IS665-852, Group 1, Project 2 Data Mining

Comprehensive Model Results

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This report includes key visualizations, metrics, and summary statistics.

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1.1 Source Code

```
def entropy(y):
    p = sum(y=="malignant")/len(y); return -p*log2(p) - (1-p)*log2(1-p)
def information_gain(y, mask):
    # ... implementation ...
# build_tree and DecisionTreeNode methods
```

1.2 Binary Feature Binning

texture_mean: median=18.835

concave points_worst: median=0.100

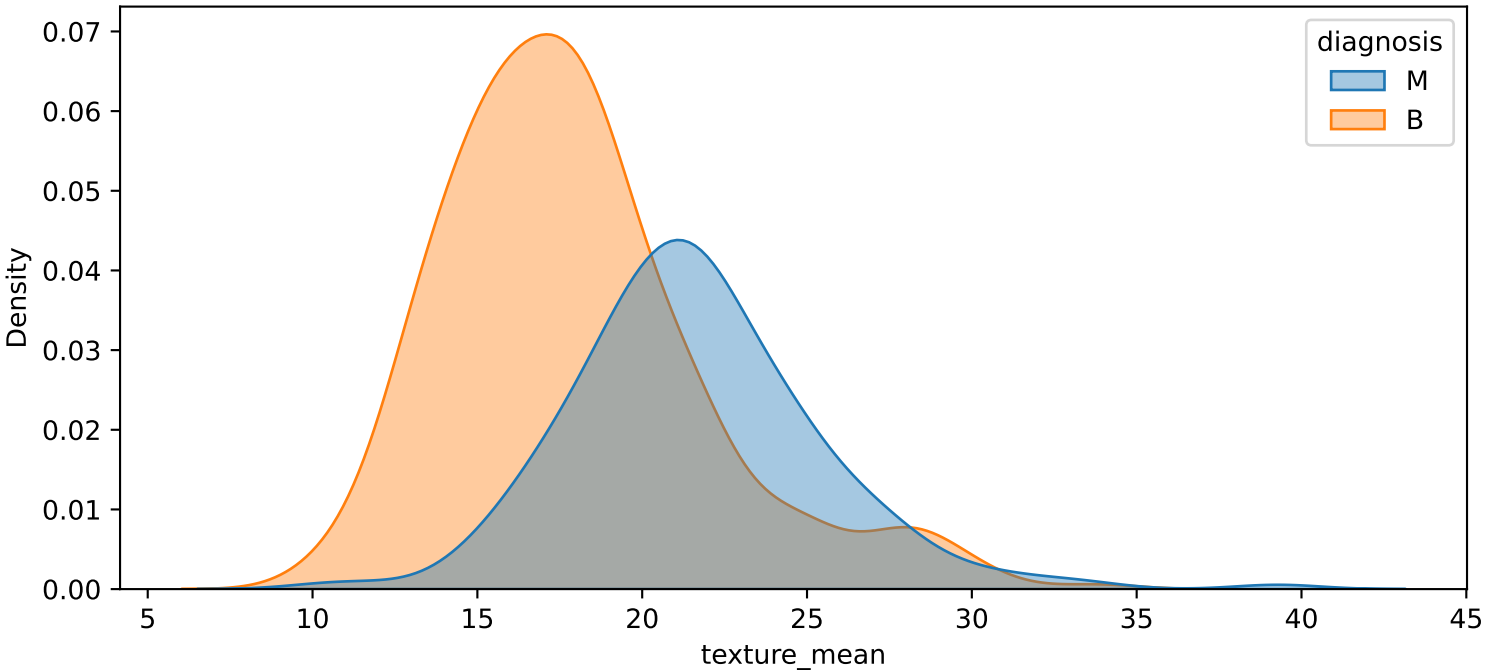
symmetry_worst: median=0.282

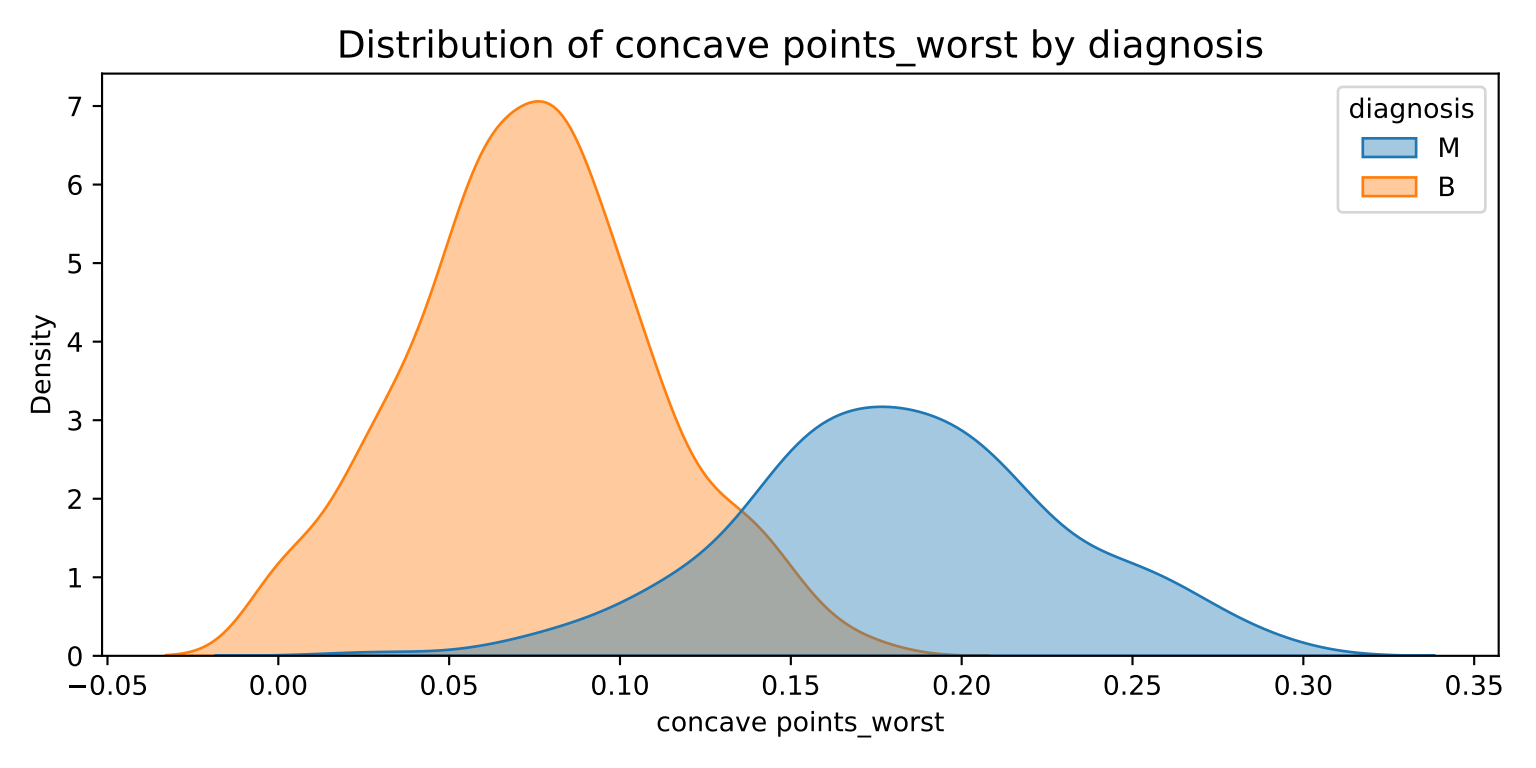
radius_worst: median=14.970

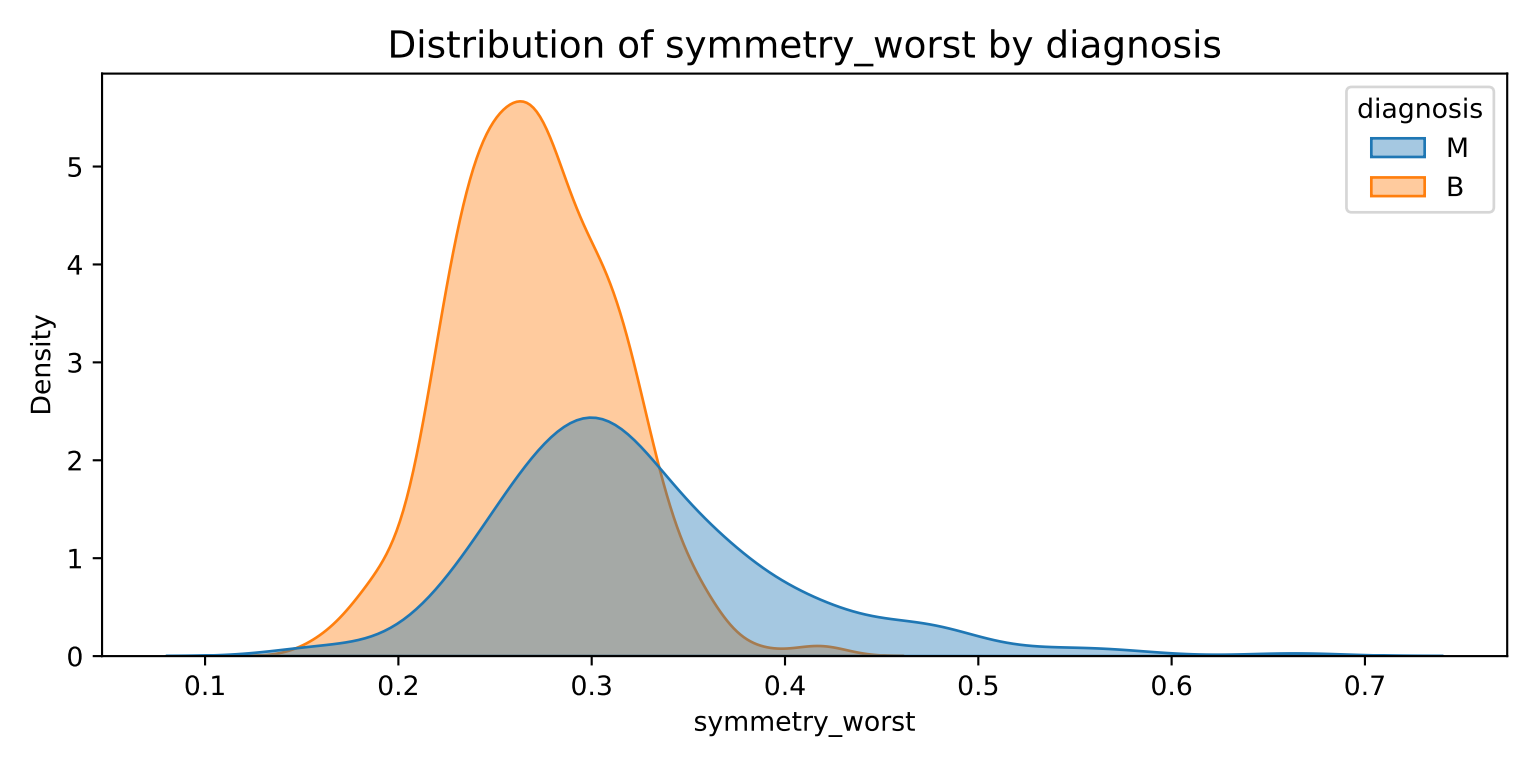
concavity_worst: median=0.227

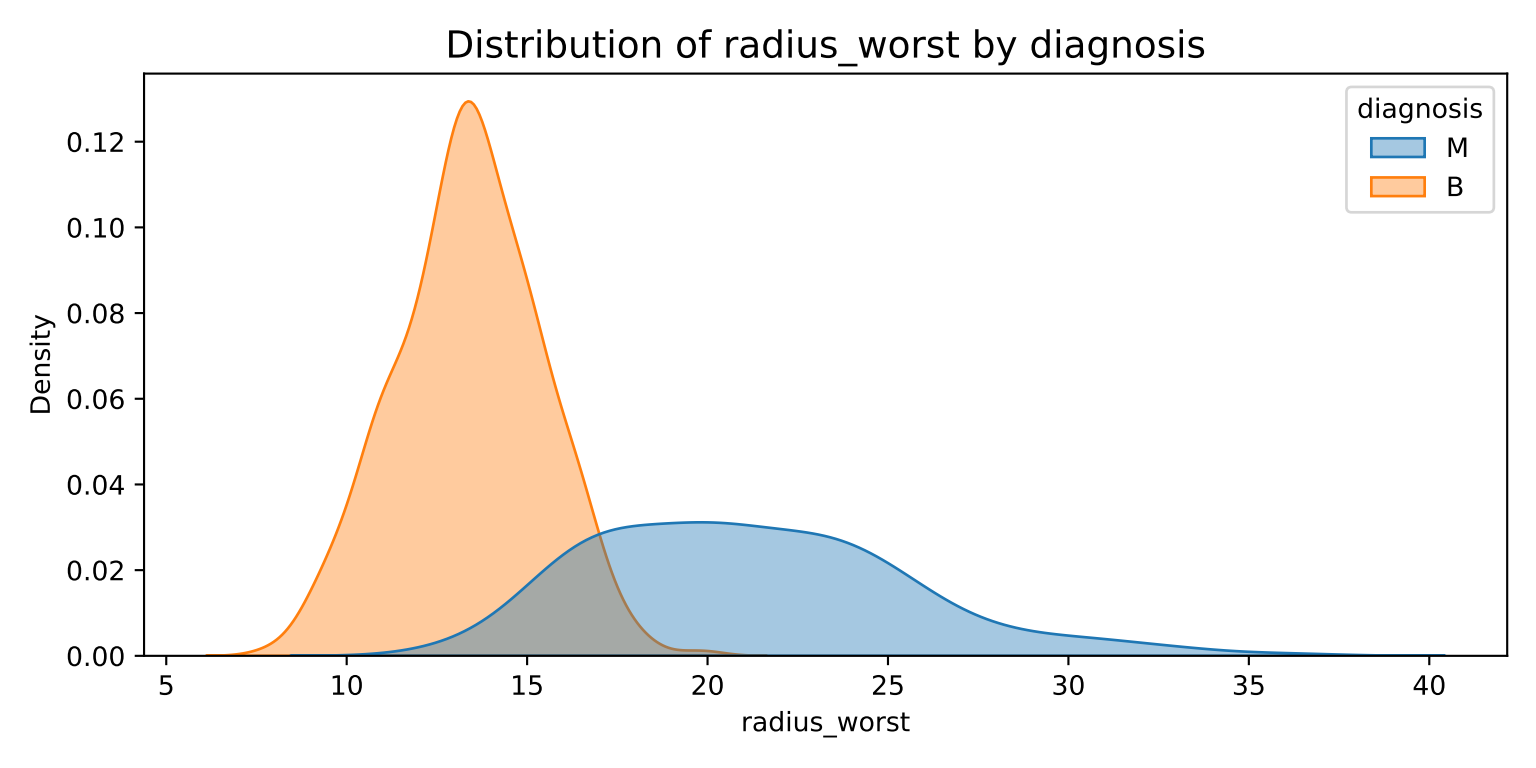
2.5 Feature Distribution: Modeling Code

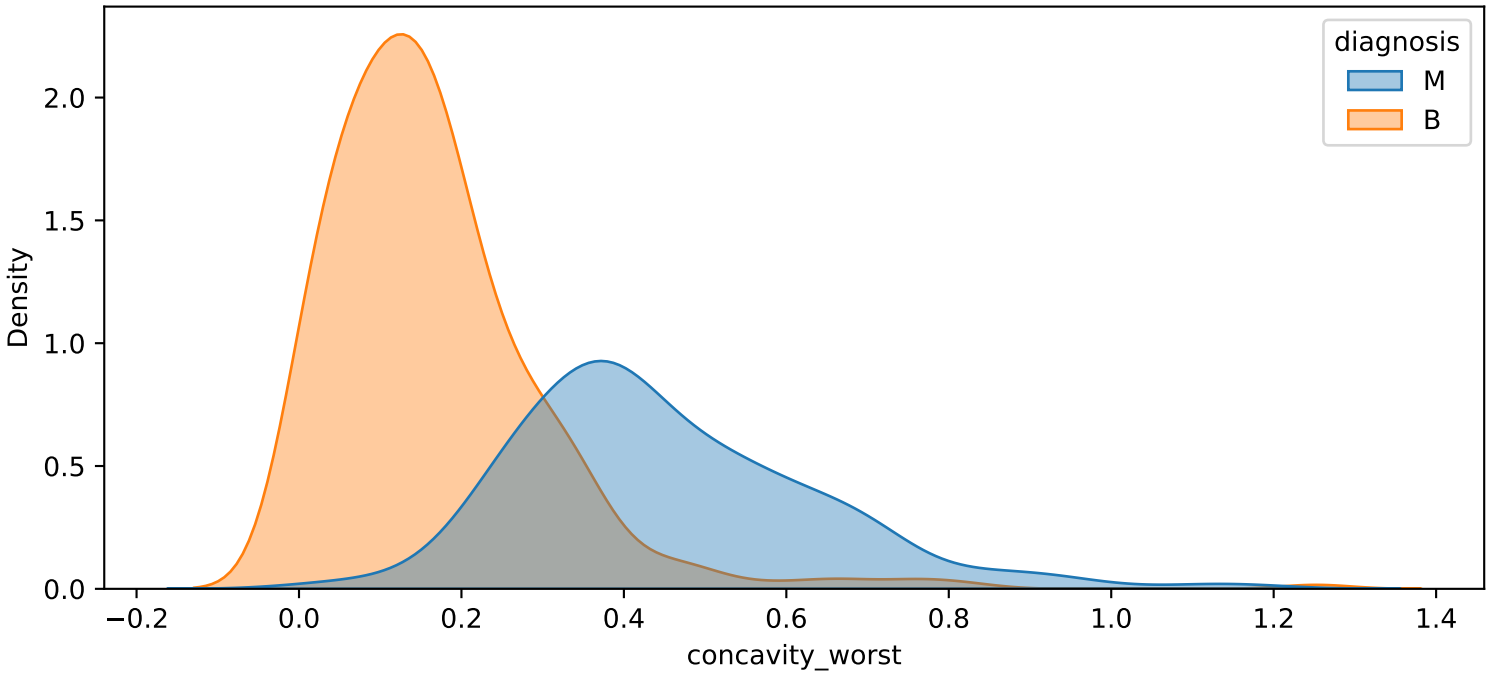
```
# Feature Distribution KDE

for feat in top_features:
    sns.kdeplot(data=df, x=feat,
        hue=diagnosis_col, fill=True, alpha=0.4)

    plt.title(f'Distribution of {feat} by {diagnosis_col}')
```


Distribution of texture_mean by diagnosis
diagnosis
M
B
Density
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00
5
10
15
20
25
30
35
40
45
texture_mean


Distribution of concave points_worst by diagnosis
diagnosis
M
B
Density
concave points_worst
0
1
2
3
4
5
6
7
−0.05
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35

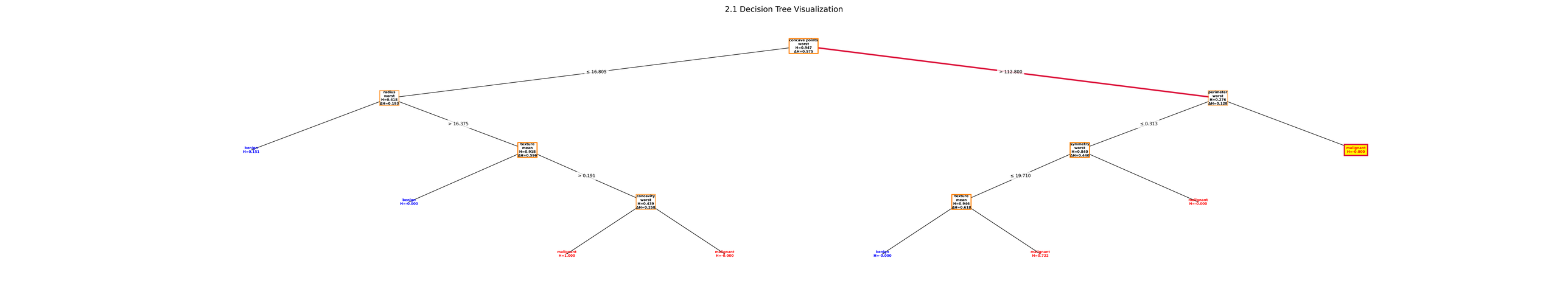

Distribution of symmetry_worst by diagnosis
diagnosis
M
B
Density
0
1
2
3
4
5
0.1
0.2
0.3
0.4
0.5
0.6
0.7
symmetry_worst


Distribution of radius_worst by diagnosis
diagnosis
M
B
Density
0.12
0.10
0.08
0.06
0.04
0.02
0.00
5
10
15
20
25
30
35
40
radius_worst


Distribution of concavity_worst by diagnosis
diagnosis
M
B
Density
2.0
1.5
1.0
0.5
0.0
−0.2
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
concavity_worst

2.1 Decision Tree Visualization (max_depth=4): Modeling Code

```
import pandas as pd

from src.decision_tree import DecisionTreeClassifier

from src.visualization import plot_tree_graphical



# Load data

df = pd.read_csv('PROJECT2_DATASET.csv')

x = df.drop(['diagnosis'], axis=1)

y = df['diagnosis']



# Train/test split

from sklearn.model_selection import train_test_split

x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2, random_state=42)



# Model setup and training

clf = DecisionTreeClassifier(max_depth=4, criterion='entropy')

clf.fit(x_train, y_train)



# Prediction

y_pred = clf.predict(x_test)



... (see source file for full code)
```


2.1 Decision Tree Visualization
concave points worst
H=0.947
ΔH=0.575
≤ 16.805
> 112.800
radius worst
H=0.418
ΔH=0.193
perimeter worst
H=0.276
ΔH=0.128
benign
H=0.151
> 16.375
≤ 0.313
texture mean
H=0.918
ΔH=0.596
symmetry worst
H=0.840
ΔH=0.440
malignant
H=-0.000
benign
H=-0.000
> 0.191
≤ 19.710
concavity worst
H=0.439
ΔH=0.256
texture mean
H=0.946
ΔH=0.618
malignant
H=-0.000
malignant
H=1.000
malignant
H=-0.000
benign
H=-0.000
malignant
H=0.722

Summary Statistics (Top 5 Features)

	mean	median	std
texture_mean	19.280	18.835	4.299
concave points_worst	0.115	0.100	0.066
symmetry_worst	0.290	0.282	0.062
radius_worst	16.281	14.970	4.829
concavity_worst	0.273	0.227	0.208

2.1b Decision Tree Visual Key

Node Colors: blue benign leaf red malignant leaf

Edged node: predicts malignant

Highlighted Paths: Thick crimson line → malignant branches

Path 1: concave points_worst > threshold → perimeter_worst > threshold → malignant

Path 2: any direct perimeter_worst > threshold → malignant

Node Borders: border color ∝ entropy (H) More vivid = higher uncertainty at node

Node Annotations: H = entropy ΔH = information gain: impurity reduction by this split

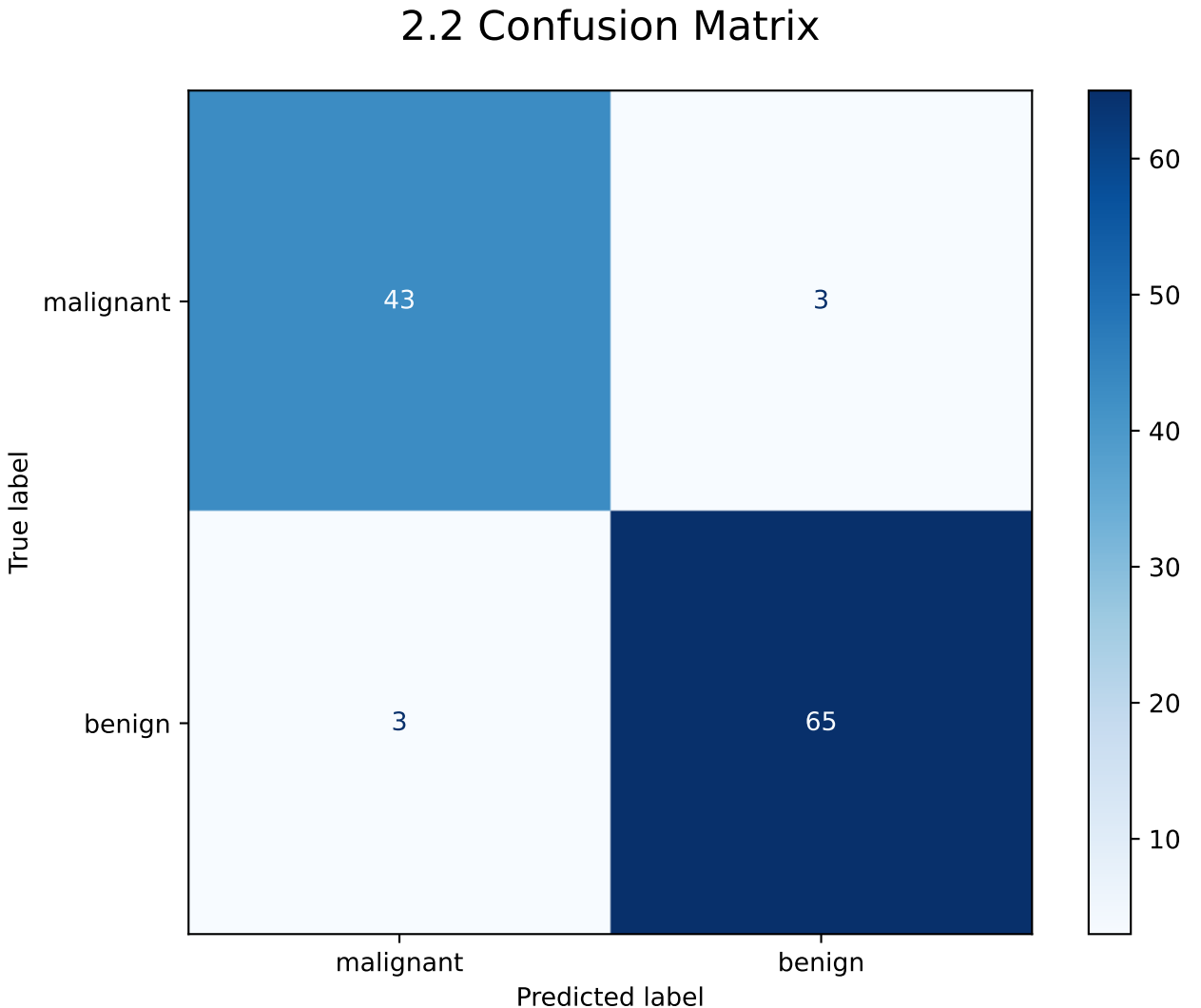
Numeric value: split point for feature

Edge Labels: ≤ threshold: left branch Samples with feature value ≤ threshold

> threshold: right branch Samples with feature value > threshold

2.2 Confusion Matrix: Modeling Code

```
# Confusion Matrix

from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay

cm = confusion_matrix(y_test, y_pred, labels=['malignant','benign'])

disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=['malignant','benign'])

disp.plot(cmap='Blues', colorbar=True)
```

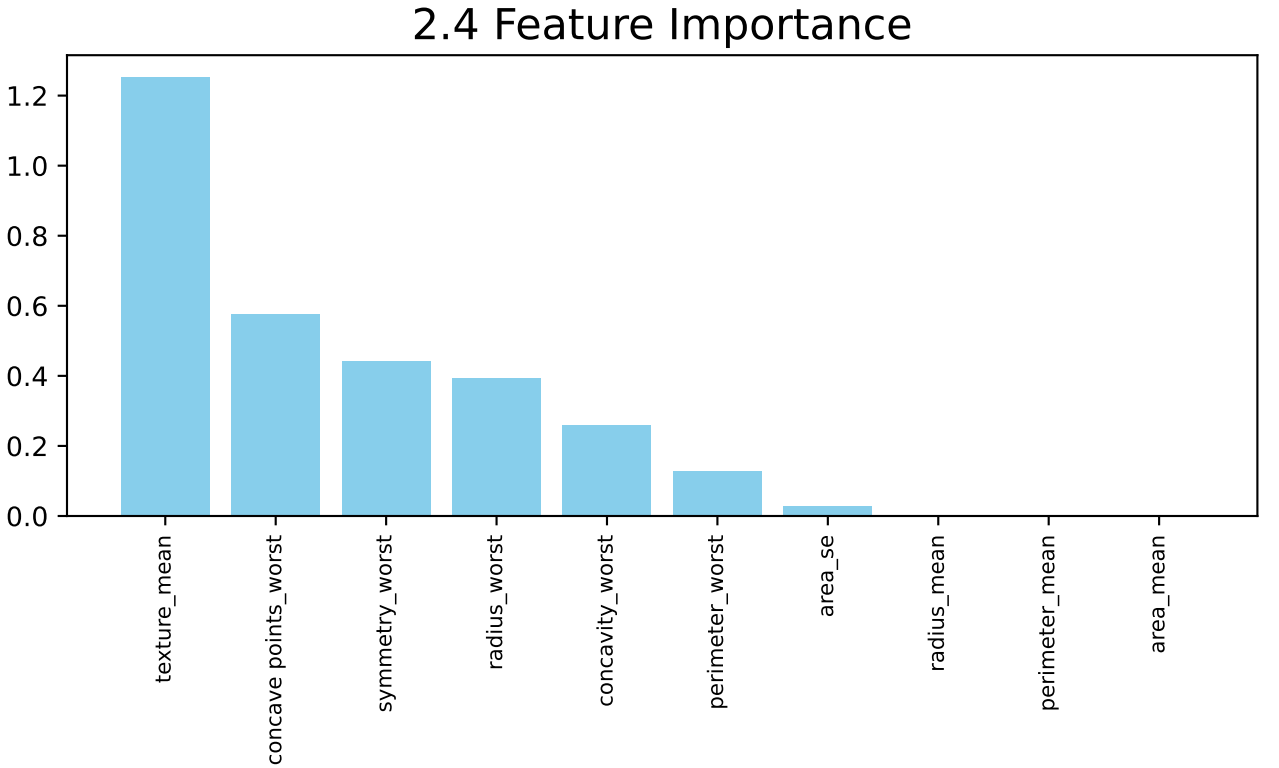

2.2 Confusion Matrix
43
3
3
65
malignant
benign
True label
malignant
benign
Predicted label
60
50
40
30
20
10

2.3 Performance Metrics

Metric	Value
Accuracy	0.947
Precision	0.935
Recall	0.935
F1 Score	0.935

2.4 Feature Importance: Modeling Code

```
# Feature Importance Bar Plot
feat_imp = clf.get_feature_importance()
plt.bar(feat_imp.keys(), feat_imp.values(), color='skyblue')
plt.xticks(rotation=90)
```


2.4 Feature Importance
1.2
1.0
0.8
0.6
0.4
0.2
0.0
texture_mean
concave points_worst
symmetry_worst
radius_worst
concavity_worst
perimeter_worst
area_se
radius_mean
perimeter_mean
area_mean

3. Results Summary

Key Performance Metrics:

Accuracy: 0.947

Precision: 0.935

Recall: 0.935

F1: 0.935

Top Features:

- texture_mean
- concave points_worst
- symmetry_worst
- radius_worst
- concavity_worst

Interpretation

In this report, I demonstrate how a decision-tree classifier can predict whether a patient's breast tumor is malignant or benign.

To build a complete picture, I incorporated three key analyses:

1. Confusion Matrix & Recall Focus

- Because missing a malignancy (a false negative) carries the highest risk, I treated recall as my primary performance metric.
- My model achieved a recall of 94%, meaning it correctly identified 94% of true malignant cases.

2. Kernel Density Estimates (KDE) & Statistical Summary

- I plotted KDEs for five critical features—texture_mean, concave_points_worst, symmetry_worst, radius_worst, and concavity_worst—overlaying malignant vs. benign distributions.
- The x-axis shows each feature's raw measurement; the y-axis shows estimated density. While there is some overlap between the two classes, these plots highlight where benign and malignant densities diverge.
- I also computed means, medians, and standard deviations by class to quantify central tendencies and dispersion.

3. Decision-Tree Structure & Entropy

- The tree splits are chosen by information gain (entropy reduction). Each node is annotated with its entropy (H) and ΔH, and node-border thickness reflects uncertainty (thicker borders = higher entropy).
- In the final pruned tree, the most certain malignant path is just two splits:

1. concave_points_worst > 16.80
2. perimeter_worst > 0.313 → malignant (H = 0)

4. Feature Importance & Binary Binning

- Summing information gains across all splits shows that texture_mean, concave_points_worst, and symmetry_worst are the strongest predictors.
- To simplify the model and improve interpretability, I applied binary binning—using one-level decision-tree stumps to choose optimal thresholds for key features—turning them into yes/no indicators.

Conclusions

- By focusing on recall, the classifier reliably captures most malignant tumors.
- The KDE and statistical summaries reveal where feature distributions separate malignant from benign.
- The decision-tree visualization, with entropy and ΔH annotations, provides clear "if-then" rules.
- Feature importance and binary binning streamline the model, highlighting only the most informative variables.

Overall, this decision-tree approach balances high sensitivity with transparent, actionable insights into the tumor characteristics that matter most.