In [ ]:
```python
# Importing Libraries
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt

# Sikit-Learn Libraries
from sklearn.preprocessing import OneHotEncoder
from sklearn.impute import SimpleImputer
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report, accuracy_score, confusion_m
```

In [ ]:
```python
# Load dataset from seaborn
df = sns.load_dataset('penguins')
print(f" The Penguins dataset has {df.shape[0]} rows {df.shape[1]} columns")
df.head()
```

```
The Penguins dataset has 344 rows 7 columns
```

Out[ ]:

	species	island	bill_length_mm	bill_depth_mm	flipper_length_mm	body_m
0	Adelie	Torgersen	39.1	18.7	181.0	
1	Adelie	Torgersen	39.5	17.4	186.0	
2	Adelie	Torgersen	40.3	18.0	195.0	
3	Adelie	Torgersen	NaN	NaN	NaN	
4	Adelie	Torgersen	36.7	19.3	193.0	

Dataset Overview

The Penguins dataset contains 344 observations and 7 columns, where each row represents an individual penguin.

The goal in most analyses is to predict the penguin species based on physical measurements and categorical attributes.

This is a **small**, **clean**, **real-world-like dataset**, suitable for demonstrating classification workflows, especially with tree-based models such as Random Forest.

Column Descriptions

1. `species` : Target variable. The penguin species (e.g., Adelie, Chinstrap, Gentoo). This is a multiclass categorical label.

2. `island` : Categorical feature indicating the island where the penguin was observed. Acts as a geographic/contextual variable.

3. `bill_length_mm` : Numerical feature measuring the length of the penguin's bill (in millimeters). Often highly discriminative between species.

4. `bill_depth_mm` : Numerical feature measuring the depth (thickness) of the bill (in millimeters). Complements bill length for species separation.

5. `flipper_length_mm` : Numerical feature representing flipper length (in millimeters). Strongly correlated with body size and species.

6. `body_mass_g` : Numerical feature indicating body mass (in grams). Useful but can overlap across species.

7. `sex` : Categorical feature indicating biological sex (Male/Female). May help slightly but should not be overweighted.

In [ ]:
```python
# Check data types and structure
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 344 entries, 0 to 343
Data columns (total 7 columns):
 #   Column             Non-Null Count  Dtype
---  ------             --------------  -----
 0   species            344 non-null    object
 1   island             344 non-null    object
 2   bill_length_mm     342 non-null    float64
 3   bill_depth_mm      342 non-null    float64
 4   flipper_length_mm  342 non-null    float64
 5   body_mass_g        342 non-null    float64
 6   sex                333 non-null    object
dtypes: float64(4), object(3)
memory usage: 18.9+ KB
```

In [ ]:
```python
df.isna().sum()
```

```
Out[ ]:
```

	0
species	0
island	0
bill_length_mm	2
bill_depth_mm	2
flipper_length_mm	2
body_mass_g	2
sex	11

dtype: int64

```
In [ ]:
```

```python
# Class Balance/Imbalance
df['species'].value_counts()
```

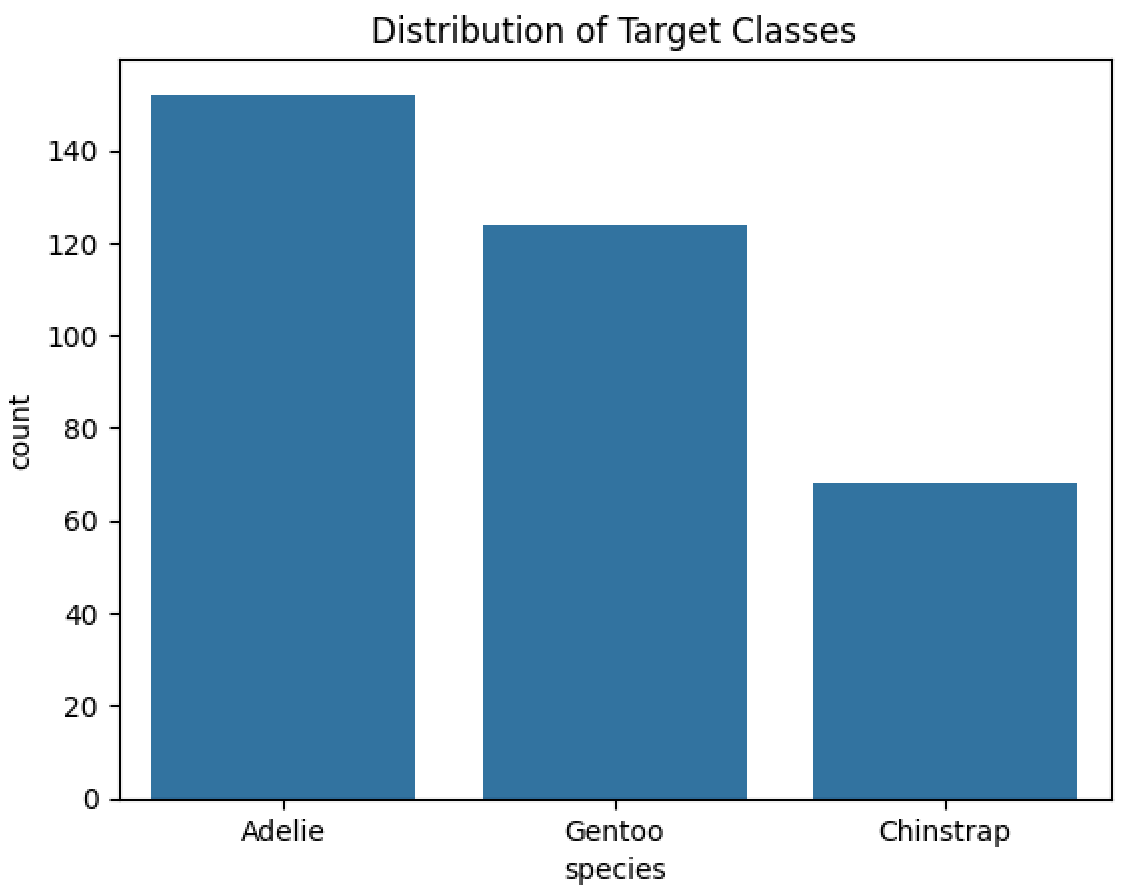
```
Out[ ]:
```

	count
species	
Adelie	152
Gentoo	124
Chinstrap	68

dtype: int64

```
In [ ]:
```

```python
# Visualizing Imbalance
sns.countplot(data=df, x='species', order=df['species'].value_counts().index)
plt.title("Distribution of Target Classes")
plt.show()
```



```
In [ ]: # Exploring numerical feature
        df.describe()
```

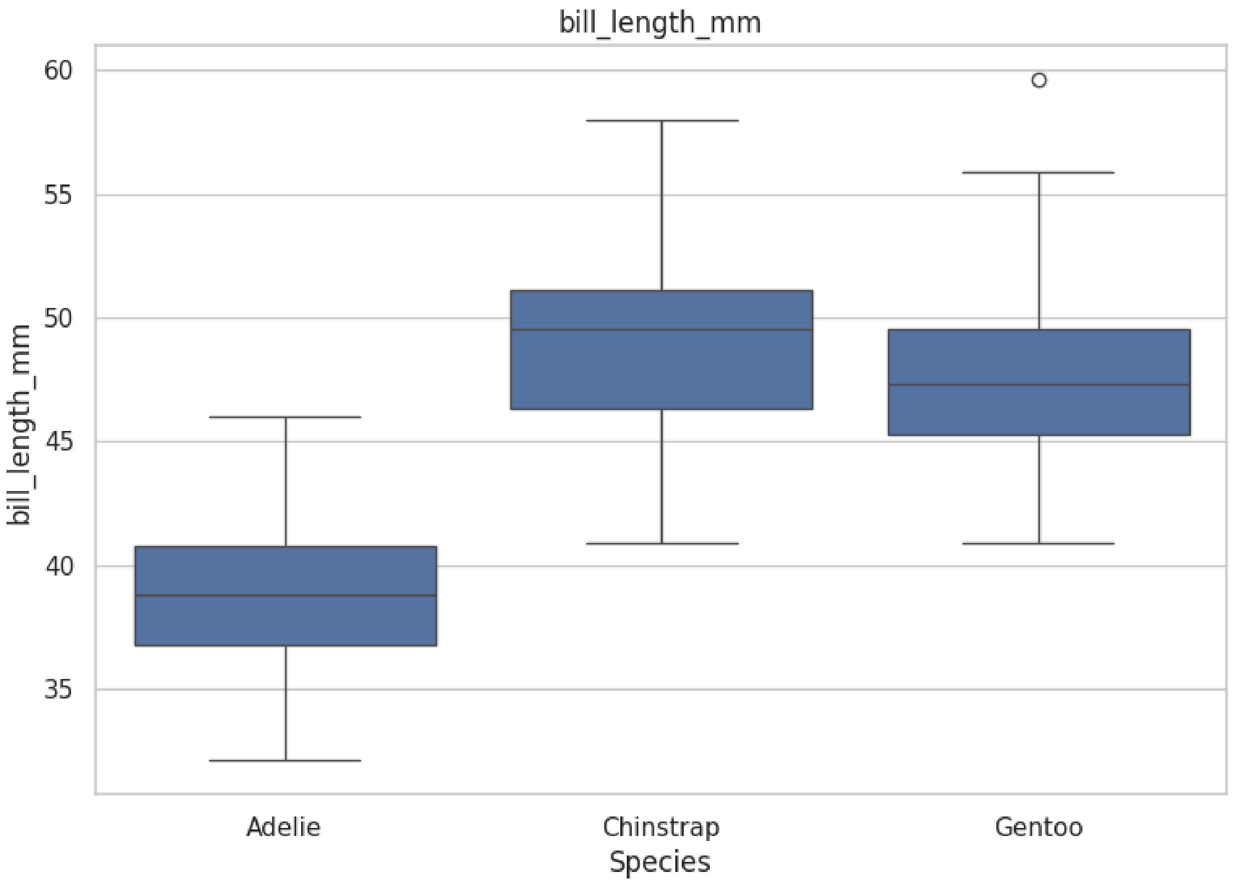
Out[ ]:

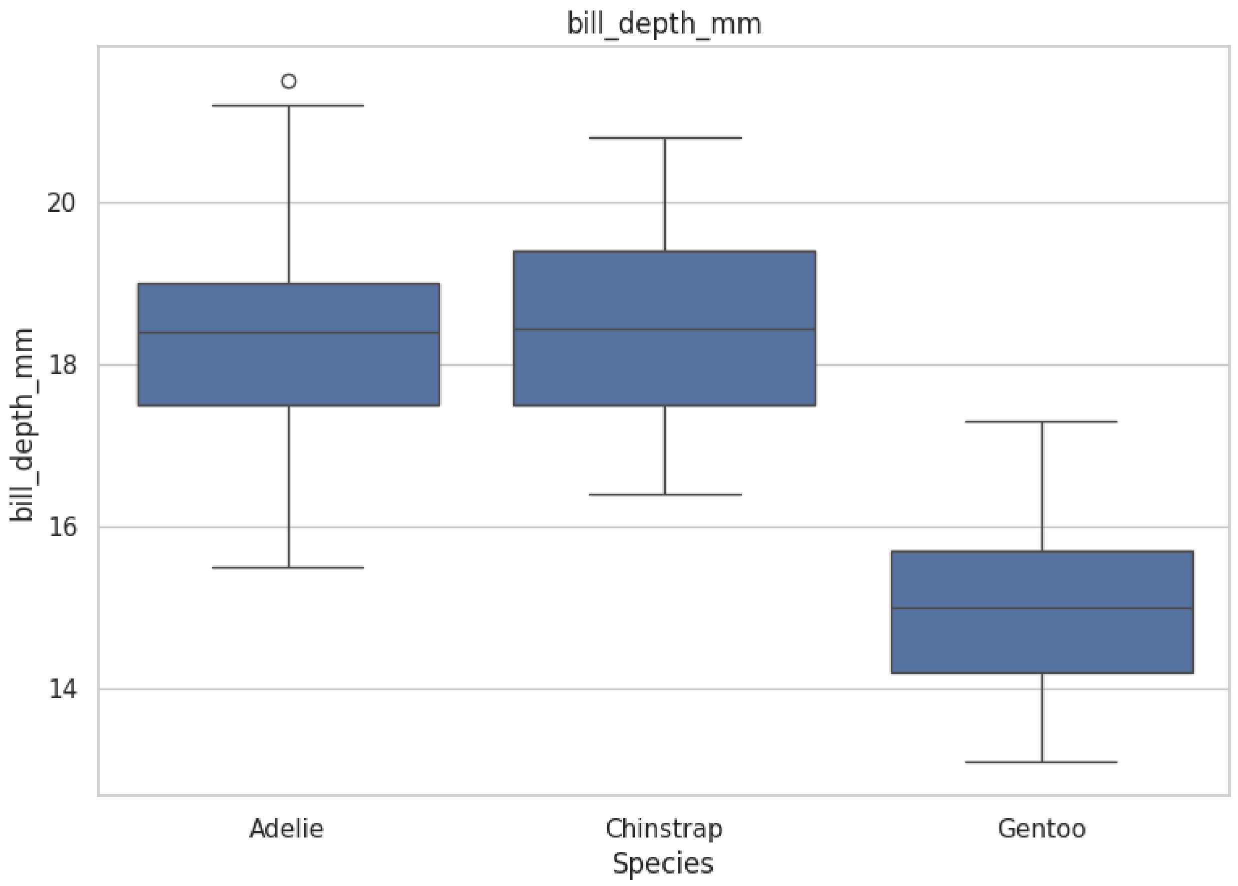
	bill_length_mm	bill_depth_mm	flipper_length_mm	body_mass_g
count	342.000000	342.000000	342.000000	342.000000
mean	43.921930	17.151170	200.915205	4201.754386
std	5.459584	1.974793	14.061714	801.954536
min	32.100000	13.100000	172.000000	2700.000000
25%	39.225000	15.600000	190.000000	3550.000000
50%	44.450000	17.300000	197.000000	4050.000000
75%	48.500000	18.700000	213.000000	4750.000000
max	59.600000	21.500000	231.000000	6300.000000

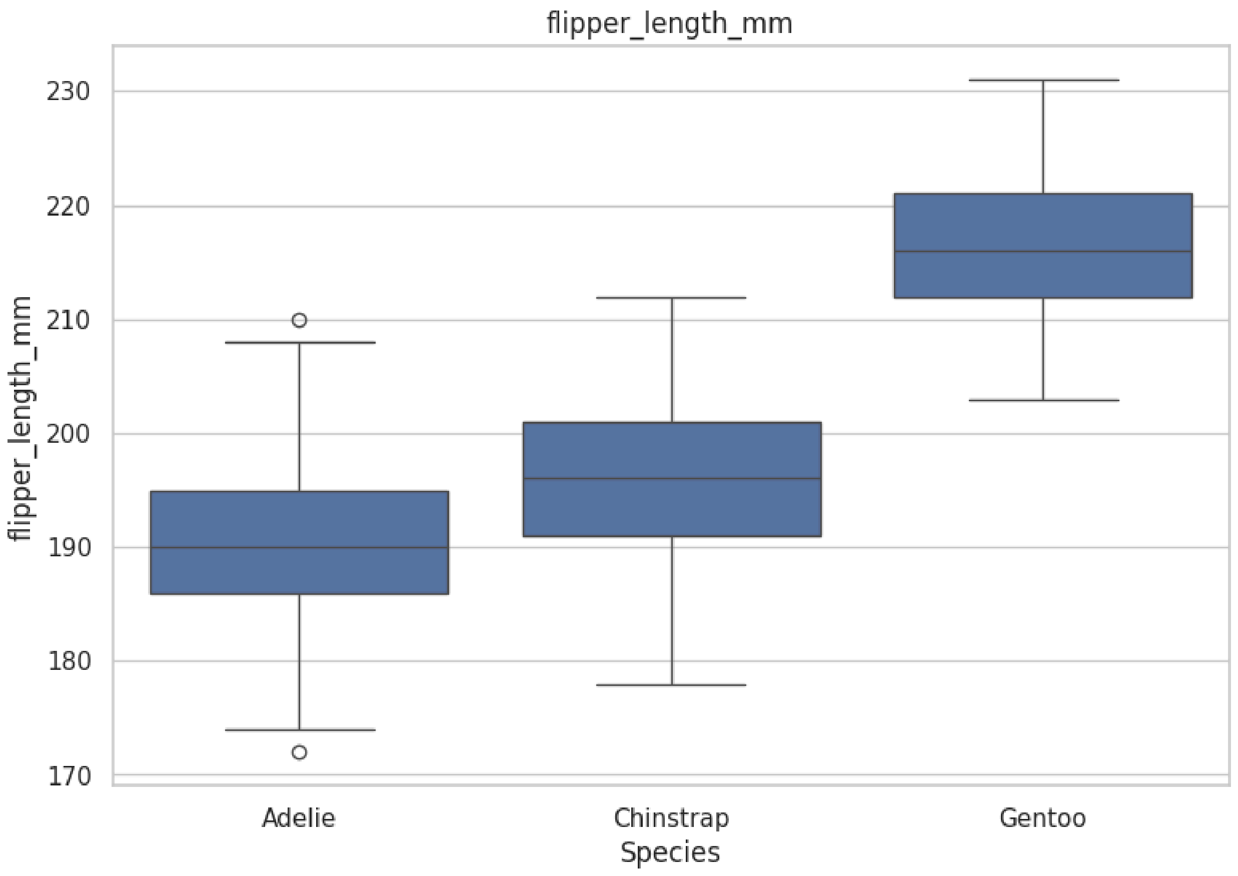
```
In [ ]: df.columns
```

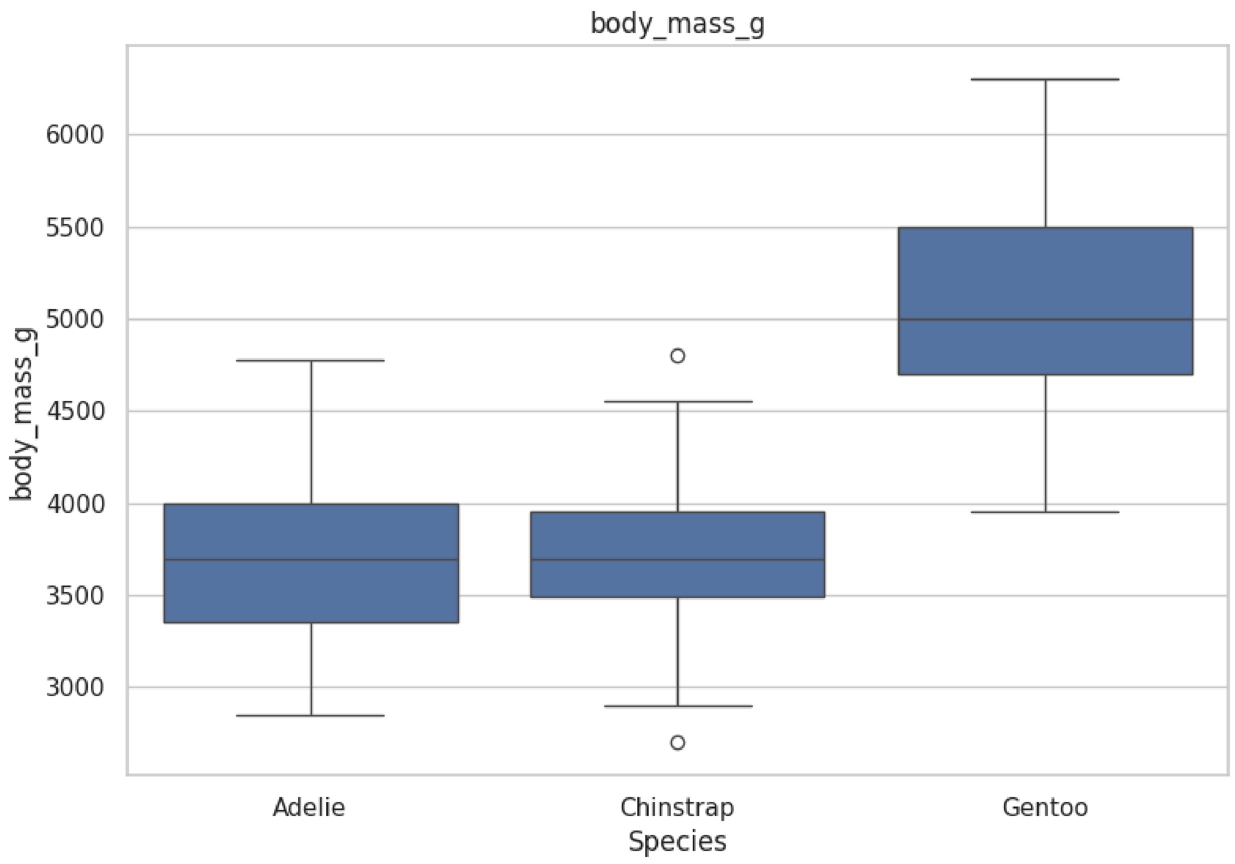
```
Out[ ]: Index(['species', 'island', 'bill_length_mm', 'bill_depth_mm',
               'flipper_length_mm', 'body_mass_g', 'sex'],
              dtype='object')
```

```
In [ ]: # Boxplot for understanding the separation in dataset
        sns.set(style="whitegrid")

        for col in df.columns[2:6]:
            plt.figure(figsize=(9, 6))
            sns.boxplot(x='species', y=col, data=df)
            plt.title(col)
            plt.xlabel('Species')
            plt.ylabel(col)
            plt.show()
```

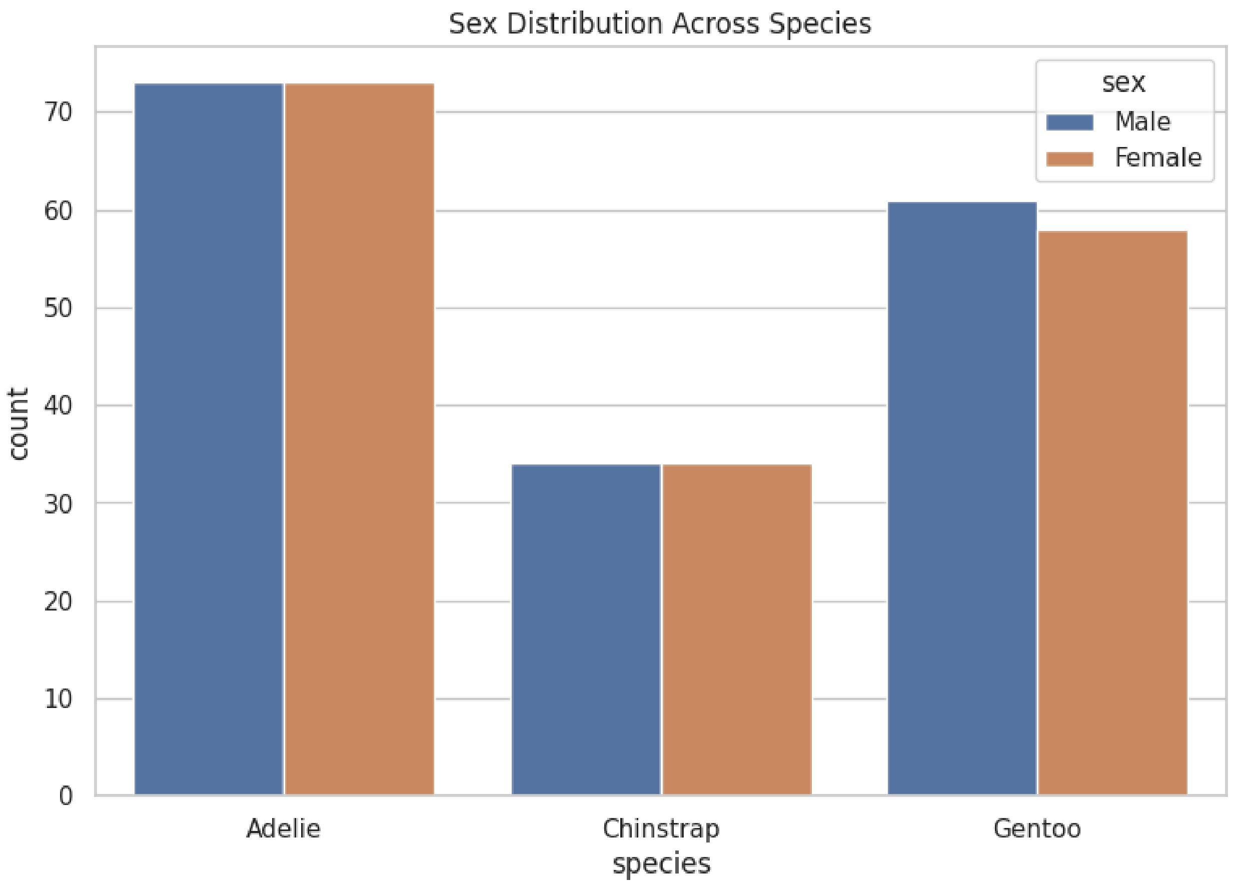



bill_depth_mm
bill_depth_mm
20
18
16
14
Adelie
Chinstrap
Gentoo
Species


flipper_length_mm
flipper_length_mm
230
220
210
200
190
180
170
Adelie
Chinstrap
Gentoo
Species



```
In [ ]: # Relationship between sex and species
        plt.figure(figsize=(9, 6))
        sns.countplot(
            data=df,
            x='species',
            hue='sex'
        )
        plt.title("Sex Distribution Across Species")
        plt.show()
```



Random Forest Model building

In [ ]:
```
# Spliting dataset in X (input) and y (output/target)
X = df.drop(columns='species')
y = df['species']

# 80% training, 20% testing
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, strat
```

In [ ]:
```
# Separateing feature types
numeric_features = ['bill_length_mm', 'bill_depth_mm', 'flipper_length_mm', 'b

categorical_features = ['island', 'sex']
```

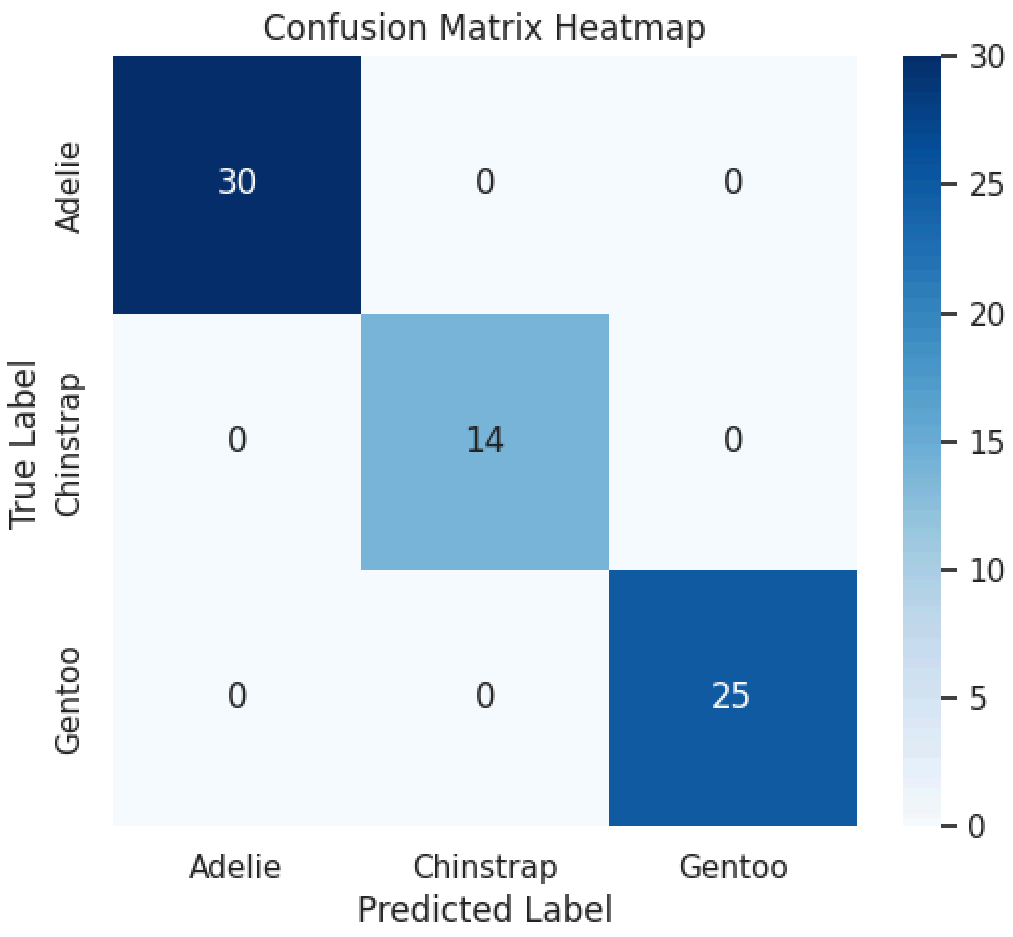
In [ ]:
```
# Building the preprocessing pipeline

# Numerical pipeline
numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median'))
])

# Categorical pipeline
categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='most_frequent')),
    ('onehot', OneHotEncoder(handle_unknown='ignore'))
])

# Combining them
preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numeric_features),
        ('cat', categorical_transformer, categorical_features)
    ]
)
```

In [ ]:
```
# Building and adding the model to the pipeline

# Baseline Random Forest
model = RandomForestClassifier(n_estimators=200, random_state=42, n_jobs=-1) #

# Full pipeline
clf = Pipeline(steps=[
    ('preprocessor', preprocessor),
    ('model', model)
])
```

In [ ]:
```
# Training the model
clf.fit(X_train, y_train)

# Evaluation
y_pred = clf.predict(X_test)

print("Accuracy:", accuracy_score(y_test, y_pred))
print(classification_report(y_test, y_pred))
```

```
Accuracy: 1.0
              precision    recall  f1-score   support

      Adelie       1.00      1.00      1.00        30
   Chinstrap       1.00      1.00      1.00        14
      Gentoo       1.00      1.00      1.00        25

    accuracy                           1.00        69
   macro avg       1.00      1.00      1.00        69
weighted avg       1.00      1.00      1.00        69
```

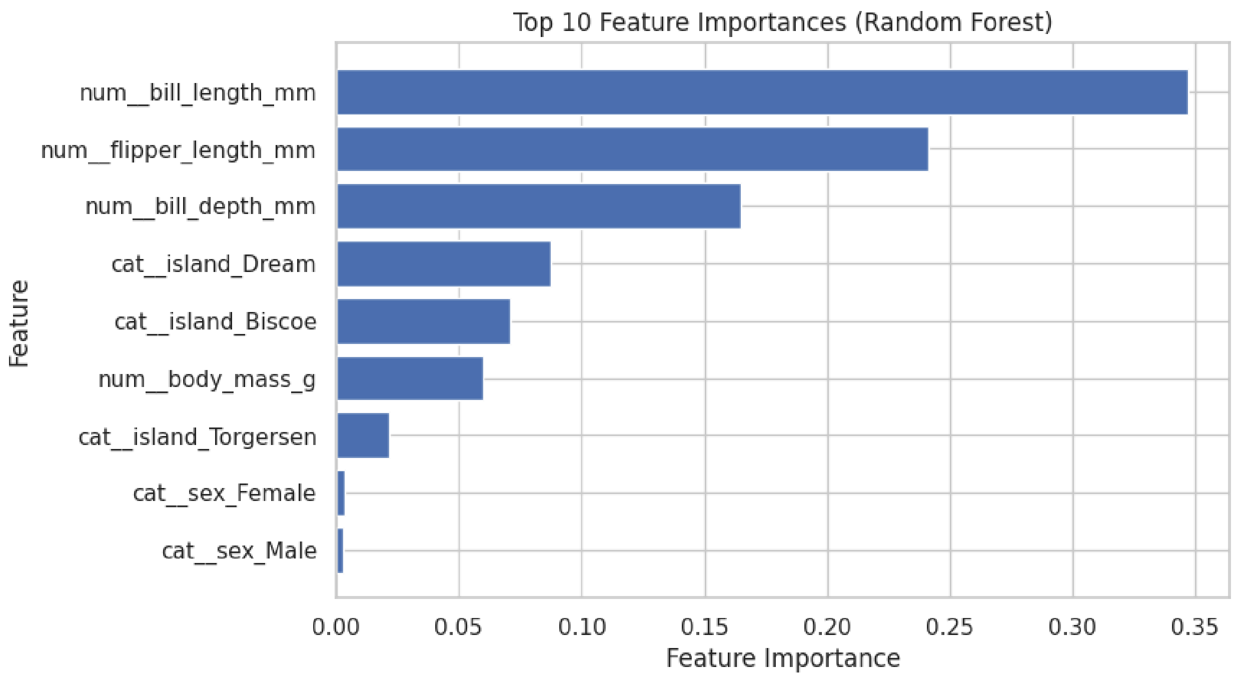
In [ ]:
```
# Computing confusion matrix
cm = confusion_matrix(y_test, y_pred)

# Ploting heatmap
plt.figure(figsize=(6, 5))
sns.heatmap(
    cm,
    annot=True,
    fmt='d',
    cmap='Blues',
    xticklabels=clf.classes_,
    yticklabels=clf.classes_
)

plt.xlabel("Predicted Label")
plt.ylabel("True Label")
plt.title("Confusion Matrix Heatmap")
plt.show()
```



In [ ]:

```
# Extracting feature names
feature_names = clf.named_steps['preprocessor'].get_feature_names_out()

# Extracting feature importances from Random Forest
importances = clf.named_steps['model'].feature_importances_

# Creating a clean importance table
feature_importance_df = pd.DataFrame({
    'feature': feature_names,
    'importance': importances
}).sort_values(by='importance', ascending=False)

# Selecting Top 10 features
top_10_features = feature_importance_df.head(10)
top_10_features
```

```python
# Visualizing Top 10 feature importances
plt.figure(figsize=(8, 5))
plt.barh(
    top_10_features['feature'],
    top_10_features['importance']
)
plt.xlabel("Feature Importance")
plt.ylabel("Feature")
plt.title("Top 10 Feature Importances (Random Forest)")
plt.gca().invert_yaxis()
plt.show()
```



Random Forest - Final Insights & Project Conclusion

Project Objective Recap

The goal of this project was to build a **robust multiclass classification model** to predict penguin species (**Adelie, Chinstrap, Gentoo**) using physical measurements and contextual features from the Palmer Penguins dataset. The emphasis was not only on model accuracy, but also on correct methodology: proper EDA, leakage-free preprocessing, and interpretable evaluation.

Key Insights from Exploratory Data Analysis:

1. **Dataset Quality**
    - The dataset contains **344 observations** and **7 features**, with low missingness.
    - **Missing values** were **limited** and **non-systematic**, making imputation preferable to row deletion.
    - No invalid or biologically implausible values were observed.
2. **Target Distribution**
    - **Species classes** were **mildly imbalanced (Adelie > Gentoo > Chinstrap)**, but not severely.
    - Stratified splitting was sufficient; resampling techniques were unnecessary.
3. **Feature Behavior**
    - Numerical features (bill length, bill depth, flipper length, body mass) showed clear inter-species separation, especially for Gentoo.
    - Overlaps between Adelie and Chinstrap were expected biological variation, not noise.
    - The `sex` feature showed balanced distributions across species, indicating weak standalone predictive power but acceptable as a supporting feature.

Modeling and Preprocessing Decisions

1. **Preprocessing Strategy**
    - Separate pipelines were used for numerical and categorical features due to fundamentally different statistical requirements.
    - Median imputation for numerical features ensured robustness to outliers.
    - Mode imputation followed by one-hot encoding handled categorical features safely.
    - All preprocessing was implemented inside a `Pipeline` and `ColumnTransformer`, ensuring:
        - **No data leakage**
        - **Correct train–test separation**
        - **Reproducibility and deployment readiness**

2. **Model Choice**

    - A **Random Forest classifier** was selected due to:
        - Strong performance on tabular data
        - Ability to model nonlinear relationships
        - Robustness to feature scaling and mild noise
    - A baseline configuration (200 trees, no tuning) was used to establish a reliable performance benchmark.

Model Performance and Evaluation

1. **Overall Performance**

    - The model achieved very high accuracy on the test set.
    - Precision, recall, and F1-scores were consistently strong across all three species.

2. **Class-Level Behavior**

    - The confusion matrix showed:
        - Near-perfect classification for Gentoo
        - Minor, expected confusion between Adelie and Chinstrap
    - No evidence of majority-class dominance or minority-class neglect was observed.

3. **Feature Importance**

    - The most influential features were:
        - `flipper_length_mm`
        - `bill_length_mm`
        - `bill_depth_mm`
        - `body_mass_g`
    - Categorical features (`island`, `sex`) contributed marginally, acting as contextual signals rather than primary drivers.
    - Feature importance was interpreted as model behavior insight, not causal inference.

Final Conclusion

This project demonstrates that the Penguins dataset is highly suitable for supervised multiclass classification when handled with proper preprocessing and evaluation discipline. The **Random Forest model**, combined with a **leakage-safe pipeline**, delivers **strong and stable performance without the need for aggressive tuning or complex feature engineering**.

More importantly, the project validates correct machine learning practice:

- EDA guided decisions instead of assumptions
- Preprocessing was learned only from training data
- Pipelines enforced consistency and prevented silent errors
- Evaluation focused on class-level performance, not just accuracy

If extended further, this work could incorporate:

- Hyperparameter tuning for marginal gains
- Permutation importance or SHAP for more reliable interpretability
- Cross-validation for performance stability estimates

```
In [ ]:
```