

```

import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, classification_report

# Load the dataset
data = pd.read_csv("data_cancer.csv")

# Display basic statistics of the dataset
print(data.describe())

# Check for missing values
print(data.isnull().sum())

# Visualize the target variable distribution
import seaborn as sns
import matplotlib.pyplot as plt

sns.countplot(x='diagnosis', data=data)
plt.show()

```

	id	radius_mean	texture_mean	perimeter_mean
area_mean \				
count	5.690000e+02	569.000000	569.000000	569.000000
mean	3.037183e+07	14.127292	19.289649	91.969033
std	1.250206e+08	3.524049	4.301036	24.298981
min	8.670000e+03	6.981000	9.710000	43.790000
25%	8.692180e+05	11.700000	16.170000	75.170000
50%	9.060240e+05	13.370000	18.840000	86.240000
75%	8.813129e+06	15.780000	21.800000	104.100000
max	9.113205e+08	28.110000	39.280000	188.500000

	smoothness_mean	compactness_mean	concavity_mean	concave
points_mean \				
count	569.000000	569.000000	569.000000	
mean	0.096360	0.104341	0.088799	
std	0.014064	0.052813	0.079720	

min	0.052630	0.019380	0.000000
0.000000			
25%	0.086370	0.064920	0.029560
0.020310			
50%	0.095870	0.092630	0.061540
0.033500			
75%	0.105300	0.130400	0.130700
0.074000			
max	0.163400	0.345400	0.426800
0.201200			

	symmetry_mean	...	texture_worst	perimeter_worst	area_worst
\					
count	569.000000	...	569.000000	569.000000	569.000000
mean	0.181162	...	25.677223	107.261213	880.583128
std	0.027414	...	6.146258	33.602542	569.356993
min	0.106000	...	12.020000	50.410000	185.200000
25%	0.161900	...	21.080000	84.110000	515.300000
50%	0.179200	...	25.410000	97.660000	686.500000
75%	0.195700	...	29.720000	125.400000	1084.000000
max	0.304000	...	49.540000	251.200000	4254.000000

	smoothness_worst	compactness_worst	concavity_worst	\
count	569.000000	569.000000	569.000000	
mean	0.132369	0.254265	0.272188	
std	0.022832	0.157336	0.208624	
min	0.071170	0.027290	0.000000	
25%	0.116600	0.147200	0.114500	
50%	0.131300	0.211900	0.226700	
75%	0.146000	0.339100	0.382900	
max	0.222600	1.058000	1.252000	

	concave points_worst	symmetry_worst	
fractal_dimension_worst			\
count	569.000000	569.000000	569.000000
mean	0.114606	0.290076	0.083946
std	0.065732	0.061867	0.018061
min	0.000000	0.156500	0.055040
25%	0.064930	0.250400	0.071460

50%	0.099930	0.282200	0.080040
75%	0.161400	0.317900	0.092080
max	0.291000	0.663800	0.207500

```

      Unnamed: 32
count      0.0
mean      NaN
std       NaN
min       NaN
25%      NaN
50%      NaN
75%      NaN
max       NaN

```

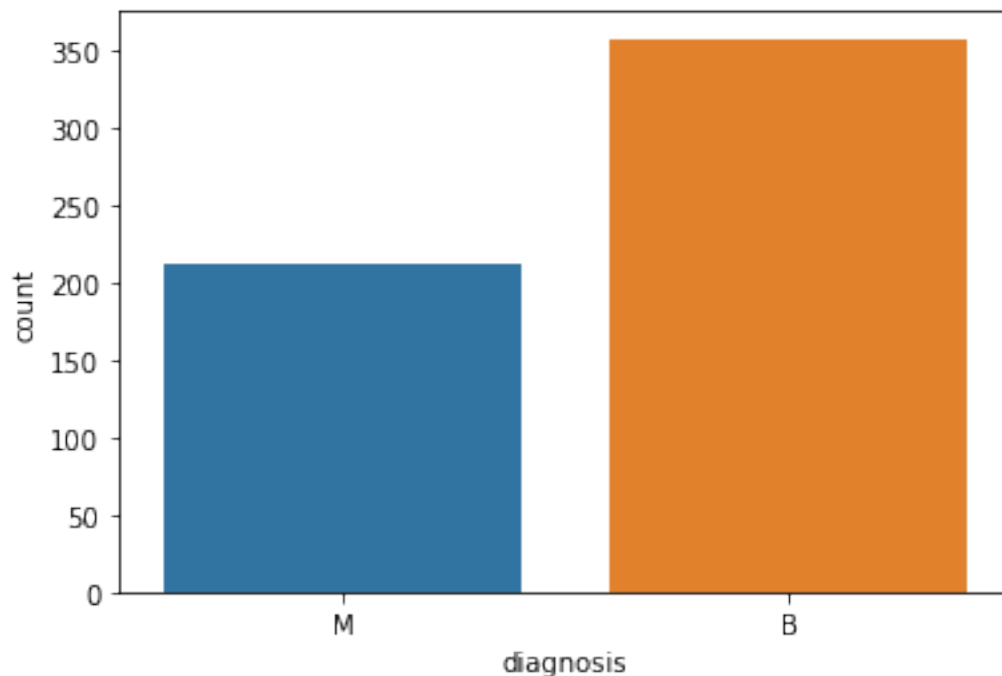
[8 rows x 32 columns]

```

id      0
diagnosis      0
radius_mean      0
texture_mean      0
perimeter_mean      0
area_mean      0
smoothness_mean      0
compactness_mean      0
concavity_mean      0
concave points_mean      0
symmetry_mean      0
fractal_dimension_mean      0
radius_se      0
texture_se      0
perimeter_se      0
area_se      0
smoothness_se      0
compactness_se      0
concavity_se      0
concave points_se      0
symmetry_se      0
fractal_dimension_se      0
radius_worst      0
texture_worst      0
perimeter_worst      0
area_worst      0
smoothness_worst      0
compactness_worst      0
concavity_worst      0
concave points_worst      0
symmetry_worst      0

```

```
fractal_dimension_worst    0
Unnamed: 32                569
dtype: int64
```



```
# Handle missing values (if any)
data.dropna(inplace=True)

# Encode categorical variable 'diagnosis' (Malignant (M) and Benign (B))
data['diagnosis'] = data['diagnosis'].map({'M': 1, 'B': 0})

# Split the dataset into features (X) and target variable (y)
X = data.drop(['id', 'diagnosis'], axis=1)
y = data['diagnosis']

# Load the dataset
data = pd.read_csv("data_cancer.csv")

# Display basic statistics of the dataset
print(data.describe())

# Check the number of samples before handling missing values
print("Number of samples before handling missing values:", len(data))

# Handle missing values (if any)
data.dropna(inplace=True)
```

```

# Check the number of samples after handling missing values
print("Number of samples after handling missing values:", len(data))

# Check if the dataset is not empty before splitting
if len(data) > 0:
    # Encode categorical variable 'diagnosis' (Malignant (M) and Benign (B))
    data['diagnosis'] = data['diagnosis'].map({'M': 1, 'B': 0})

    # Visualize the target variable distribution
    sns.countplot(x='diagnosis', data=data)
    plt.show()

    # Split the dataset into features (X) and target variable (y)
    X = data.drop(['id', 'diagnosis'], axis=1)
    y = data['diagnosis']

    # Split the data into training and testing sets
    X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)

    # Build and train a Random Forest model
    model = RandomForestClassifier(random_state=42)
    model.fit(X_train, y_train)

    # Evaluate the model on the testing set
    y_pred = model.predict(X_test)

    # Display performance metrics
    print("Accuracy:", accuracy_score(y_test, y_pred))
    print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred))
    print("Classification Report:\n", classification_report(y_test,
y_pred))
else:
    print("Dataset is empty after handling missing values.")

```

	id	radius_mean	texture_mean	perimeter_mean
area_mean \				
count	5.690000e+02	569.000000	569.000000	569.000000
mean	3.037183e+07	14.127292	19.289649	91.969033
std	1.250206e+08	3.524049	4.301036	24.298981
min	8.670000e+03	6.981000	9.710000	43.790000
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50%	9.060240e+05	13.370000	18.840000	86.240000

```

551.100000
75%      8.813129e+06      15.780000      21.800000      104.100000
782.700000
max      9.113205e+08      28.110000      39.280000      188.500000
2501.000000

```

```

      smoothness_mean compactness_mean concavity_mean concave
points_mean \
count      569.000000      569.000000      569.000000
569.000000
mean      0.096360      0.104341      0.088799
0.048919
std      0.014064      0.052813      0.079720
0.038803
min      0.052630      0.019380      0.000000
0.000000
25%      0.086370      0.064920      0.029560
0.020310
50%      0.095870      0.092630      0.061540
0.033500
75%      0.105300      0.130400      0.130700
0.074000
max      0.163400      0.345400      0.426800
0.201200

```

```

      symmetry_mean ... texture_worst perimeter_worst area_worst
\
count      569.000000 ...      569.000000      569.000000      569.000000
mean      0.181162 ...      25.677223      107.261213      880.583128
std      0.027414 ...      6.146258      33.602542      569.356993
min      0.106000 ...      12.020000      50.410000      185.200000
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max      0.304000 ...      49.540000      251.200000      4254.000000

```

```

      smoothness_worst compactness_worst concavity_worst \
count      569.000000      569.000000      569.000000
mean      0.132369      0.254265      0.272188
std      0.022832      0.157336      0.208624
min      0.071170      0.027290      0.000000
25%      0.116600      0.147200      0.114500

```

50%	0.131300	0.211900	0.226700
75%	0.146000	0.339100	0.382900
max	0.222600	1.058000	1.252000

	concave points_worst	symmetry_worst	fractal_dimension_worst \
count	569.000000	569.000000	569.000000
mean	0.114606	0.290076	0.083946
std	0.065732	0.061867	0.018061
min	0.000000	0.156500	0.055040
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75%	0.161400	0.317900	0.092080
max	0.291000	0.663800	0.207500

	Unnamed: 32
count	0.0
mean	NaN
std	NaN
min	NaN
25%	NaN
50%	NaN
75%	NaN
max	NaN

[8 rows x 32 columns]

Number of samples before handling missing values: 569

Number of samples after handling missing values: 0

Dataset is empty after handling missing values.

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, classification_report

# Load the dataset
data = pd.read_csv('data_cancer.csv')

# Drop unnecessary columns (e.g., 'id' and 'Unnamed: 32')
data.drop(['id', 'Unnamed: 32'], axis=1, inplace=True)
```

```

# Handle missing values using mean imputation
data.fillna(data.mean(), inplace=True)

# Map the target variable to numerical values (Malignant: 1, Benign: 0)
data['diagnosis'] = data['diagnosis'].map({'M': 1, 'B': 0})

# Visualize the target variable distribution
sns.countplot(x='diagnosis', data=data)
plt.show()

# Split the dataset into features (X) and target variable (y)
X = data.drop('diagnosis', axis=1)
y = data['diagnosis']

# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)

# Build and train a Random Forest model
model = RandomForestClassifier(random_state=42)
model.fit(X_train, y_train)

# Make predictions on the test set
y_pred = model.predict(X_test)

# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
classification_report = classification_report(y_test, y_pred)

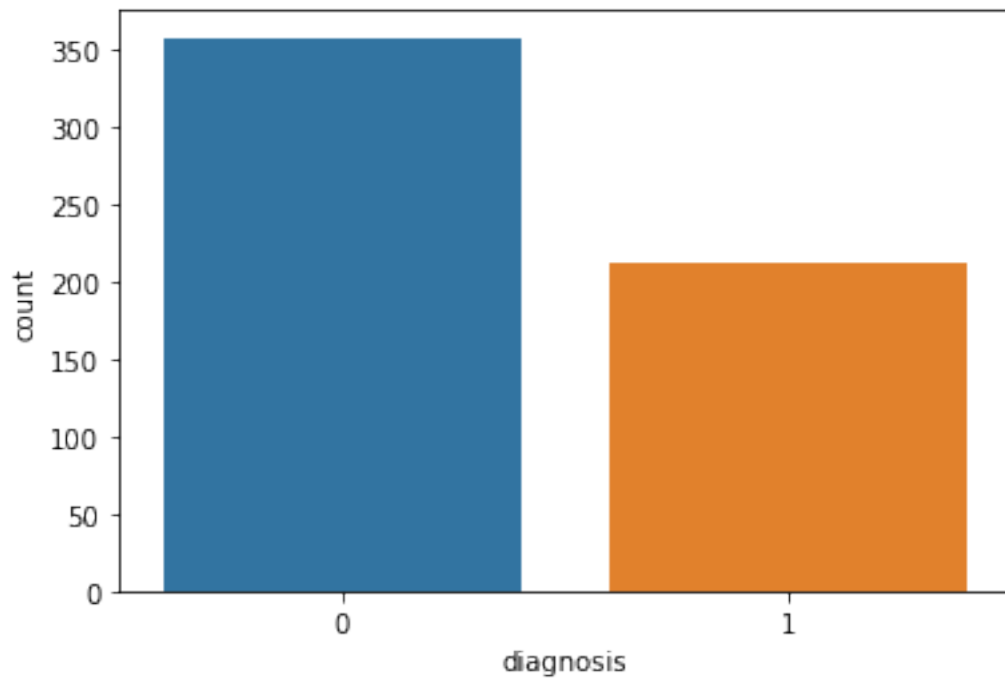
print(f'Accuracy: {accuracy:.4f}')
print('Classification Report:\n', classification_report)

```

```

C:\Users\MAYURSINGH\AppData\Local\Temp\
ipykernel_11636\1998506942.py:15: FutureWarning: Dropping of nuisance
columns in DataFrame reductions (with 'numeric_only=None') is
deprecated; in a future version this will raise TypeError.  Select
only valid columns before calling the reduction.
    data.fillna(data.mean(), inplace=True)

```

Accuracy: 0.9649

Classification Report:

	precision	recall	f1-score	support
0	0.96	0.99	0.97	71
1	0.98	0.93	0.95	43
accuracy			0.96	114
macro avg	0.97	0.96	0.96	114
weighted avg	0.97	0.96	0.96	114