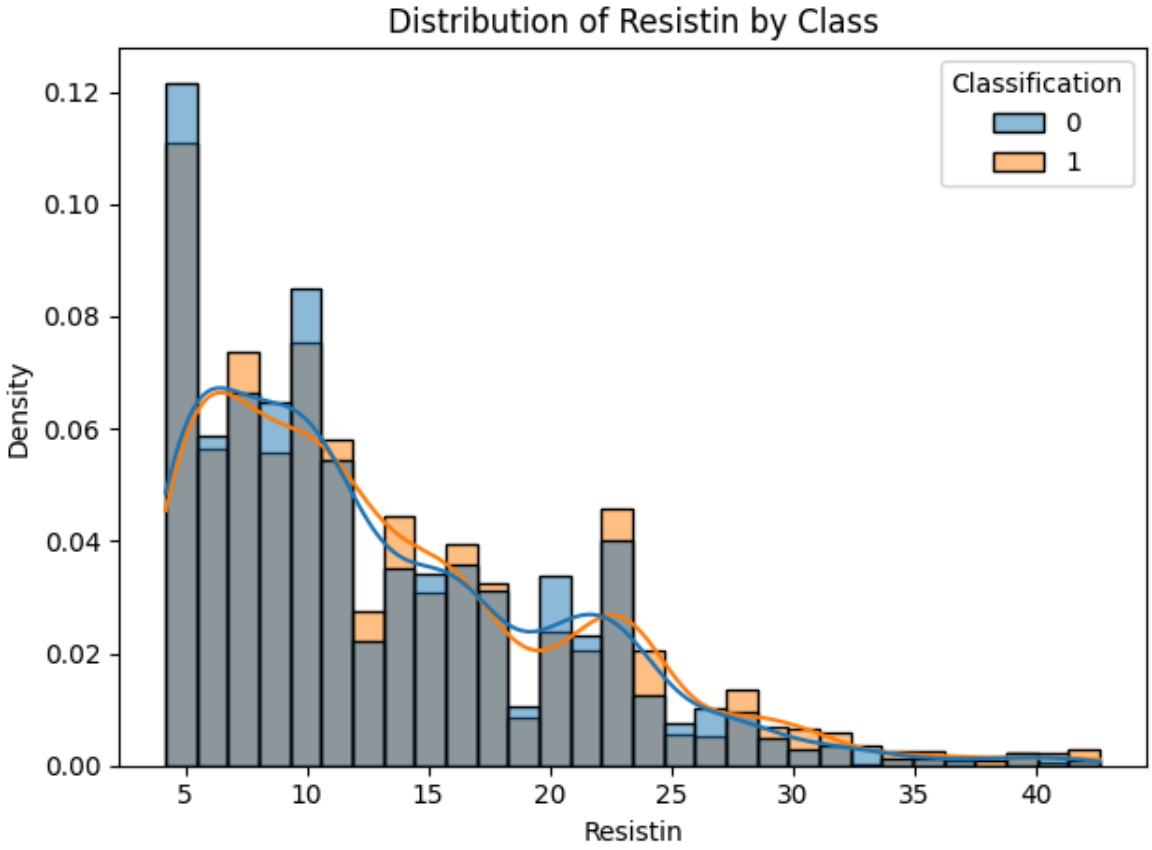

Distribution of Glucose by Class
Classification
0
1
Density
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00
80
90
100
110
120
130
140
Glucose

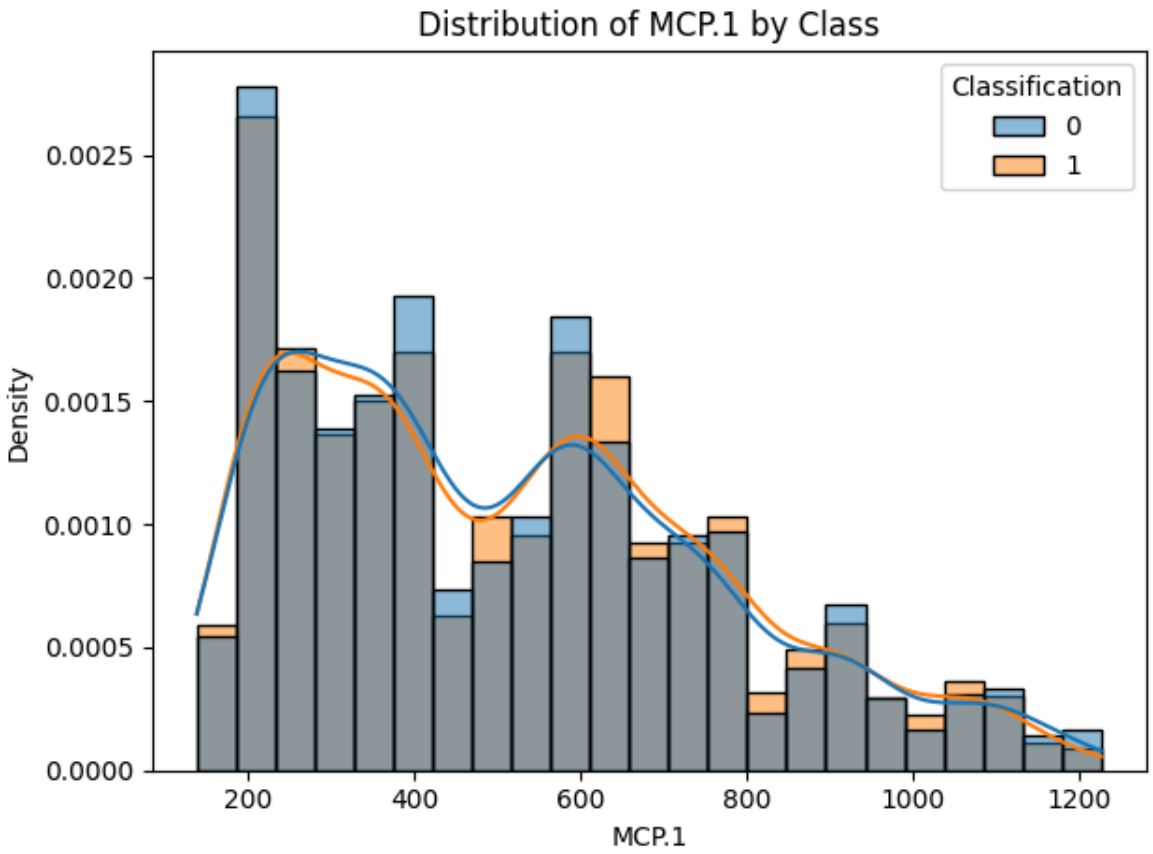

Distribution of Insulin by Class
Classification
0
1
Density
0.200
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
5
10
15
20
25
30
Insulin


Distribution of HOMA by Class
Classification
0
1
Density
HOMA
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
1
2
3
4
5
6
7
8


Distribution of Leptin by Class
Classification
0
1
Density
Leptin
0.00
0.01
0.02
0.03
0.04
10
20
30
40
50
60
70


Distribution of Adiponectin by Class
Classification
0
1
Density
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
Adiponectin


Distribution of Resistin by Class
Classification
0
1
Density
0.12
0.10
0.08
0.06
0.04
0.02
0.00
5
10
15
20
25
30
35
40
Resistin



4. Boxplots & Violin Plots by Class

Boxplots and violin plots confirm the overlapping distributions between healthy and patient groups.

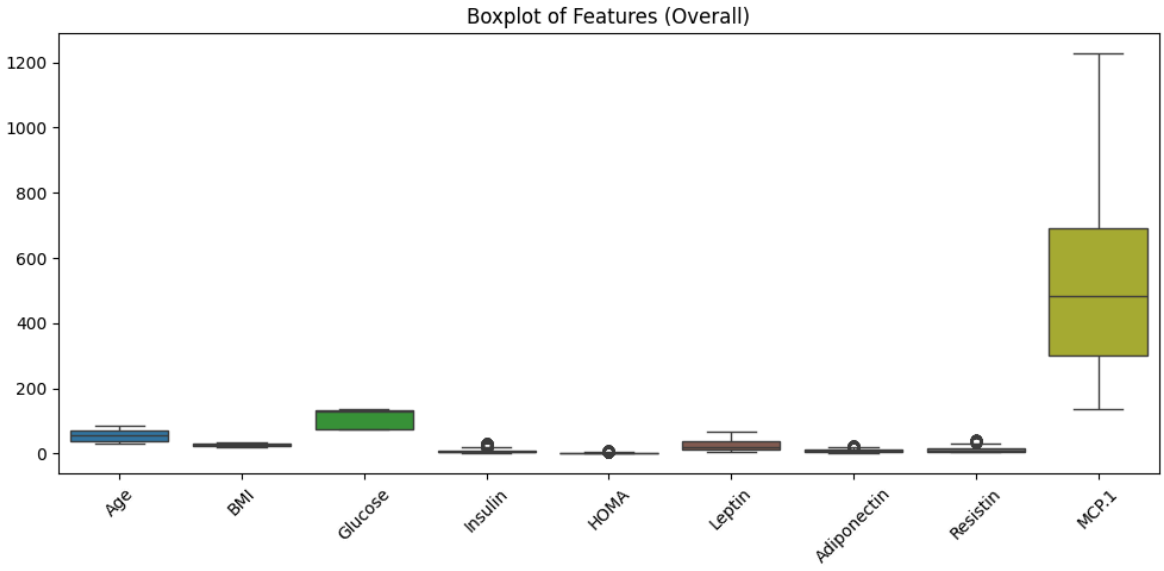
Observations

- Medians for all features are nearly identical between classes.
- Significant outliers are present in:
  - **Insulin**
  - **HOMA**
  - **Resistin**
- The violin plot shapes further reinforce the lack of clear separation.

Interpretation

The dataset likely contains **weak individual predictors**, requiring combined or interaction-based modeling.

In [14]:
```
# Overall boxplots (not stratified by class)
plt.figure(figsize=(10, 5))
sns.boxplot(data=df[feature_cols])
plt.xticks(rotation=45)
plt.title("Boxplot of Features (Overall)")
plt.tight_layout()
plt.show()
```



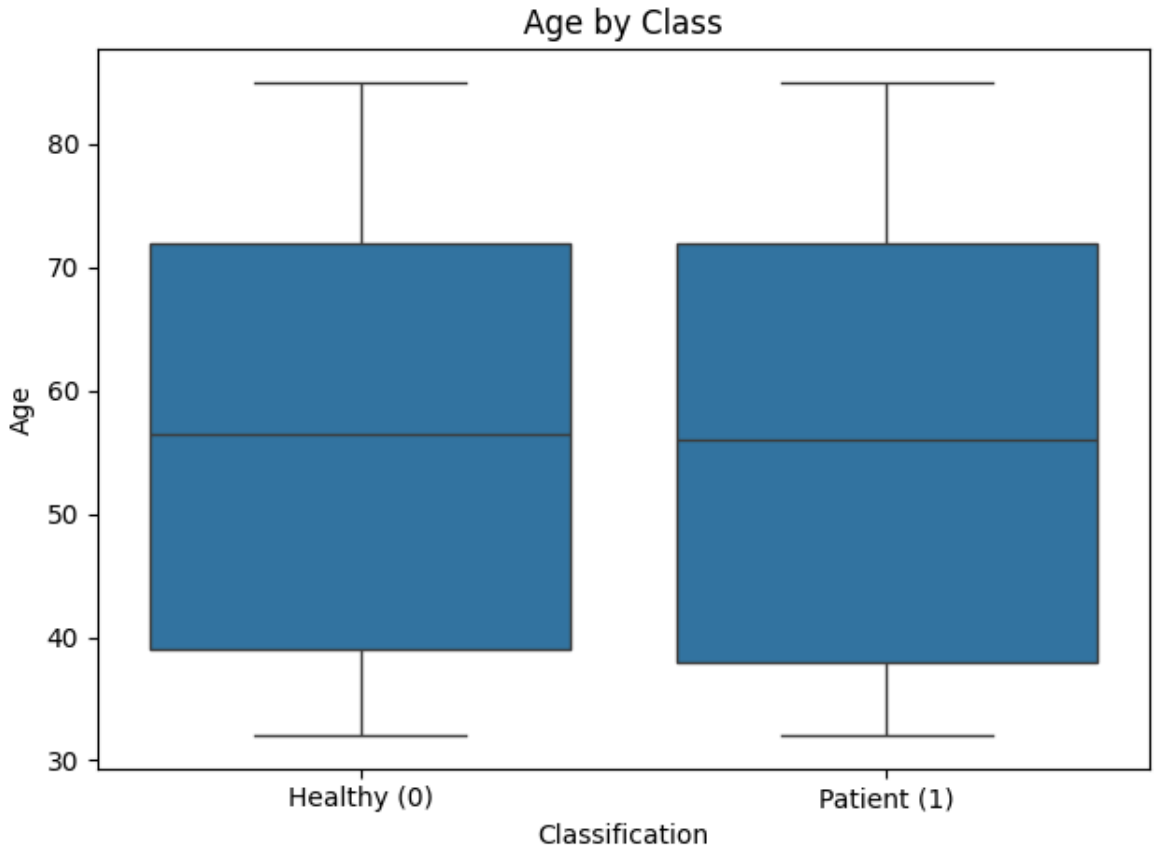
In [15]:
```
# Summary statistics per class
grouped_stats = df.groupby(TARGET_COL)[feature_cols].describe().transpose()
grouped_stats
```

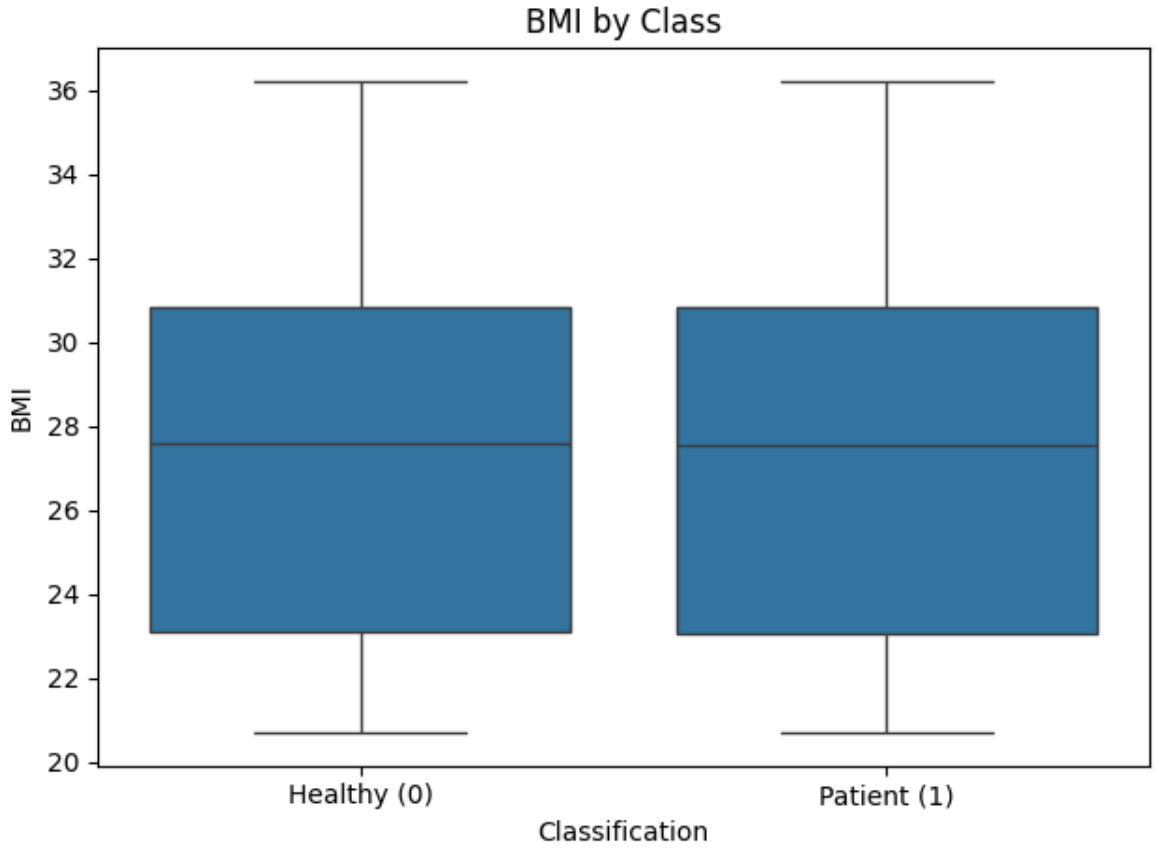
Out[15]:

	Classification	0	1
Age	**count**	1784.000000	2216.000000
	mean	56.368834	56.083484
	std	17.702713	17.898252
	min	32.000000	32.000000
	25%	39.000000	38.000000
...	**...**	...	...
MCP.1	**min**	137.488000	138.903000
	25%	300.156250	299.263750
	50%	473.118000	483.763000
	75%	679.262500	696.078500
	max	1223.677000	1227.250000

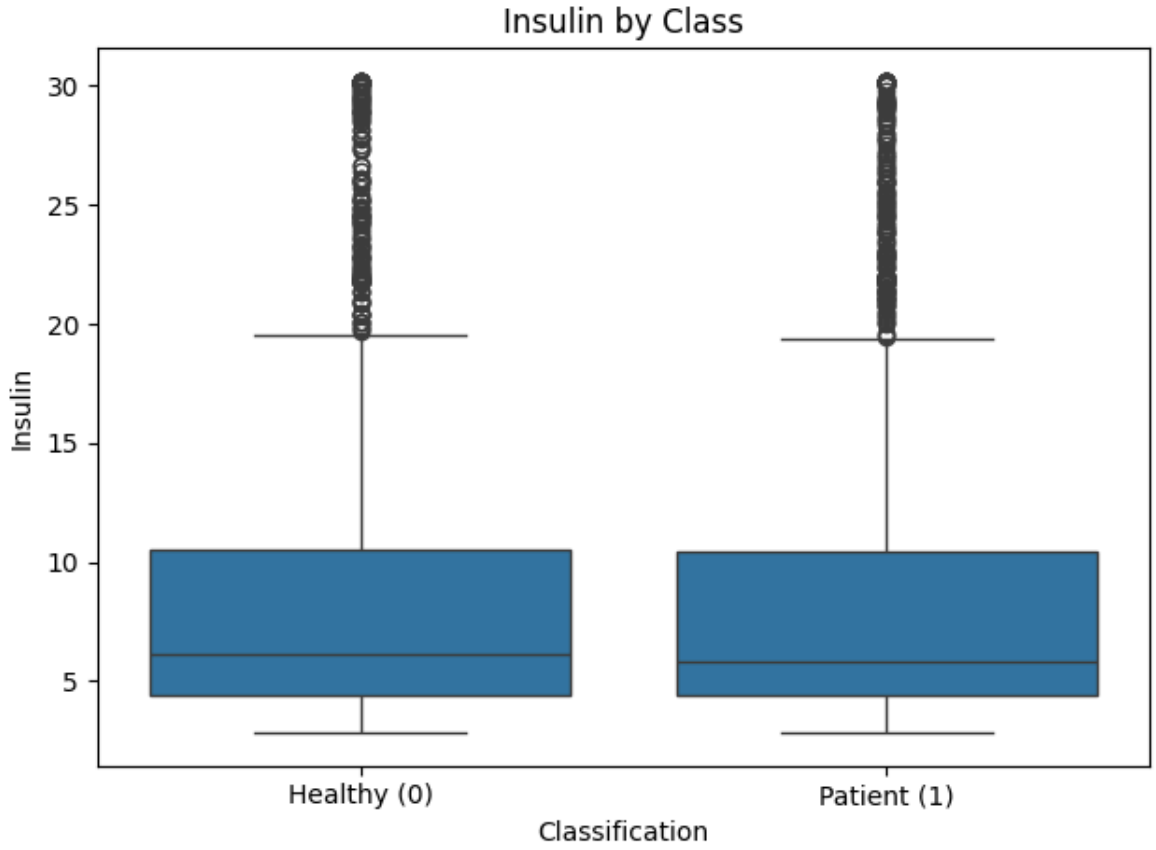
72 rows × 2 columns

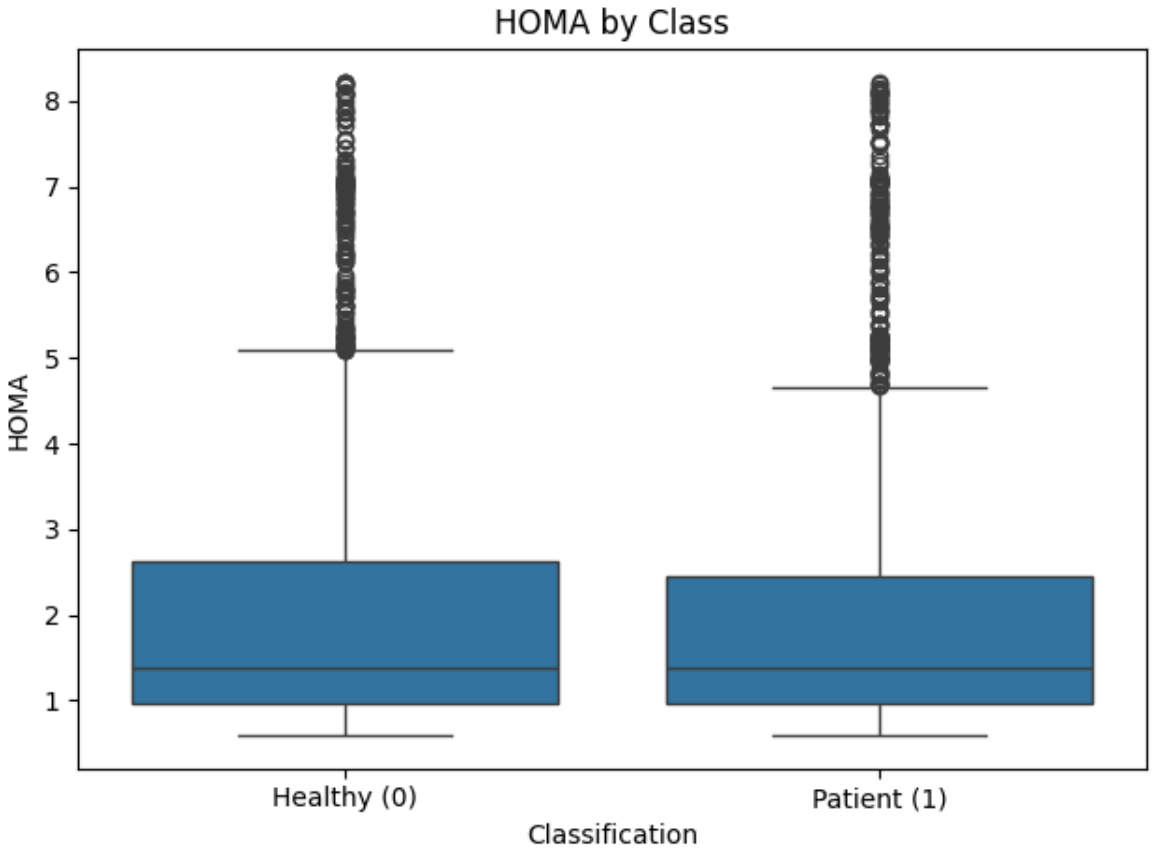
In [ ]:
```
for col in feature_cols:
    fig, ax = plt.subplots()
    sns.boxplot(x=TARGET_COL, y=col, data=df, ax=ax)

    ax.set_xticks([0, 1])
    ax.set_xticklabels(["Healthy (0)", "Patient (1)"])

    ax.set_title(f"{col} by Class")
    plt.tight_layout()
    plt.show()
```

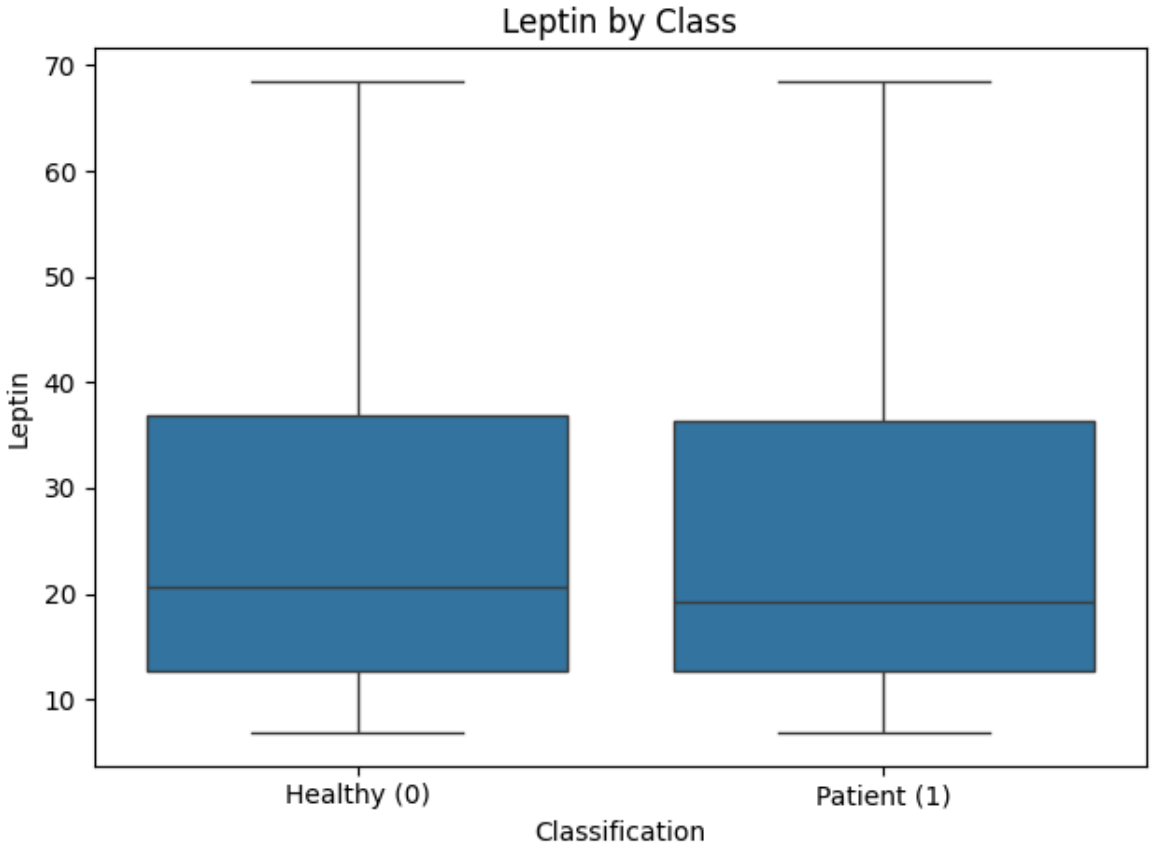

Age by Class
Age
80
70
60
50
40
30
Healthy (0)
Patient (1)
Classification

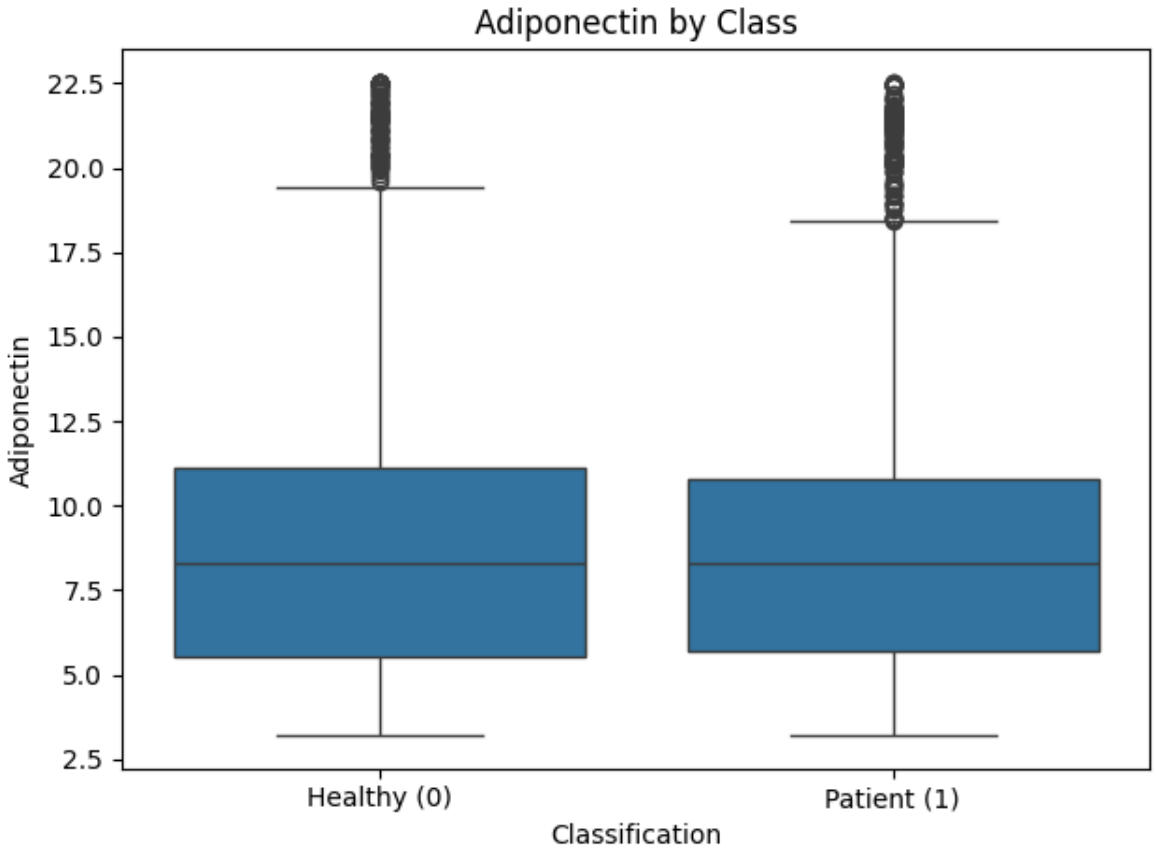

BMI by Class
BMI
36
34
32
30
28
26
24
22
20
Healthy (0)
Patient (1)
Classification

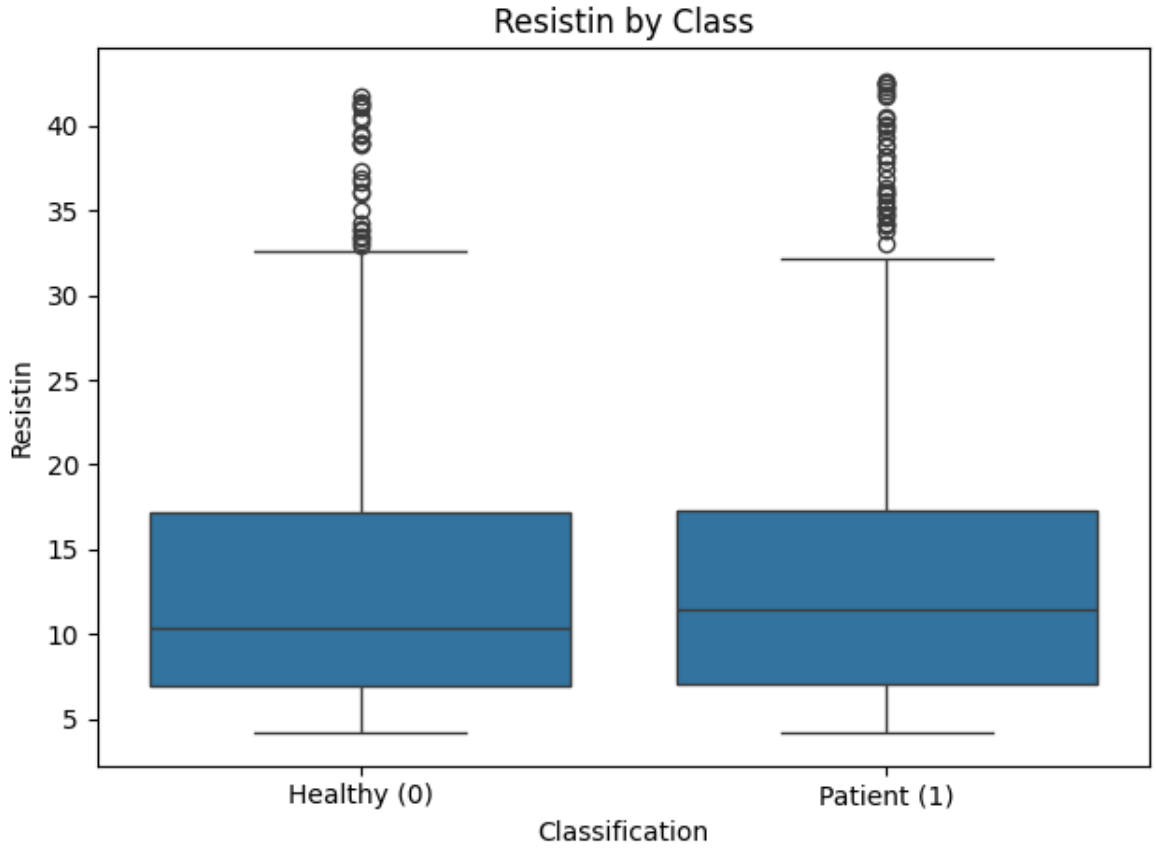

Glucose by Class
140
130
120
110
100
90
80
Glucose
Healthy (0)
Patient (1)
Classification

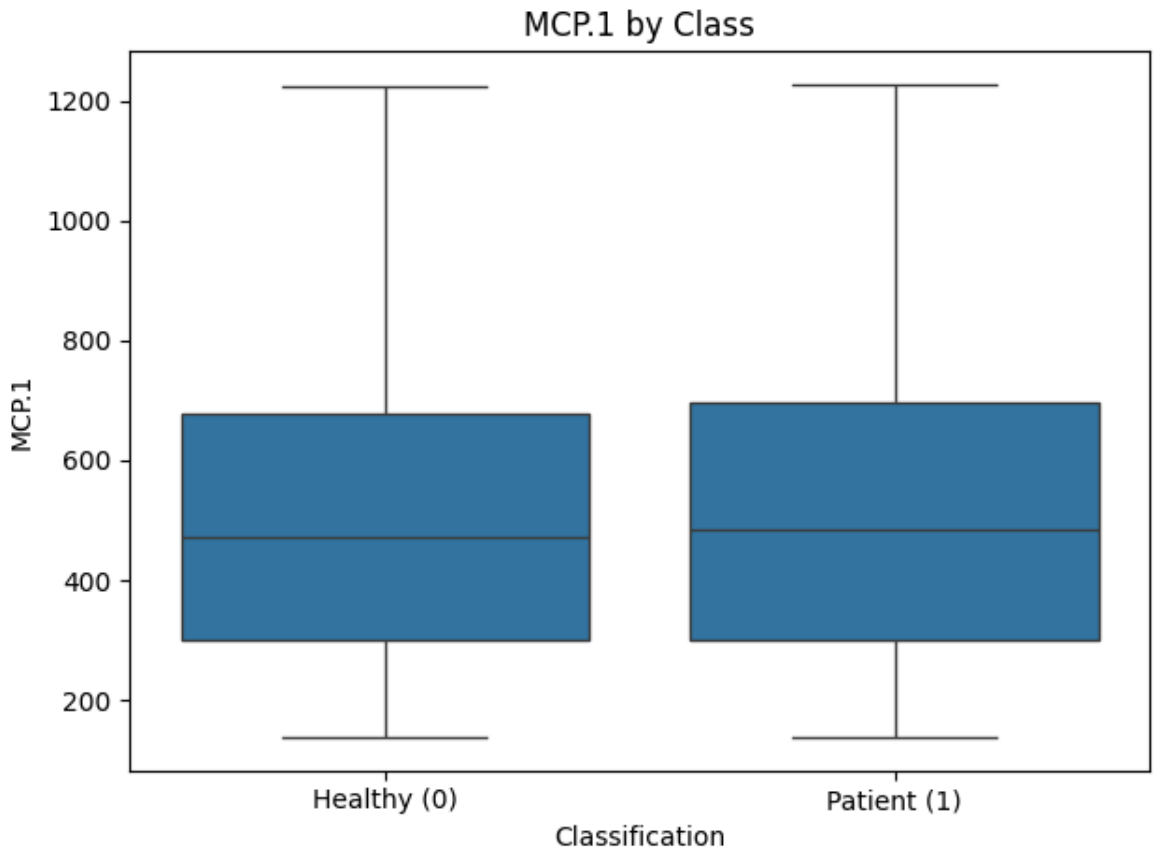

Insulin by Class
30
25
20
15
10
5
Insulin
Healthy (0)
Patient (1)
Classification


HOMA by Class
HOMA
8
7
6
5
4
3
2
1
Healthy (0)
Patient (1)
Classification

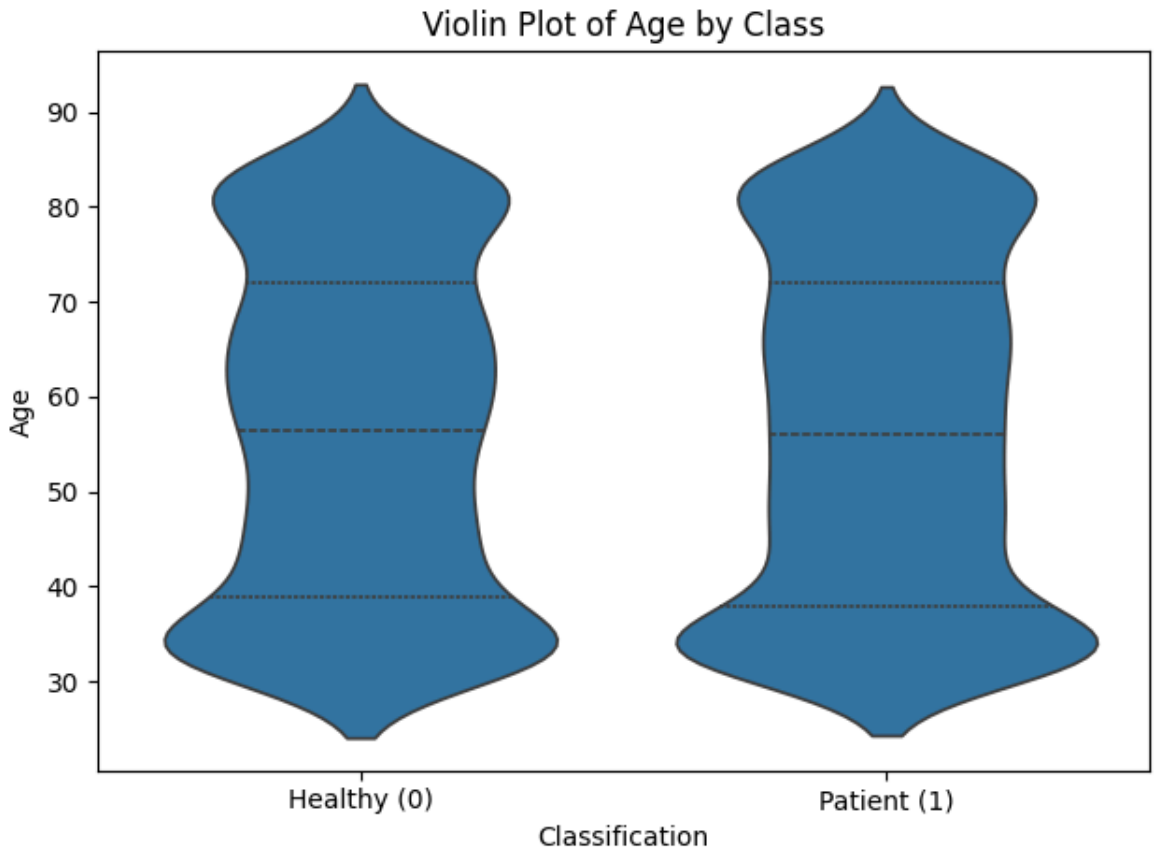

Leptin by Class
Leptin
70
60
50
40
30
20
10
Healthy (0)
Patient (1)
Classification

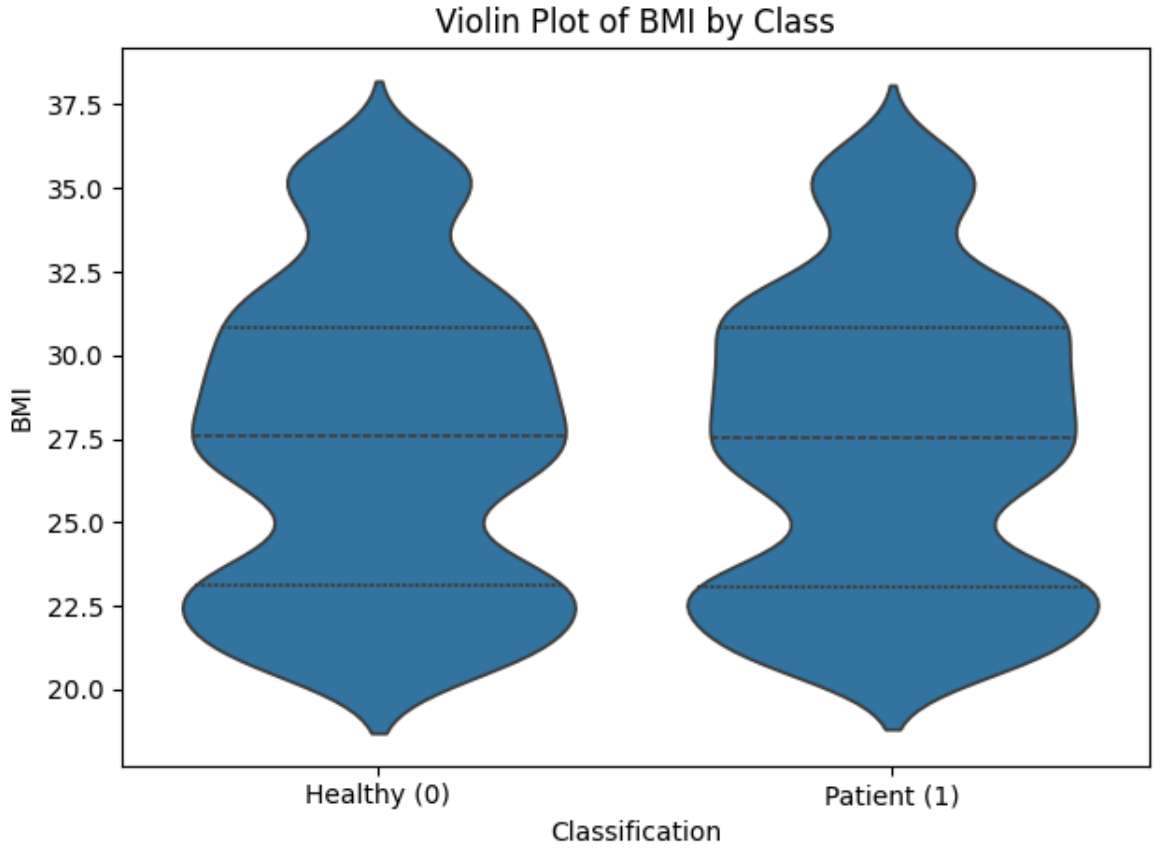

Adiponectin by Class
Adiponectin
22.5
20.0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
Healthy (0)
Patient (1)
Classification

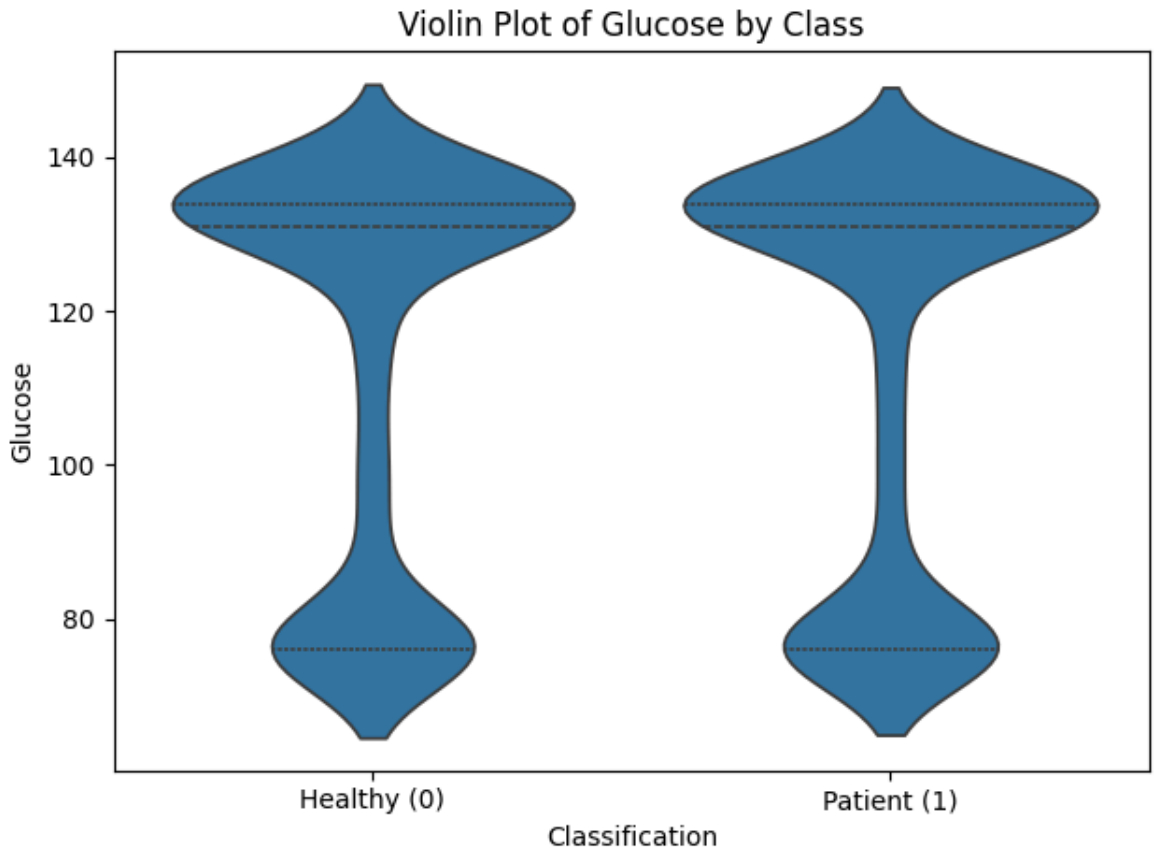

Resistin by Class
Resistin
40
35
30
25
20
15
10
5
Healthy (0)
Patient (1)
Classification

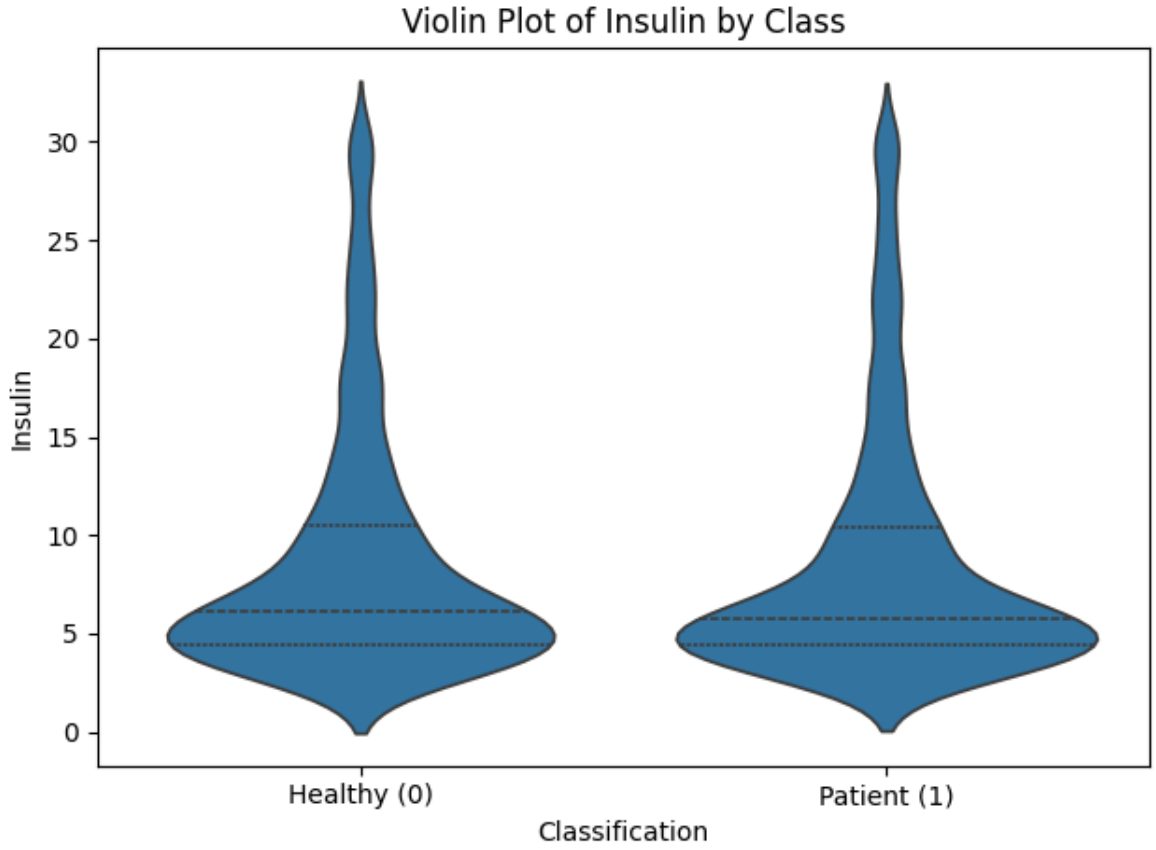


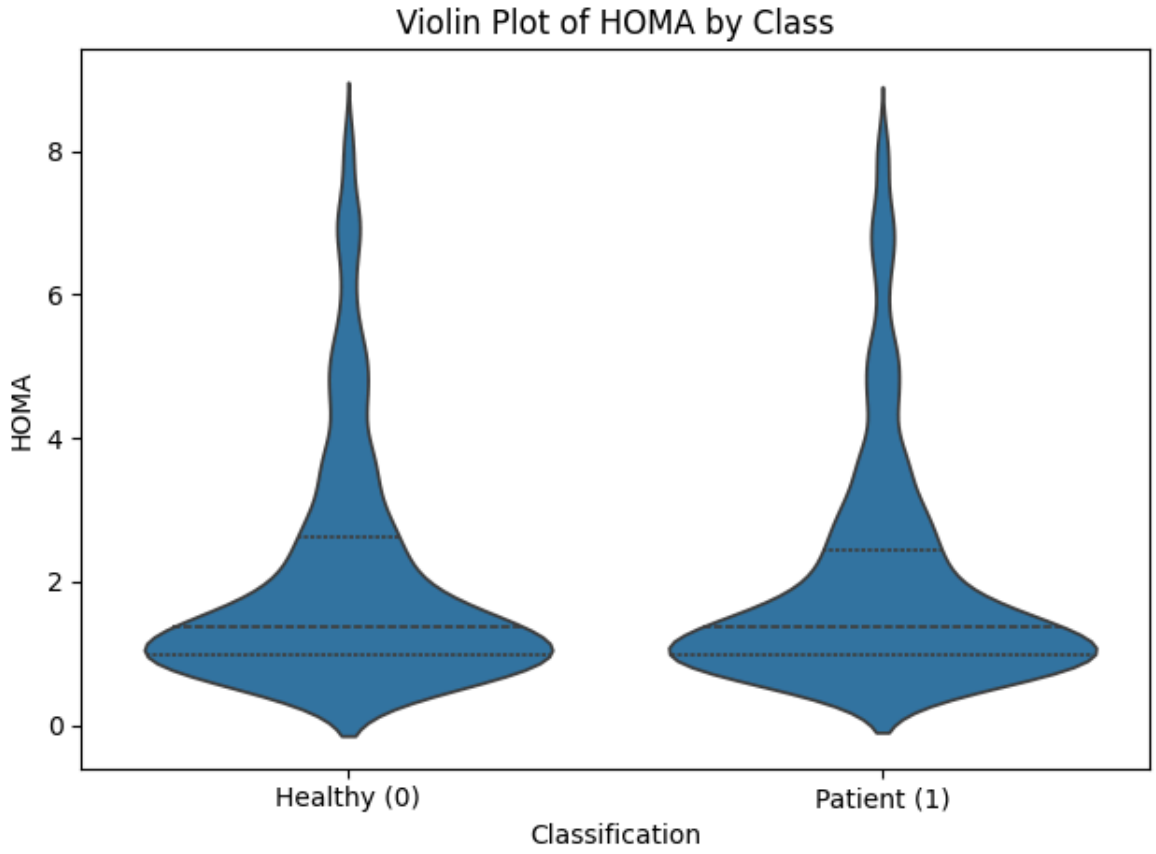
In [21]:
```
for col in feature_cols:
    fig, ax = plt.subplots()
    sns.violinplot(x=TARGET_COL, y=col, data=df, inner="quartile", ax=ax)
    ax.set_xticks([0, 1])
    ax.set_xticklabels(["Healthy (0)", "Patient (1)"])
    ax.set_title(f"Violin Plot of {col} by Class")
    plt.tight_layout()
    plt.show()
```

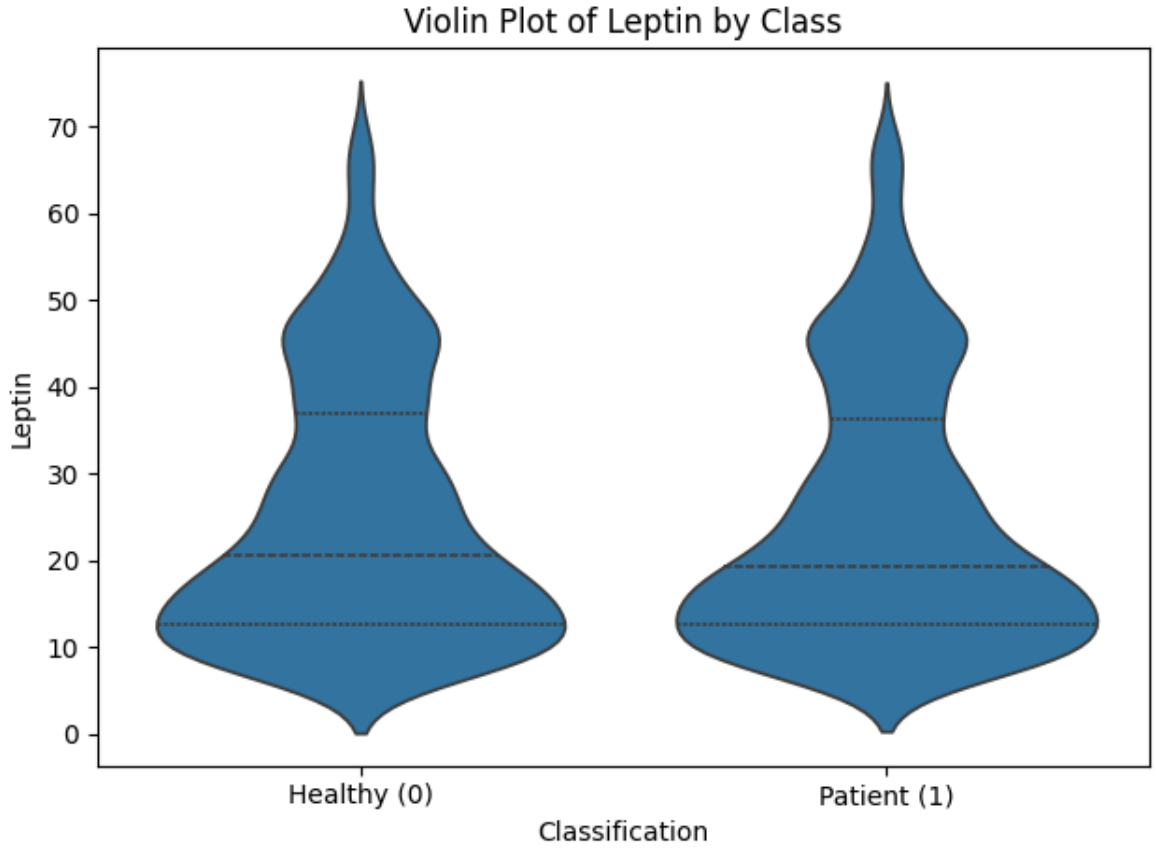

Violin Plot of Age by Class
Age
90
80
70
60
50
40
30
Healthy (0)
Patient (1)
Classification

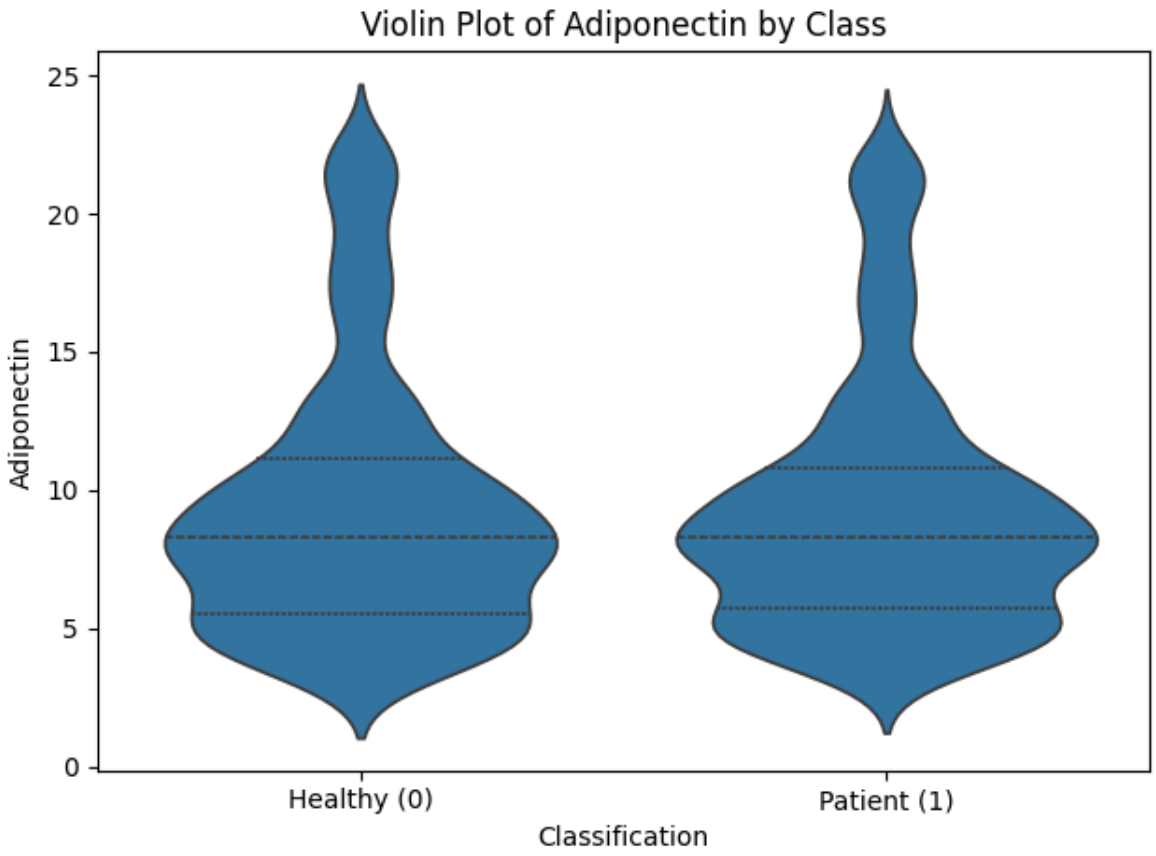

Violin Plot of BMI by Class
BMI
37.5
35.0
32.5
30.0
27.5
25.0
22.5
20.0
Healthy (0)
Patient (1)
Classification

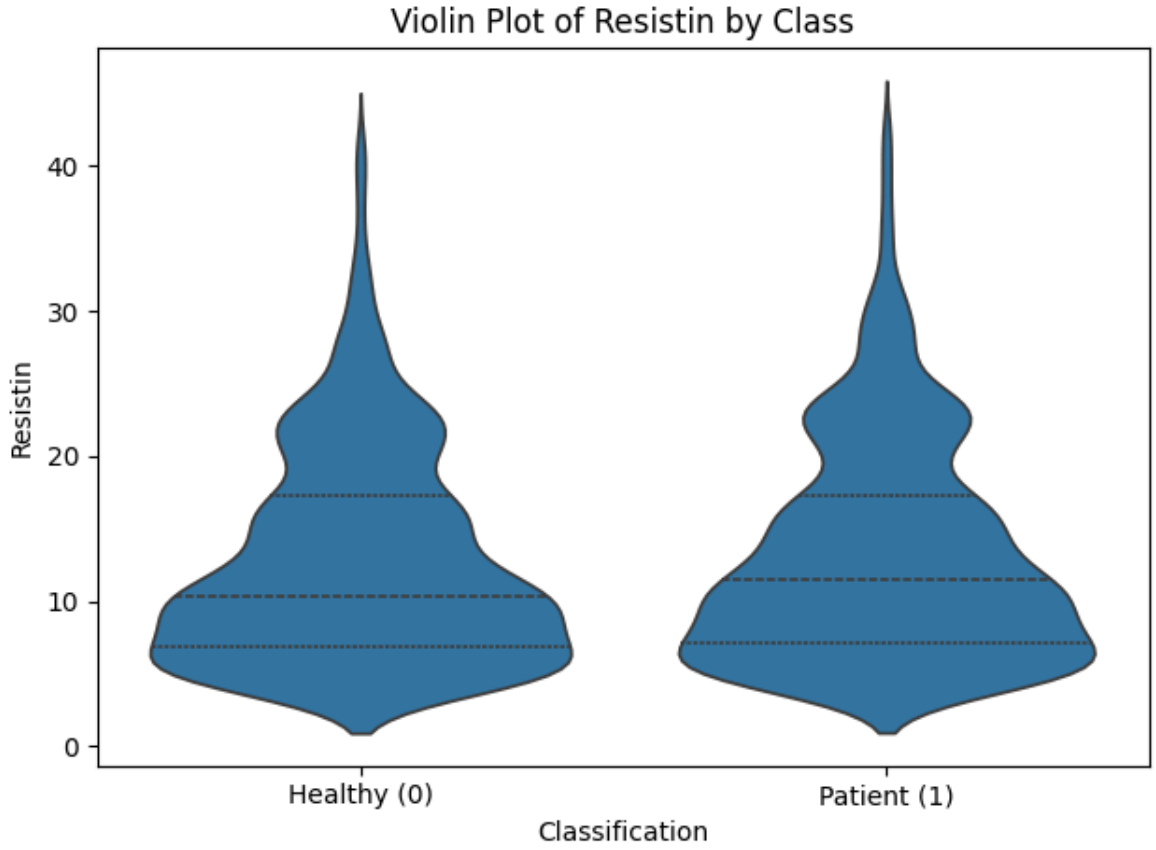

Violin Plot of Glucose by Class
Glucose
140
120
100
80
Healthy (0)
Patient (1)
Classification

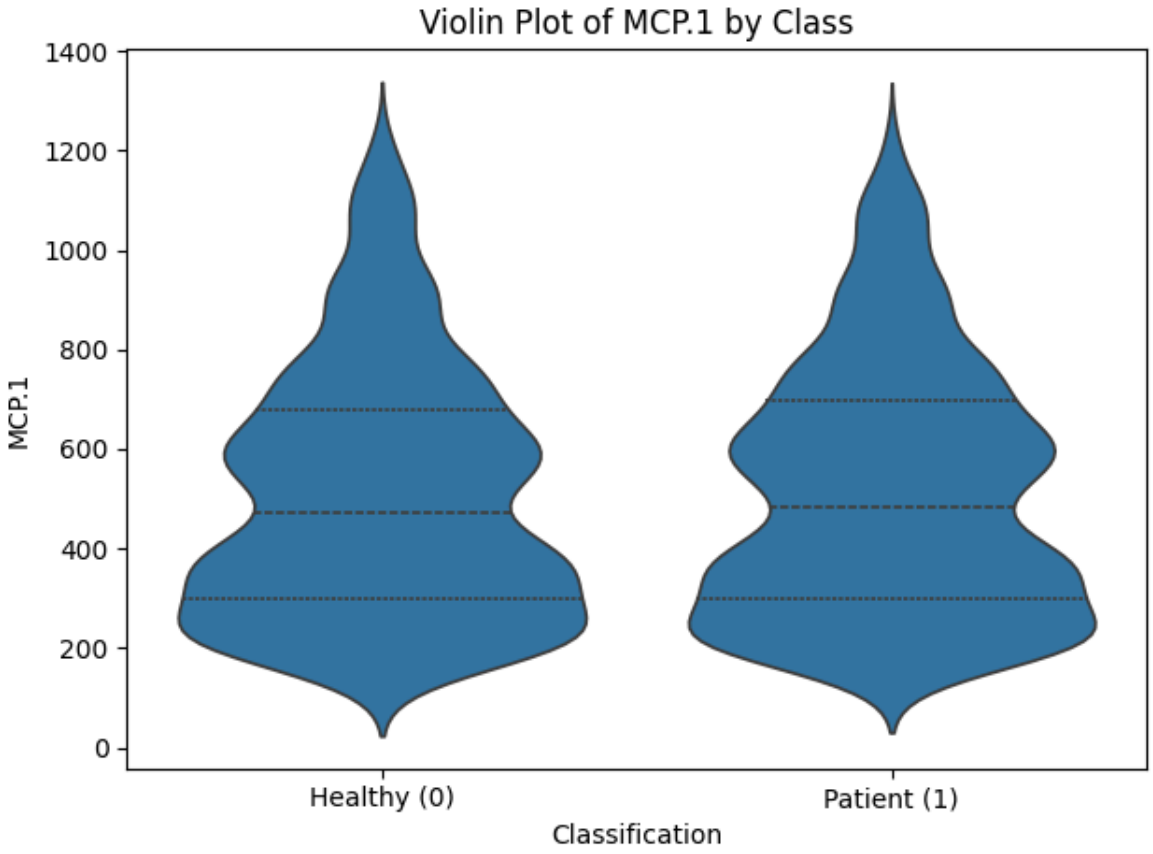

Violin Plot of Insulin by Class
Insulin
30
25
20
15
10
5
0
Healthy (0)
Patient (1)
Classification


Violin Plot of HOMA by Class
HOMA
0
2
4
6
8
Healthy (0)
Patient (1)
Classification


Violin Plot of Leptin by Class
Leptin
0
10
20
30
40
50
60
70
Healthy (0)
Patient (1)
Classification


Violin Plot of Adiponectin by Class
Adiponectin
0
5
10
15
20
25
Healthy (0)
Patient (1)
Classification


Violin Plot of Resistin by Class
Resistin
0
10
20
30
40
Healthy (0)
Patient (1)
Classification



5. Statistical Tests (t-test & Mann-Whitney U)

For each feature, both **t-tests** and **Mann-Whitney U tests** were performed.

Most distinguishable features (still weak):

Feature	Mann-Whitney p-value	Interpretation
Insulin	0.074	Weak difference; borderline significance
Resistin	0.091	Weak difference
Others	> 0.6	No meaningful difference

Conclusion

- The dataset shows **very limited statistical separation** between classes.
- Insulin and Resistin contain minor signals but not strong enough alone.

In [22]:
```
results = []

for col in feature_cols:
    # Split by class
    group0 = df[df[TARGET_COL] == 0][col]
    group1 = df[df[TARGET_COL] == 1][col]

    # Normality check (optional, small n so not super reliable)
    # Shapiro-Wilk test
    # shapiro0 = stats.shapiro(group0)
    # shapiro1 = stats.shapiro(group1)
```

```
    # Here we just do both t-test and Mann-Whitney and report them.
    t_stat, t_p = stats.ttest_ind(group0, group1, equal_var=False)
    u_stat, u_p = stats.mannwhitneyu(group0, group1, alternative="two-sided")

    results.append({
        "feature": col,
        "t_statistic": t_stat,
        "t_pvalue": t_p,
        "mannwhitney_u": u_stat,
        "mannwhitney_pvalue": u_p,
        "mean_class0": group0.mean(),
        "mean_class1": group1.mean()
    })

stats_df = pd.DataFrame(results).set_index("feature")
stats_df.sort_values("mannwhitney_pvalue", inplace=True)
stats_df
```

Out[22]:

feature	t_statistic	t_pvalue	mannwhitney_u	mannwhitney_pvalue	mean_clas
Insulin	1.064205	0.287303	2041508.0	0.074129	8.7746
Resistin	-1.665580	0.095878	1915307.5	0.090990	12.8357
Age	0.504255	0.614111	1994986.5	0.613757	56.3688
Leptin	0.311227	0.755645	1993972.0	0.633722	25.2204
BMI	0.590046	0.555195	1992751.0	0.657865	27.4682
MCP.1	-0.379380	0.704427	1961162.5	0.669250	510.4892
Glucose	0.309659	0.756837	1985751.5	0.800449	114.0173
HOMA	0.784348	0.432885	1985021.0	0.818131	2.0468
Adiponectin	0.471932	0.637003	1969372.5	0.840666	9.4039

In [ ]:

```
corr = df[feature_cols + [TARGET_COL]].corr(method="pearson")
corr
```

Out[ ]:

	Age	BMI	Glucose	Insulin	HOMA	Leptin	Adi
Age	1.000000	0.019139	0.002611	0.000742	0.024631	0.005058	
BMI	0.019139	1.000000	-0.014469	0.011574	0.012795	-0.011482	
Glucose	0.002611	-0.014469	1.000000	0.000558	-0.018232	-0.006461	
Insulin	0.000742	0.011574	0.000558	1.000000	-0.013142	0.005678	
HOMA	0.024631	0.012795	-0.018232	-0.013142	1.000000	0.006751	
Leptin	0.005058	-0.011482	-0.006461	0.005678	0.006751	1.000000	
Adiponectin	-0.013493	-0.002348	0.016363	-0.014560	0.003433	0.024054	
Resistin	-0.013438	0.005303	0.014179	0.036136	0.000272	0.014217	
MCP.1	-0.019410	-0.023389	0.001837	-0.011382	0.009965	-0.003359	
Classification	-0.007965	-0.009352	-0.004893	-0.016826	-0.012441	-0.004914	

6. Correlation Analysis

A Pearson correlation matrix and heatmap were generated.

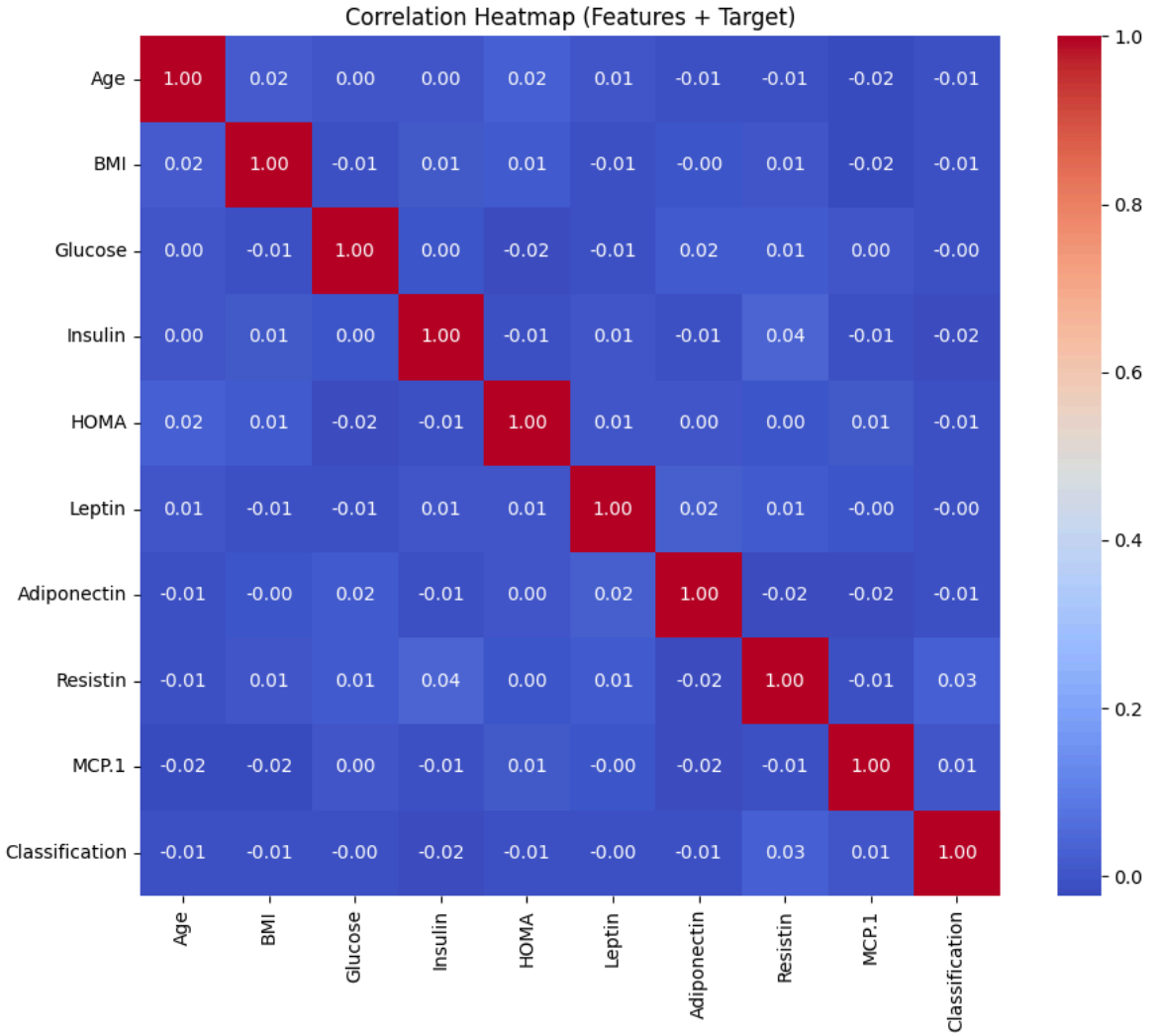
Key Findings

- **All correlations are extremely low** (|r| < 0.03 in most cases).
- No meaningful linear relationships exist between features.
- Correlation between each feature and `Classification` is close to zero.

Interpretation

The dataset lacks linear structure.
Effective models must capture **nonlinear** relationships or feature interactions.

In [24]:
```
plt.figure(figsize=(10, 8))
sns.heatmap(corr, annot=True, fmt=".2f", cmap="coolwarm", square=True)
plt.title("Correlation Heatmap (Features + Target)")
plt.tight_layout()
plt.show()
```



7. Outlier Detection

Z-score analysis flagged outliers using the threshold |z| > 3:

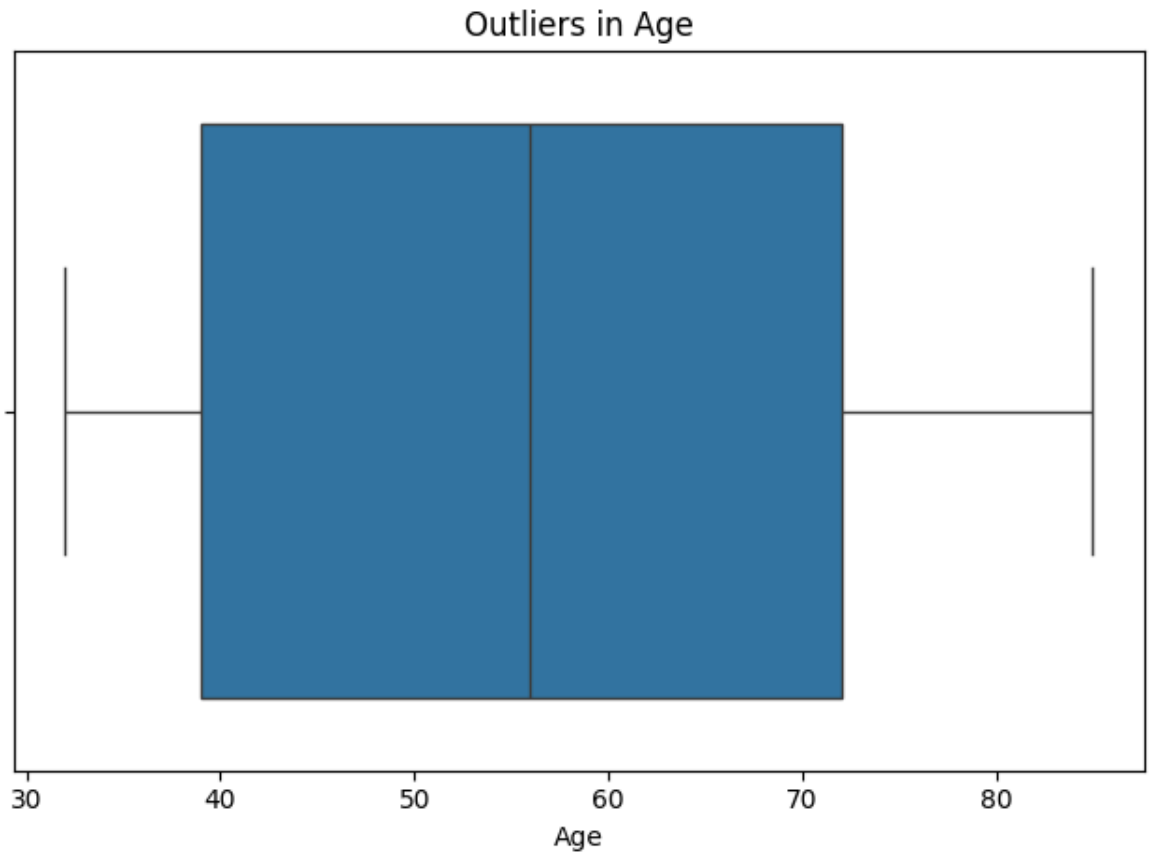
Feature	Outlier Count
Insulin	110
HOMA	112
Resistin	43
Others	0

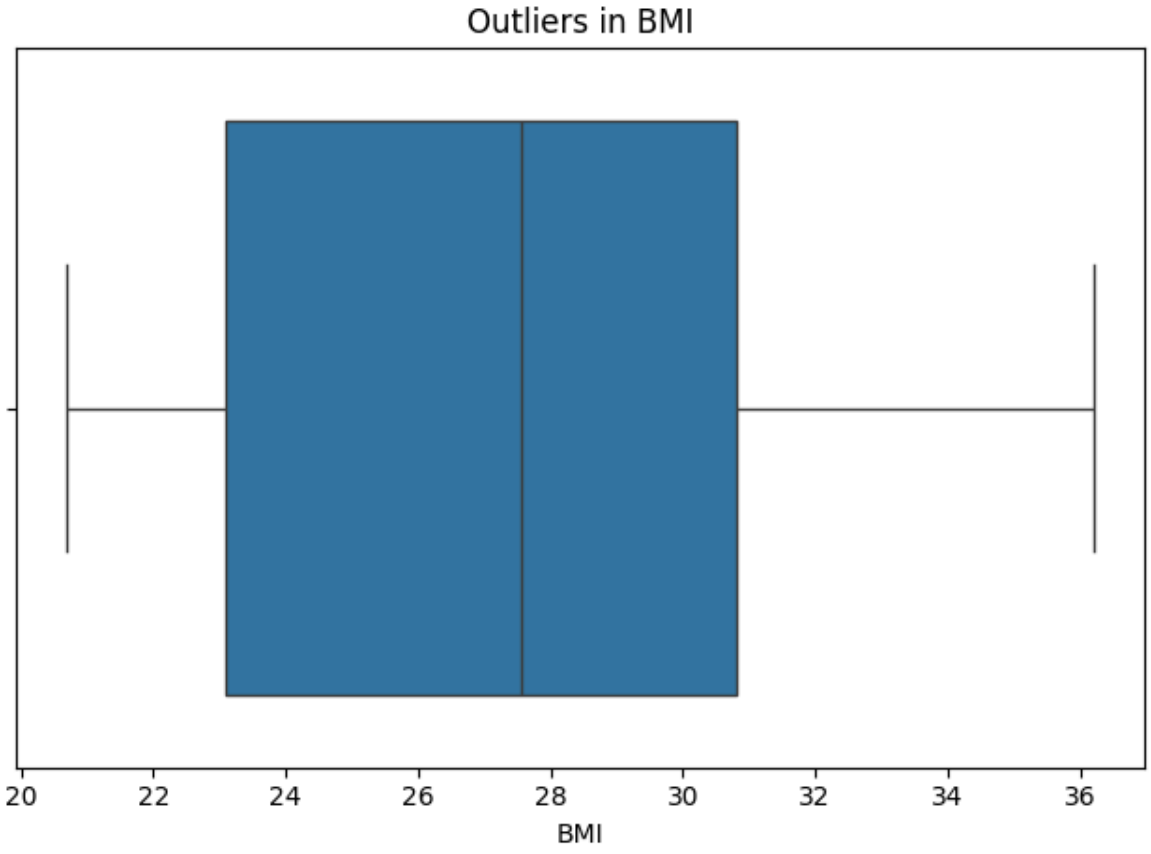
Interpretation

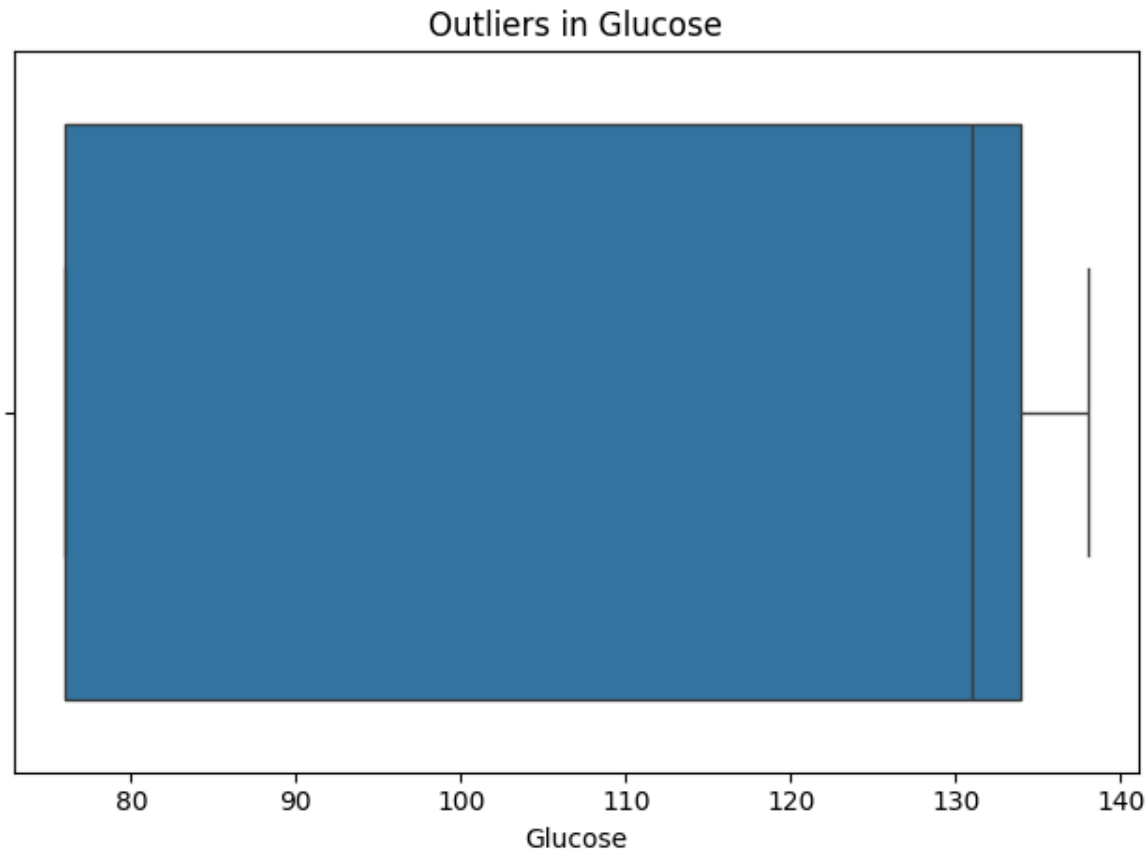
Outliers are concentrated in metabolic markers, which commonly display high biological variability.
Given the dataset size, retaining them is reasonable, but scaling becomes crucial.

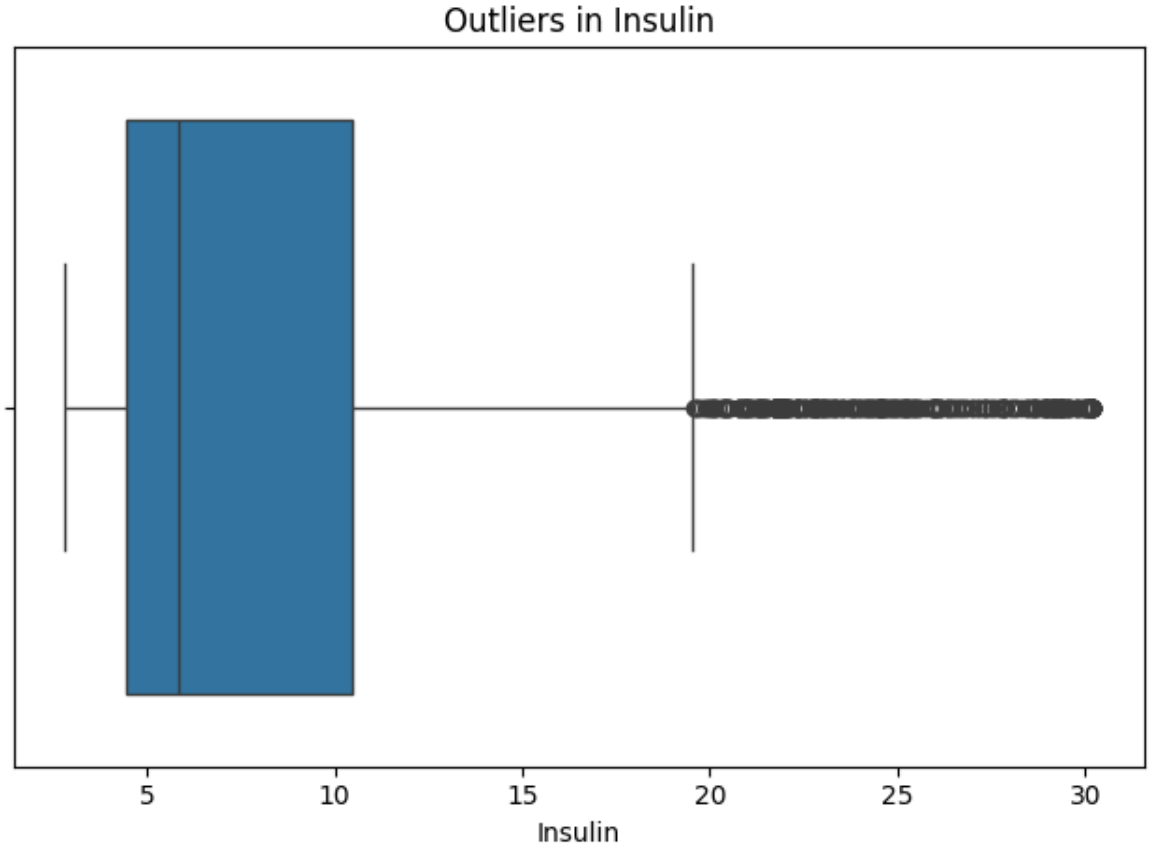
In [ ]:
```
for col in feature_cols:
    fig, ax = plt.subplots()
    sns.boxplot(x=df[col], ax=ax)
    ax.set_title(f"Outliers in {col}")
```

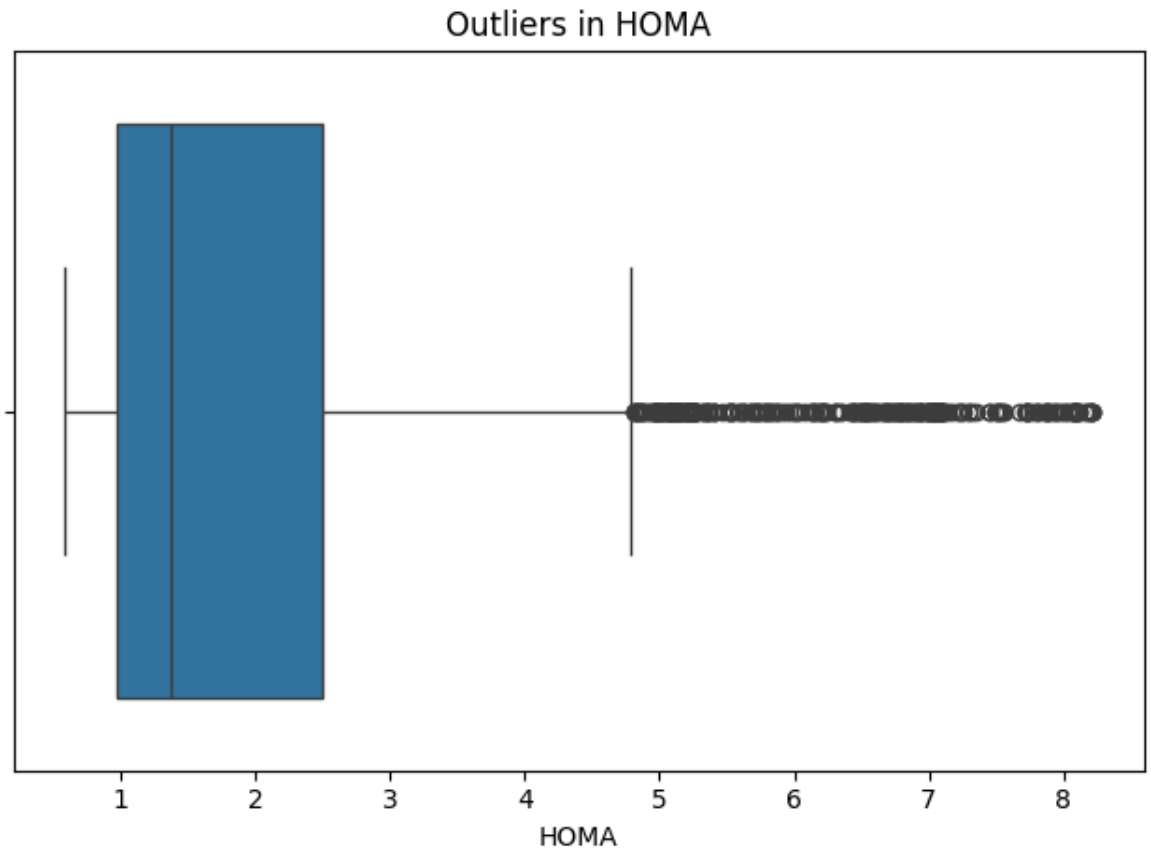
```
    plt.tight_layout()
    plt.show()
```

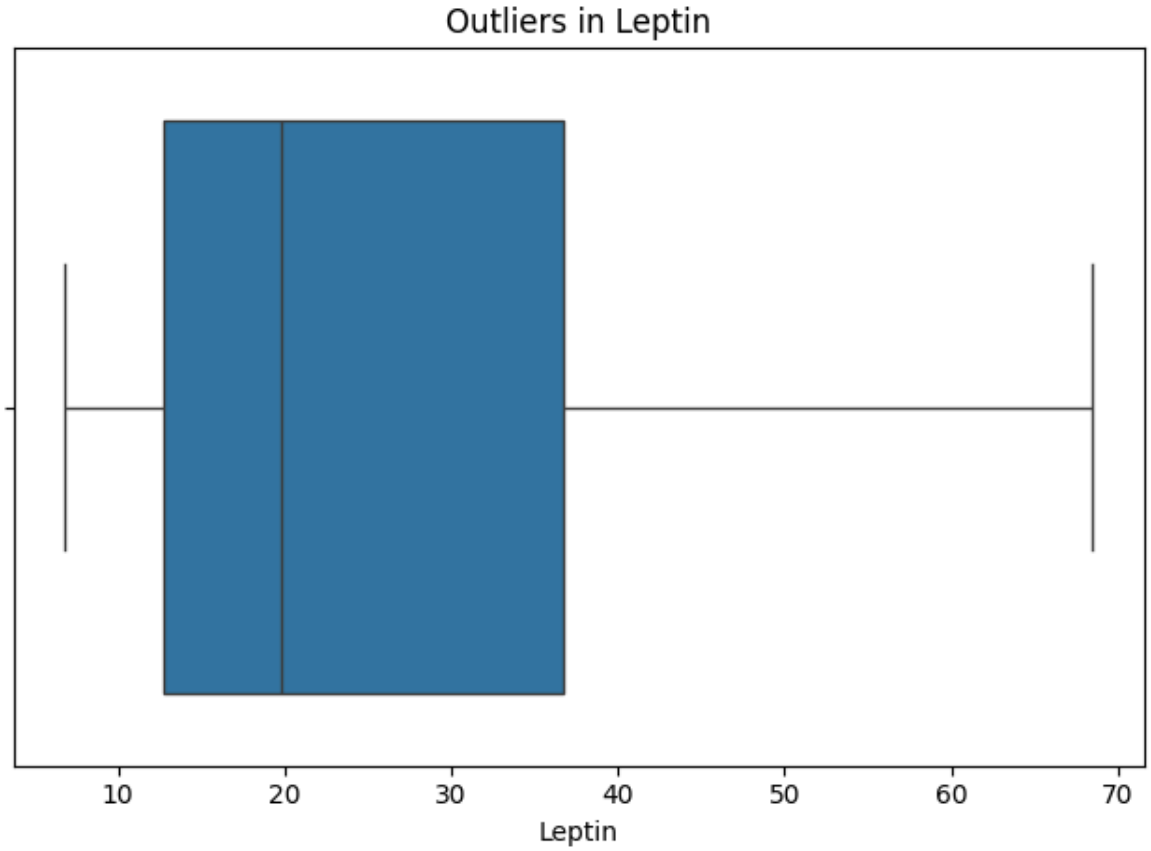


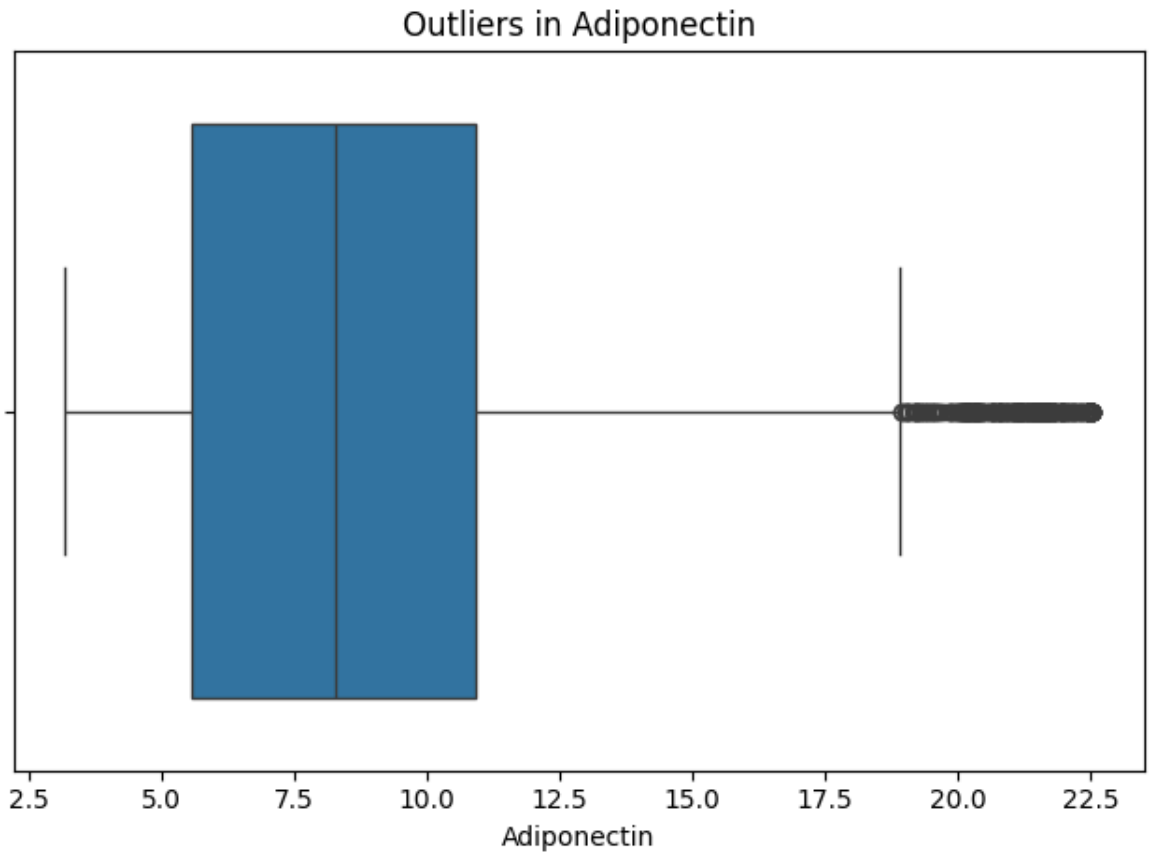


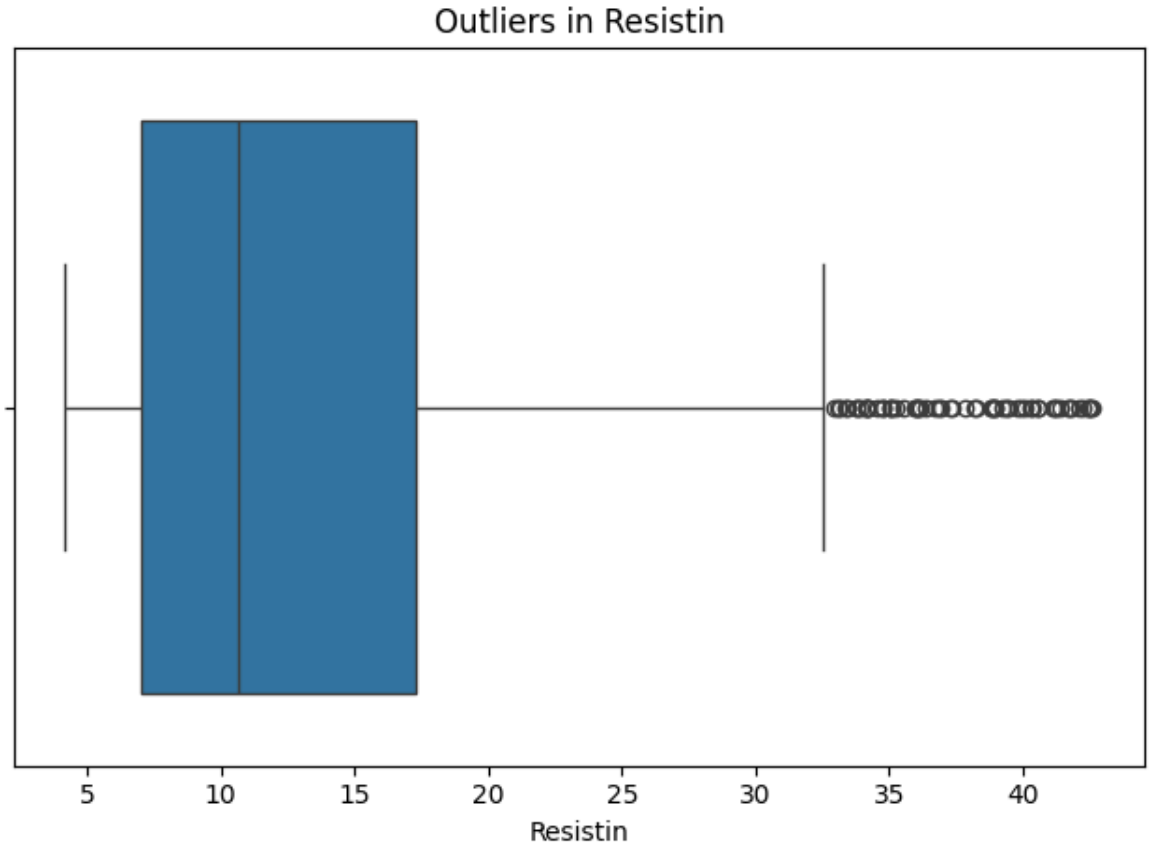

Outliers in Glucose
80
90
100
110
120
130
140
Glucose

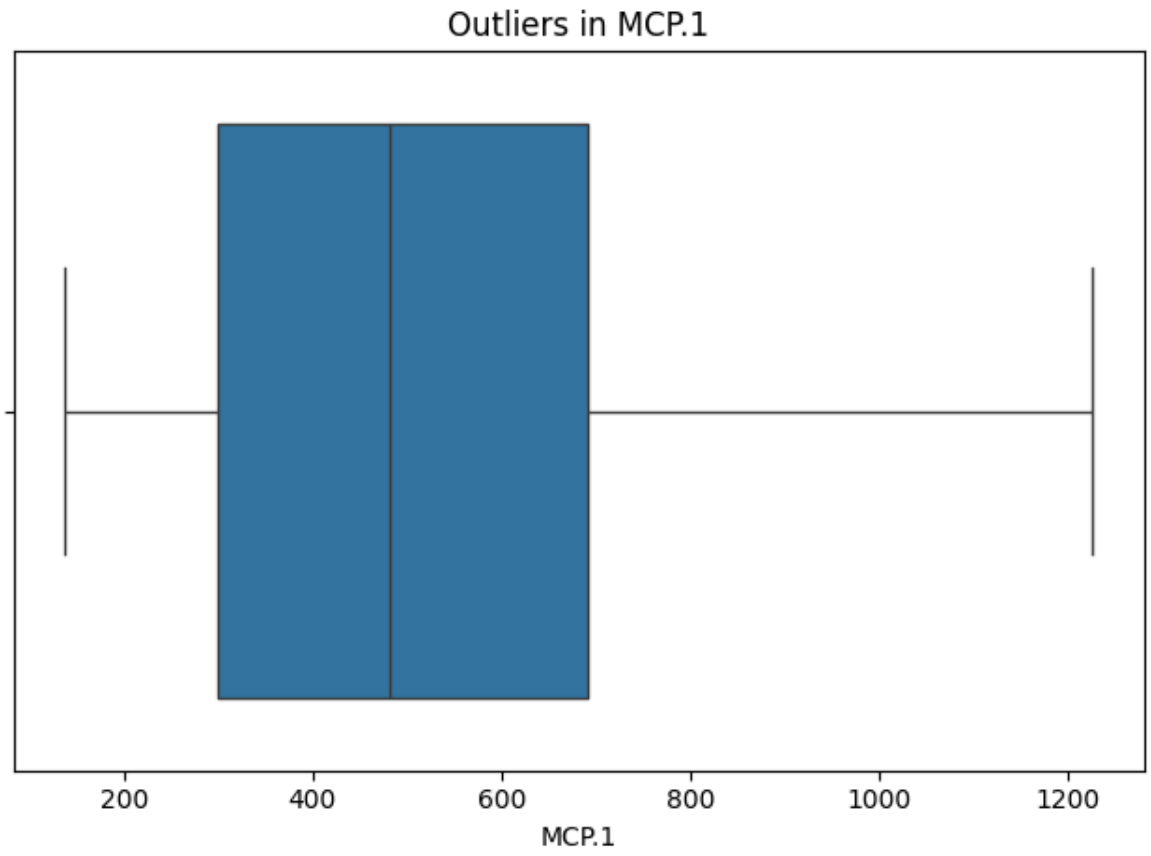

Outliers in Insulin
5
10
15
20
25
30
Insulin


Outliers in HOMA
1
2
3
4
5
6
7
8
HOMA


Outliers in Leptin
10
20
30
40
50
60
70
Leptin


Outliers in Adiponectin
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
Adiponectin


Outliers in Resistin
5
10
15
20
25
30
35
40
Resistin



In [26]:
```
z_scores = np.abs(stats.zscore(df[feature_cols]))
z_df = pd.DataFrame(z_scores, columns=feature_cols)

# Consider |z| > 3 as outlier
outlier_mask = z_df > 3
outlier_counts = outlier_mask.sum()

print("Outlier counts per feature (|z| > 3):")
outlier_counts
```

```
Outlier counts per feature (|z| > 3):
```

Out[26]:
```
Age              0
BMI              0
Glucose          0
Insulin        110
HOMA           112
Leptin           0
Adiponectin      0
Resistin        43
MCP.1            0
dtype: int64
```

8. Scaling Effects

StandardScaler was applied to all numerical features.

Results

- All features successfully standardized to ~0 mean and unit variance.
- Skewed features remain skewed (scaling does not normalize distribution).

Why scaling matters

Essential for algorithms such as:

- Logistic Regression
- SVM
- kNN
- Neural Networks

Particularly important because the Coimbra dataset contains **wide variance differences** across metabolic markers.

In [27]:
```
scaler = StandardScaler()
scaled_features = scaler.fit_transform(df[feature_cols])
scaled_df = pd.DataFrame(scaled_features, columns=feature_cols)

print("Original feature summary:")
display(df[feature_cols].describe().T)

print("\nScaled feature summary (mean ~0, std ~1):")
display(scaled_df.describe().T)
```

```
Original feature summary:
```

	count	mean	std	min	25%	50%	
Age	4000.0	56.210750	17.809650	32.000000	39.000000	56.000000	7
BMI	4000.0	27.422280	4.413884	20.690751	23.079053	27.558485	3
Glucose	4000.0	113.876500	25.837795	76.000000	76.000000	131.000000	13
Insulin	4000.0	8.654001	6.435160	2.821000	4.421750	5.818000	1
HOMA	4000.0	2.024332	1.625638	0.590033	0.970090	1.373842	
Leptin	4000.0	25.137737	15.096446	6.831900	12.712750	19.805050	3
Adiponectin	4000.0	9.364896	4.674244	3.192272	5.580210	8.286938	1
Resistin	4000.0	13.053667	7.454424	4.190320	7.022095	10.692780	1
MCP.1	4000.0	512.183456	253.279015	137.488000	299.665000	482.308000	69

```
Scaled feature summary (mean ~0, std ~1):
```

	count	mean	std	min	25%	50%	75%
Age	4000.0	1.523226e-16	1.000125	-1.359587	-0.966493	-0.011835	0.88666
BMI	4000.0	-3.144152e-16	1.000125	-1.525271	-0.984115	0.030862	0.76872
Glucose	4000.0	2.664535e-16	1.000125	-1.466117	-1.466117	0.662814	0.77893
Insulin	4000.0	-1.509903e-16	1.000125	-0.906540	-0.657758	-0.440759	0.28165
HOMA	4000.0	6.572520e-17	1.000125	-0.882410	-0.648591	-0.400194	0.29434
Leptin	4000.0	3.197442e-17	1.000125	-1.212744	-0.823143	-0.353285	0.76401
Adiponectin	4000.0	1.616485e-16	1.000125	-1.320726	-0.809791	-0.230645	0.33237
Resistin	4000.0	-6.394885e-17	1.000125	-1.189154	-0.809228	-0.316749	0.56900
MCP.1	4000.0	3.126388e-16	1.000125	-1.479563	-0.839173	-0.117969	0.70732

9. Feature Importance (Mutual Information & ANOVA F-test)

Mutual Information Rankings

1. **HOMA** (0.017)
2. **Resistin** (0.006)
3. **Glucose** (0.004)
4. **Adiponectin** (0.003)
5. Others: 0.0

ANOVA F-test Rankings

- **Resistin**: F = 2.75, p ≈ 0.097
- Insulin: F ≈ 1.13
- Others: F < 1

Interpretation

- No feature demonstrates strong predictive value individually.
- HOMA and Resistin contain the most information, but signals are weak.
- Models must rely on **feature combinations** and **nonlinear effects**.

In [28]:
```
X = df[feature_cols].values
y = df[TARGET_COL].values

mi = mutual_info_classif(X, y, random_state=42)

mi_df = pd.DataFrame({
    "feature": feature_cols,
    "mutual_information": mi
}).sort_values("mutual_information", ascending=False).set_index("feature")

mi_df
```

Out[28]:

feature	mutual_information
HOMA	0.017155
Resistin	0.006323
Glucose	0.004276
Adiponectin	0.003197
Age	0.000000
BMI	0.000000
Insulin	0.000000
Leptin	0.000000
MCP.1	0.000000

In [29]:
```
f_vals, f_pvals = f_classif(X, y)

f_df = pd.DataFrame({
    "feature": feature_cols,
    "f_value": f_vals,
    "p_value": f_pvals
}).sort_values("f_value", ascending=False).set_index("feature")

f_df
```

Out[29]:

feature	f_value	p_value
Resistin	2.753596	0.097114
Insulin	1.132220	0.287367
HOMA	0.618858	0.431519
BMI	0.349664	0.554337
Age	0.253670	0.614530
Adiponectin	0.224822	0.635416
MCP.1	0.144050	0.704308
Leptin	0.096552	0.756023
Glucose	0.095709	0.757057

Final Summary

Key Findings

1. Feature distributions show strong skewness in Insulin, HOMA, Resistin.
2. Healthy vs Patient groups have heavily overlapping distributions.
3. Statistical tests show weak class separation.
4. Correlations are extremely low across all feature pairs.
5. Outliers exist mainly in metabolic markers.
6. Scaling is required due to differing magnitude ranges.
7. Feature importance scores are very small, indicating weak individual predictors.

Overall Conclusion

The Coimbra dataset does **not** contain strong linear signals in single features. Successful classification will require:

- Nonlinear models (Random Forest, Gradient Boosting, SVM RBF)
- Use of interaction terms
- Combined feature effects
- Robust preprocessing and scaling

This dataset is best modeled using **multivariate, nonlinear techniques** rather than relying on any one biomarker alone.