In [ ]:
```
# Breast Cancer Wisconsin (Original) - Exploratory Data Analysis

This notebook performs exploratory data analysis (EDA) on the cleaned
Breast Cancer Wisconsin (Original) dataset. The main goals are:

- To understand the distribution of each cytological feature.
- To analyze how each feature relates to the malignancy label.
- To visualize the results using correlation plots and boxplots.
- To train a simple Random Forest classifier and inspect feature importances.
```

In [3]:
```
# Import basic packages
import os
import numpy as np
import pandas as pd

import matplotlib.pyplot as plt
import seaborn as sns

# Make plots look nicer
plt.rcParams["figure.figsize"] = (8, 5)
plt.rcParams["axes.titlesize"] = 14
plt.rcParams["axes.labelsize"] = 12

# Set path to the cleaned CSV file
DATA_PATH = "/Users/shijietang/Desktop/143project/Analysis/breast_cancer_wiscons

DATA_PATH
```

Out[3]:
```
'/Users/shijietang/Desktop/143project/Analysis/breast_cancer_wisconsin_original
_cleaned.csv'
```

In [4]:
```
# Load the dataset
df = pd.read_csv(DATA_PATH)

print(f"Data shape: {df.shape[0]} rows, {df.shape[1]} columns")
df.head()
```

```
Data shape: 675 rows, 11 columns
```

Out[4]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Nc Nu
0	5	1	1	1	2	1.0	3	
1	5	4	4	5	7	10.0	3	
2	3	1	1	1	2	2.0	3	
3	6	8	8	1	3	4.0	3	
4	4	1	1	3	2	1.0	3	

In [5]:
```
print("Columns:", df.columns.tolist())
print("\nData types:\n", df.dtypes)

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

```
df.describe()
```

```
Columns: ['Clump Thickness', 'Uniformity of Cell Size', 'Uniformity of Cell Shap
e', 'Marginal Adhesion', 'Single Epithelial Cell Size', 'Bare Nuclei', 'Bland Chr
omatin', 'Normal Nucleoli', 'Mitoses', 'Diagnosis', 'Is_Malignant']

Data types:
 Clump Thickness                int64
Uniformity of Cell Size         int64
Uniformity of Cell Shape        int64
Marginal Adhesion               int64
Single Epithelial Cell Size     int64
Bare Nuclei                   float64
Bland Chromatin                 int64
Normal Nucleoli                 int64
Mitoses                         int64
Diagnosis                       int64
Is_Malignant                    int64
dtype: object

Missing values per column:

Clump Thickness               0
Uniformity of Cell Size       0
Uniformity of Cell Shape      0
Marginal Adhesion             0
Single Epithelial Cell Size   0
Bare Nuclei                   0
Bland Chromatin               0
Normal Nucleoli               0
Mitoses                       0
Diagnosis                     0
Is_Malignant                  0
dtype: int64
```

Out[5]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	C
count	675.000000	675.000000	675.000000	675.000000	675.000000	675.000000	67
mean	4.451852	3.146667	3.208889	2.848889	3.229630	3.537778	
std	2.820859	3.055005	2.976552	2.875917	2.208497	3.637871	
min	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	
25%	2.000000	1.000000	1.000000	1.000000	2.000000	1.000000	
50%	4.000000	1.000000	1.000000	1.000000	2.000000	1.000000	
75%	6.000000	5.000000	5.000000	4.000000	4.000000	6.000000	
max	10.000000	10.000000	10.000000	10.000000	10.000000	10.000000	1

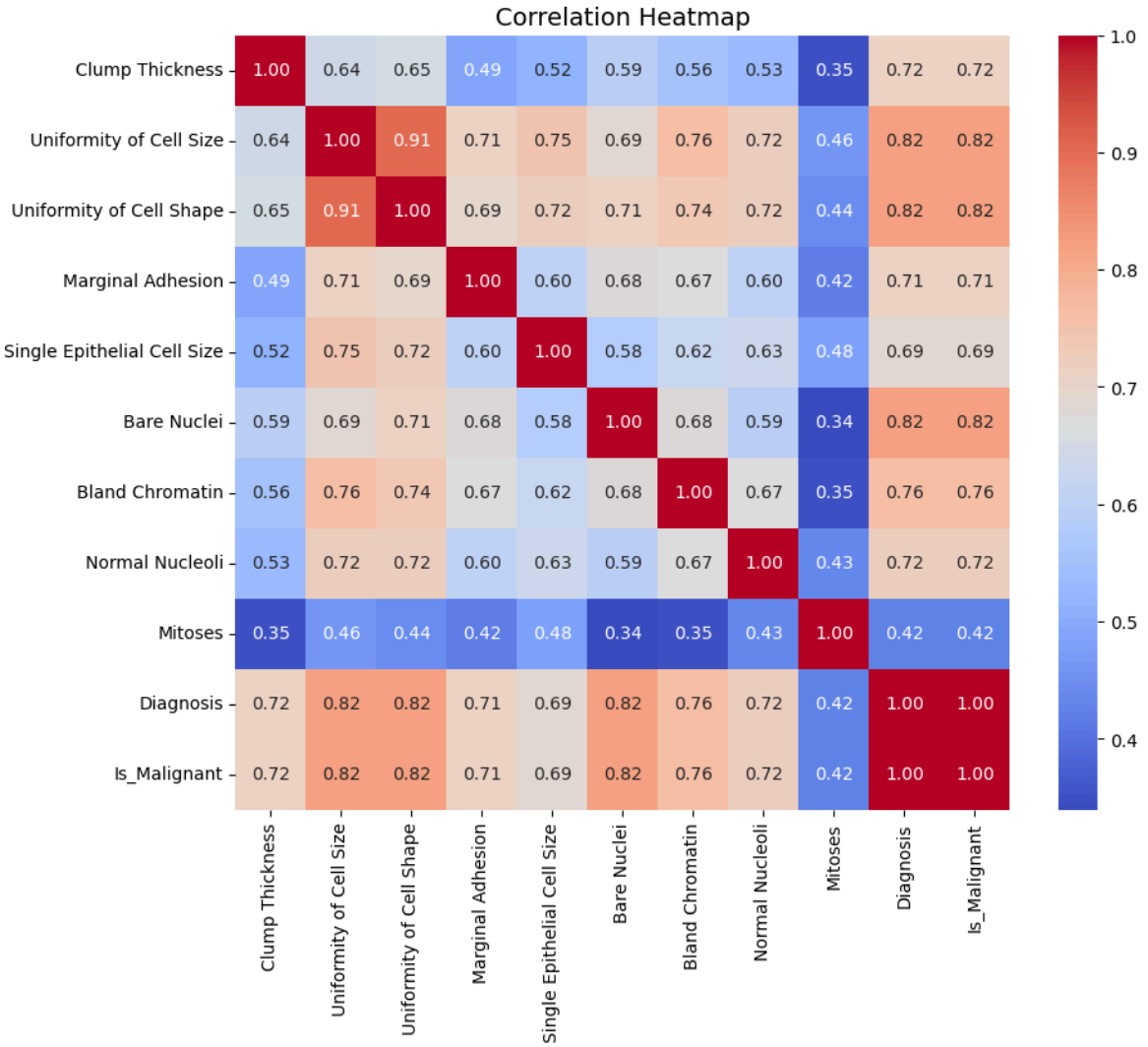
In [6]:

```
counts = df["Is_Malignant"].value_counts().sort_index()
ratios = df["Is_Malignant"].value_counts(normalize=True).sort_index()

print("Class distribution for Is_Malignant:")
for c in counts.index:
```

```
    label = "Benign (0)" if c == 0 else "Malignant (1)"
    print(f"{label}: {counts[c]} samples ({ratios[c] * 100:.2f}%)")
```

```
Class distribution for Is_Malignant:
Benign (0): 439 samples (65.04%)
Malignant (1): 236 samples (34.96%)
```

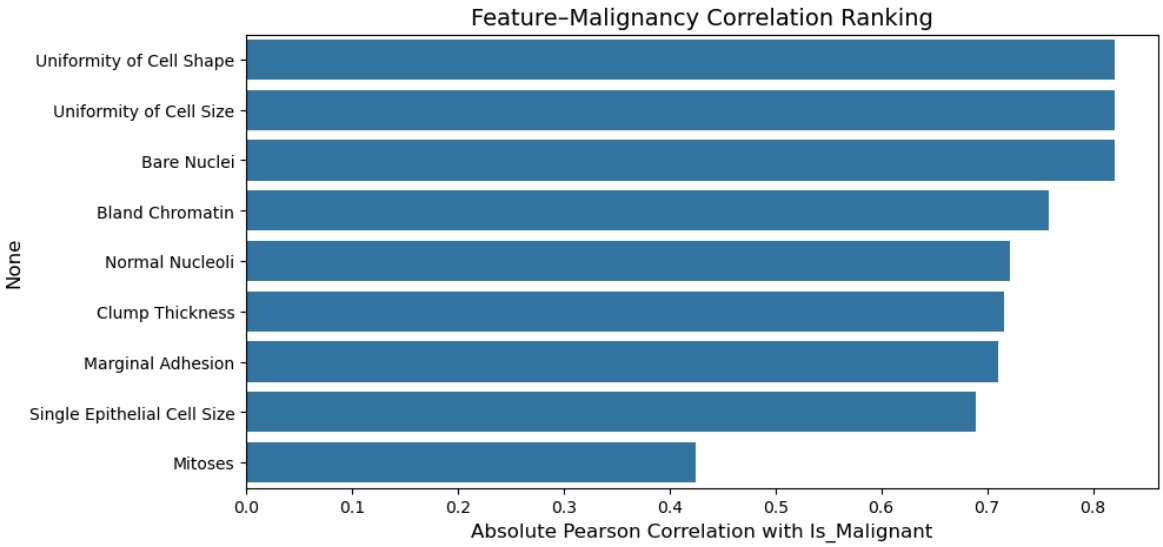
In [7]:
```
numeric_cols = df.select_dtypes(include=[np.number]).columns.tolist()
corr_matrix = df[numeric_cols].corr()

plt.figure(figsize=(10, 8))
sns.heatmap(corr_matrix, annot=True, fmt=".2f", cmap="coolwarm", square=True)
plt.title("Correlation Heatmap")
plt.show()
```



In [8]:
```
corr_with_target = df[numeric_cols].corr()["Is_Malignant"].sort_values(ascending
corr_with_target
```

Out[8]:
```
Is_Malignant                 1.000000
Diagnosis                    1.000000
Uniformity of Cell Shape     0.820688
Uniformity of Cell Size      0.820663
Bare Nuclei                  0.820533
Bland Chromatin              0.758252
Normal Nucleoli              0.722020
Clump Thickness              0.715714
Marginal Adhesion            0.710985
Single Epithelial Cell Size  0.689544
Mitoses                      0.424399
Name: Is_Malignant, dtype: float64
```

In [9]:
```
# Remove the target & original diagnosis code from feature ranking
corr_features_only = corr_with_target.drop(["Is_Malignant", "Diagnosis"])

plt.figure(figsize=(10, 5))
sns.barplot(x=corr_features_only.abs(), y=corr_features_only.index)
plt.xlabel("Absolute Pearson Correlation with Is_Malignant")
plt.title("Feature-Malignancy Correlation Ranking")
plt.show()
```



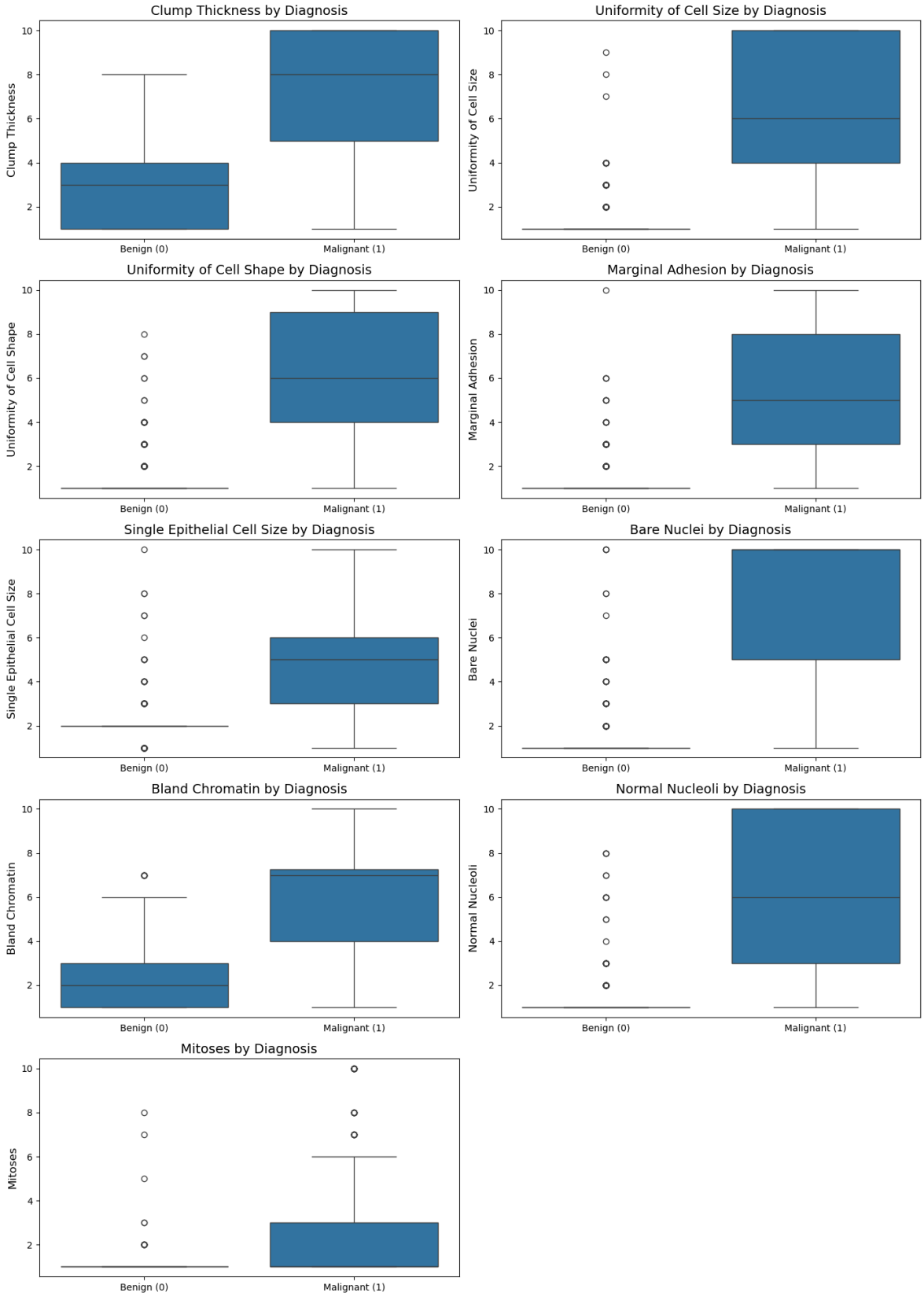
In [10]:
```
df_plot = df.copy()
df_plot["Diagnosis_Label"] = df_plot["Is_Malignant"].map({0: "Benign (0)", 1: "M

features = [col for col in numeric_cols if col not in ["Is_Malignant", "Diagnosi
features
```

Out[10]:
```
['Clump Thickness',
 'Uniformity of Cell Size',
 'Uniformity of Cell Shape',
 'Marginal Adhesion',
 'Single Epithelial Cell Size',
 'Bare Nuclei',
 'Bland Chromatin',
 'Normal Nucleoli',
 'Mitoses']
```

In [11]:
```
# Multi-panel boxplots
n_features = len(features)
n_cols = 2
n_rows = int(np.ceil(n_features / n_cols))
```

```
plt.figure(figsize=(14, 4 * n_rows))

for i, feature in enumerate(features, start=1):
    plt.subplot(n_rows, n_cols, i)
    sns.boxplot(data=df_plot, x="Diagnosis_Label", y=feature)
    plt.title(f"{feature} by Diagnosis")
    plt.xlabel("")
    plt.ylabel(feature)

plt.suptitle("Feature Distributions by Diagnosis", fontsize=16, y=1.02)
plt.tight_layout()
plt.show()
```

Feature Distributions by Diagnosis



In [12]:
```
means = df.groupby("Is_Malignant")[features].mean()
means
```

Out[12]:

Is_Malignant	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Cl
0	2.972665	1.309795	1.419134	1.350797	2.113895	1.350797	
1	7.203390	6.563559	6.538136	5.635593	5.305085	7.605932	

In [13]:
```
(means.loc[1] - means.loc[0]).sort_values(ascending=False)
```

Out[13]:
```
Bare Nuclei                   6.255135
Uniformity of Cell Size       5.253764
Uniformity of Cell Shape      5.119001
Normal Nucleoli               4.638305
Marginal Adhesion             4.284796
Clump Thickness               4.230725
Bland Chromatin               3.899087
Single Epithelial Cell Size   3.191190
Mitoses                       1.548348
dtype: float64
```

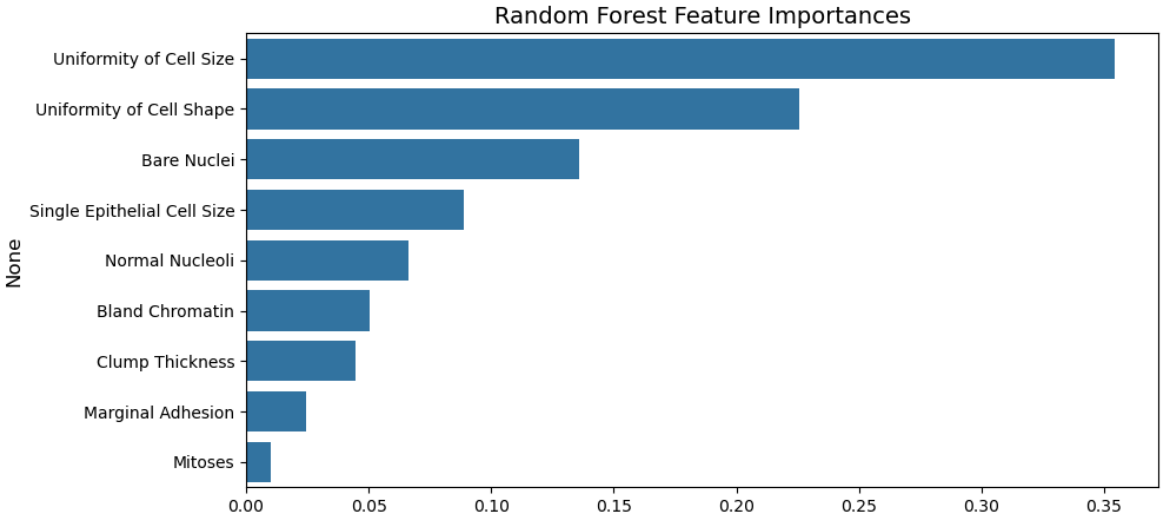
In [14]:
```
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import roc_auc_score, classification_report

X = df[features].values
y = df["Is_Malignant"].values

X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.3, stratify=y, random_state=42
)

rf = RandomForestClassifier(
    n_estimators=200,
    class_weight="balanced",
    random_state=42,
)

rf.fit(X_train, y_train)

y_prob = rf.predict_proba(X_test)[:, 1]
y_pred = rf.predict(X_test)

print("ROC-AUC:", roc_auc_score(y_test, y_prob))
print("\nClassification Report:\n", classification_report(y_test, y_pred))
```

```
ROC-AUC: 0.994771660264618

Classification Report:
              precision    recall  f1-score   support

           0       0.96      0.98      0.97       132
           1       0.96      0.93      0.94        71

    accuracy                           0.96       203
   macro avg       0.96      0.95      0.96       203
weighted avg       0.96      0.96      0.96       203
```

In [15]:
```
importances = pd.Series(rf.feature_importances_, index=features).sort_values(asc
importances
```

Out[15]:
```
Uniformity of Cell Size         0.354379
Uniformity of Cell Shape        0.225554
Bare Nuclei                     0.135997
Single Epithelial Cell Size     0.088600
Normal Nucleoli                 0.066054
Bland Chromatin                 0.050582
Clump Thickness                 0.044595
Marginal Adhesion               0.024356
Mitoses                         0.009884
dtype: float64
```

In [16]:
```
plt.figure(figsize=(10, 5))
sns.barplot(x=importances.values, y=importances.index)
plt.title("Random Forest Feature Importances")
plt.show()
```



In [ ]: