

```
df=pd.read_csv("data.csv")
df.head()
```

```
df.head()
```

```
df.info()
```

1/5

memory usage: 142.4+ KB

```
df['diagnosis'].unique()
```

```
↔ array(['M', 'B'], dtype=object)
```

```
df['diagnosis'] = df['diagnosis'].map({'M': 1, 'B': 0})
```

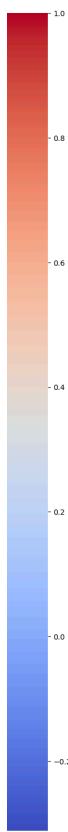
```
correlation_matrix = df.corr()
```

```
plt.figure(figsize=(20, 20))
```

```
sns.heatmap(correlation_matrix, annot=True, fmt=".2f", cmap='coolwarm', square=True, linewidths=0.5)
```

```
plt.title('Correlation Matrix of Breast Cancer Dataset')
```

```
plt.show()
```

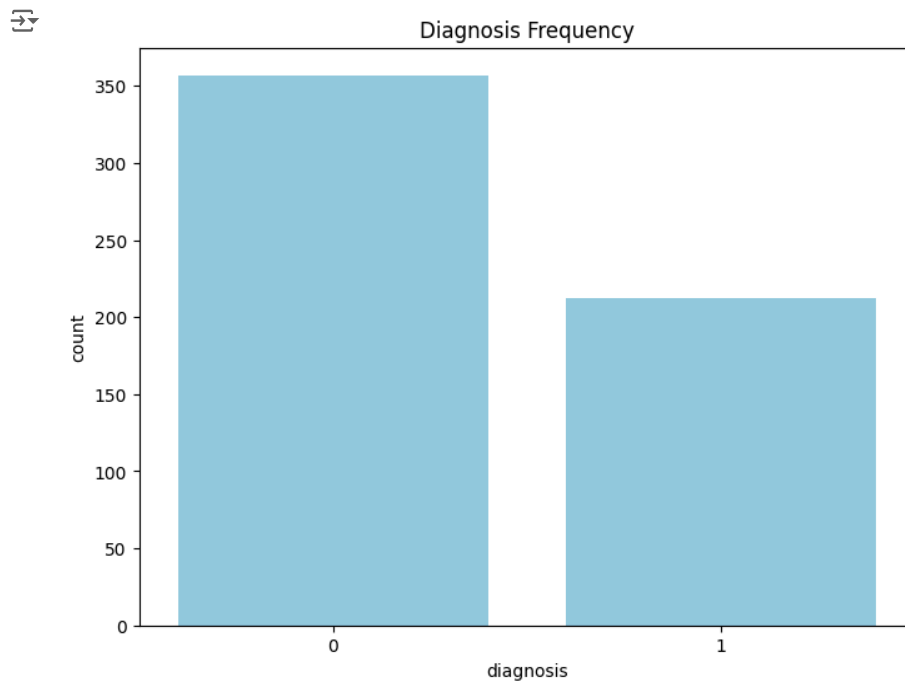


The heatmap shows how features in the Breast Cancer dataset are related to each other. Correlation values range from -1 to 1, where -1 means a perfect negative relationship, 0 means no relationship, and 1 means a perfect positive relationship.

High correlation: Some features are almost perfectly related, like "mean radius" and "mean perimeter" (0.997). You can choose just one for analysis to avoid redundancy. Low correlation: Some features are almost unrelated, like "mean symmetry" and "mean fractal dimension" (0.008). These independent features can be useful for building accurate models.

```
# Distribution Plots
sns.pairplot(df, hue='diagnosis', vars=['radius_mean', 'texture_mean', 'perimeter_mean', 'area_mean'])
plt.show()

plt.figure(figsize=(8, 6))
sns.countplot(x='diagnosis', data=df, color='skyblue')
plt.title('Diagnosis Frequency')
plt.show()
```




```
threshold = 0.5
high_corr_features = correlation_matrix.index(abs(correlation_matrix['diagnosis']) > threshold).tolist()
high_corr_features.remove('diagnosis')

len(high_corr_features)
high_corr_features
```

```
['radius_mean',
 'perimeter_mean',
 'area_mean',
 'compactness_mean',
 'concavity_mean',
 'concave_points_mean',
 'radius_se',
 'perimeter_se',
 'area_se',
 'radius_worst',
 'perimeter_worst',
 'area_worst',
 'compactness_worst',
 'concavity_worst',
 'concave_points_worst']
```

```
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
```

```
X = df[high_corr_features]
y = df['diagnosis']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
model = LogisticRegression(max_iter=10000)
model.fit(X_train, y_train)
```


 **LogisticRegression**
LogisticRegression(max_iter=10000)

```
logisticRegression_y_pred = model.predict(X_test)
```

```
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
from sklearn.preprocessing import StandardScaler
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
```

```
accuracy = accuracy_score(y_test, logisticRegression_y_pred)
```

```
print("Accuracy:", accuracy)
```


 Accuracy: 0.9824561403508771

```
knn_model = KNeighborsClassifier(n_neighbors=3)
knn_model.fit(X_train, y_train)
```

```
knn_y_pred = knn_model.predict(X_test)
```

```
accuracy = accuracy_score(y_test, knn_y_pred)
```

```
print("Accuracy:", accuracy)
```

 Accuracy: 0.9298245614035088

```
numerical_cols = [col for col in numerical_cols if 'id' not in col]
id_ = "id"
if id_ in numerical_cols:
```