Complete data visualization on Mushroom dataset using Matplotlib and Seaborn libraries

Dataset link:- https://archive.ics.uci.edu/dataset/73/mushroom

This data set includes descriptions of hypothetical samples corresponding to 23 species of gilled mushrooms in the Agaricus and Lepiota Family (pp. 500-525). Each species is identified as definitely edible, definitely poisonous, or of unknown edibility and not recommended. This latter class was combined with the poisonous one. The Guide clearly states that there is no simple rule for determining the edibility of a mushroom; no rule like ``leaflets three, let it be" for Poisonous Oak and Ivy.

In [ ]:

```
import pandas as pd
import numpy as np

# Load the dataset into a DataFrame
df = pd.read_csv("desktop\python\mushroom.csv")
# Display the column names and data types
print(df.columns)
print(df.dtypes)

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

# Check the unique values in each column
for column in df.columns:
    unique_values = df[column].unique()
    print(column, ":", unique_values)
import matplotlib.pyplot as plt
import seaborn as sns

# Example visualizations
# Plot the count of edible and poisonous mushrooms
plt.figure(figsize=(8, 6))
sns.countplot(x='class', data=df)
plt.title("Edible vs. Poisonous Mushrooms")
plt.xlabel("Class")
plt.ylabel("Count")
plt.show()

# Plot the distribution of cap shapes
plt.figure(figsize=(8, 6))
sns.countplot(x='cap-shape', hue='class', data=df)
plt.title("Distribution of Cap Shapes")
plt.xlabel("Cap Shape")
plt.ylabel("Count")
plt.show()

# Plot the correlation heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(df.corr(), annot=True, cmap='coolwarm')
plt.title("Correlation Heatmap")
plt.show()
```