In [155…

```python
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

df = pd.read_csv('Black_revised.csv')


species_counts = df['scientificname'].value_counts()

# Print the species and their counts
#for species, count in species_counts.items():
 #  print(f"Species: {species}, Count: {count}")


#print(df.columns)
```

In [156…

```python
# Group the data by 'Year collected' and 'Season collected' and count unique
species_richness = df.groupby(['yearcollected', 'seasoncollected'])['scienti


species_richness.rename(columns={'scientificname': 'Species Richness'}, inpl


print(species_richness)
```

```
   yearcollected seasoncollected  Species Richness
0           1982          summer                14
1           1985          summer                60
2           1986          summer                37
3           1988          summer                 5
4           1992          summer                 9
```

In [157…

```python
# Group the data by 'Year collected' and 'Season collected' and get unique s
species_richness = df.groupby(['yearcollected', 'seasoncollected', 'scientif


#print(species_richness)
```

In [158…

```python
# Group the data by 'Year collected' and 'Season collected' and get unique s
species_richness = df.groupby(['yearcollected', 'seasoncollected', 'scientif


sorted_species = species_richness.sort_values(by='Count', ascending=False)
threshold = 2

# Filter for species with counts above the threshold
high_count_species = sorted_species[sorted_species['Count'] > threshold]


print(high_count_species)
```

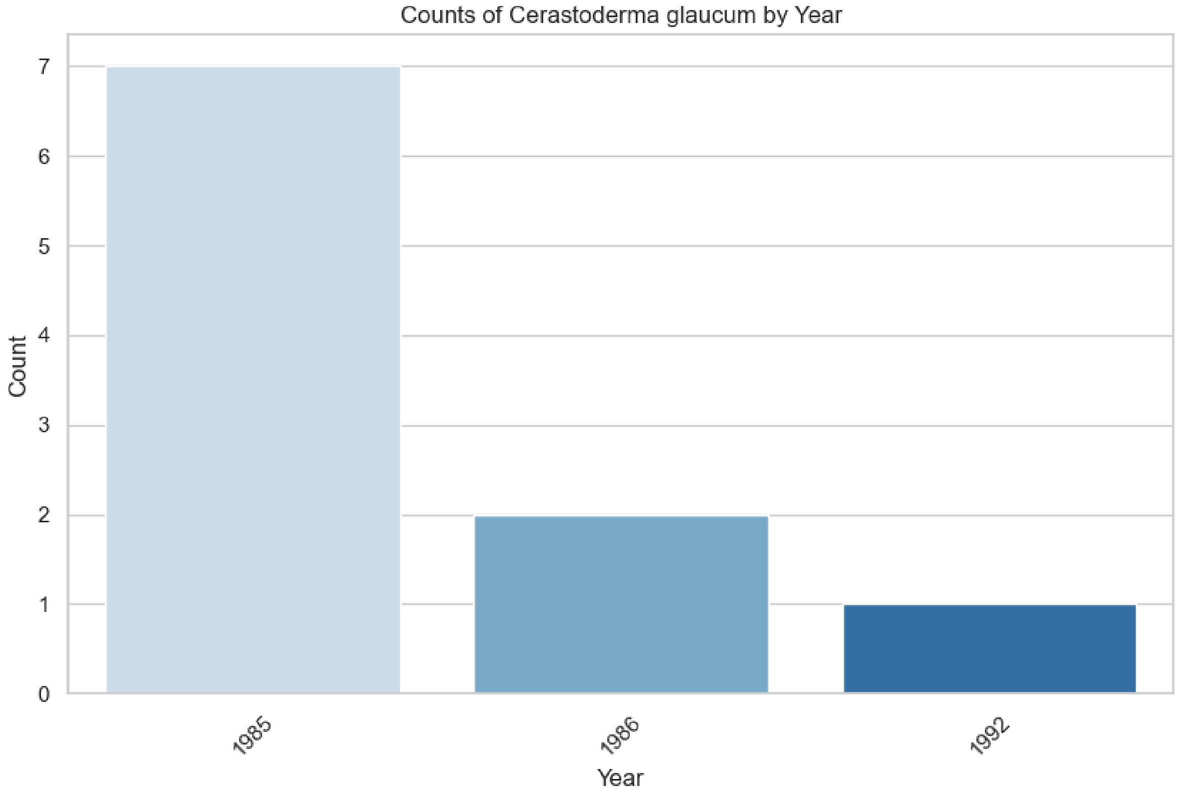
```
    yearcollected seasoncollected          scientificname  Count
26           1985          summer     Cerastoderma glaucum      7
53           1985          summer        Nephtys hombergii      6
27           1985          summer         Chamelea gallina      6
25           1985          summer       Capitella capitata      6
39           1985          summer           Hydrobia acuta      6
62           1985          summer         Polydora ciliata      5
21           1985          summer      Bittium reticulatum      5
29           1985          summer       Diogenes pugilator      4
46           1985          summer     Lucinella divaricata      4
36           1985          summer      Harmothoe imbricata      3
28           1985          summer           Cyclope neritea      3
52           1985          summer          Nephtys cirrosa      3
70           1985          summer      Spisula subtruncata      3
17           1985          summer          Alitta succinea      3
18           1985          summer  Amphibalanus improvisus      3
61           1985          summer       Polititapes aureus      3
```

In [ ]:

```

```

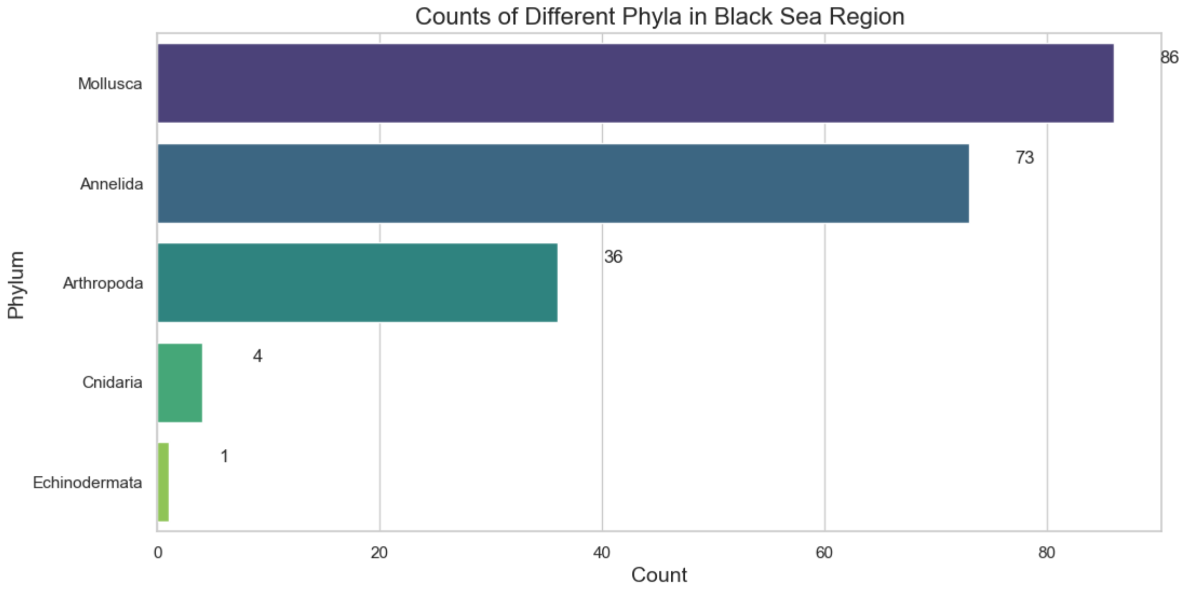
In [160…

```
# Filter the DataFrame for the species 'Cerastoderma glaucum'
cerastoderma_data = df[df['scientificname'] == 'Cerastoderma glaucum']


years_of_interest = [1992, 1986, 1988, 1985]
cerastoderma_counts = cerastoderma_data[cerastoderma_data['yearcollected'].i

# Group the filtered data by year and count the occurrences
counts_by_year = cerastoderma_counts.groupby('yearcollected')['scientificnam


plt.figure(figsize=(10, 6))
sns.barplot(x='yearcollected', y='Count', data=counts_by_year, palette='Blue
plt.xlabel('Year')
plt.ylabel('Count')
plt.title('Counts of Cerastoderma glaucum by Year')
plt.xticks(rotation=45)
plt.show()
```



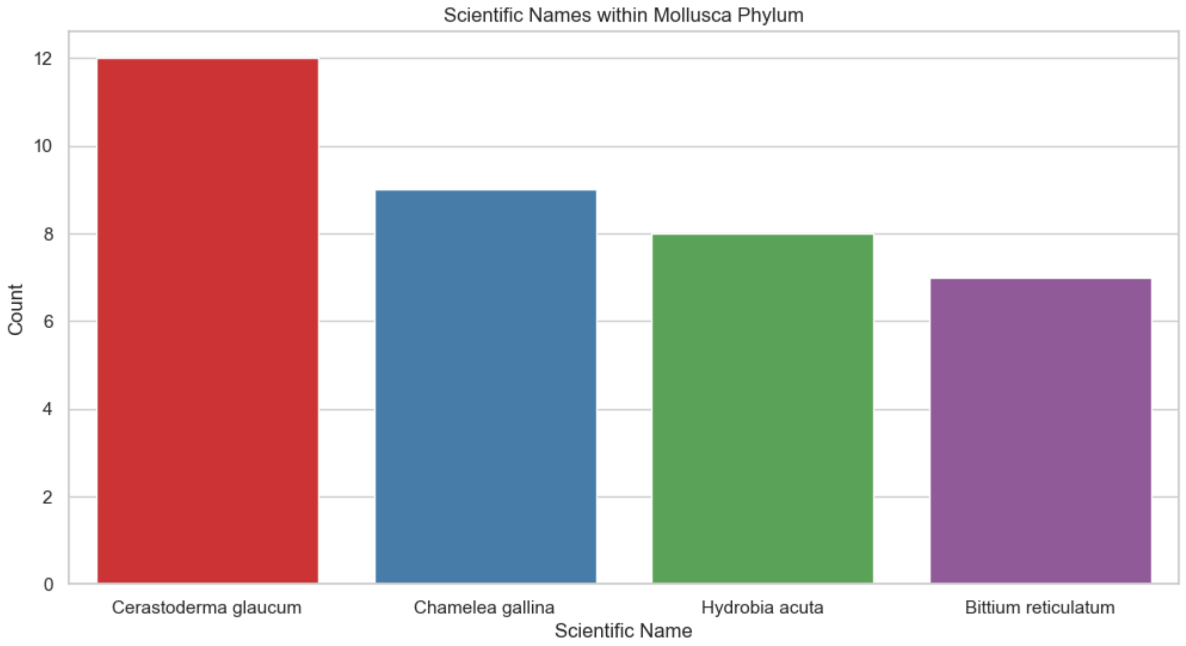
In [161…

```
# Group the data by 'phylum' and count the occurrences of each phylum
phylum_counts = df['phylum'].value_counts().reset_index()
phylum_counts.columns = ['Phylum', 'Count']


plt.figure(figsize=(12, 6))
sns.set(style="whitegrid")
ax = sns.barplot(x="Count", y="Phylum", data=phylum_counts, palette="viridis


plt.xlabel('Count', fontsize=14)
plt.ylabel('Phylum', fontsize=14)
plt.title('Counts of Different Phyla in Black Sea Region', fontsize=16)


for p in ax.patches:
    width = p.get_width()
    plt.text(width + 5, p.get_y() + p.get_height() / 2 - 0.2, int(width), ha

plt.savefig("phylum_counts_plot_Black_sea.pdf", format="pdf")
plt.show()
```



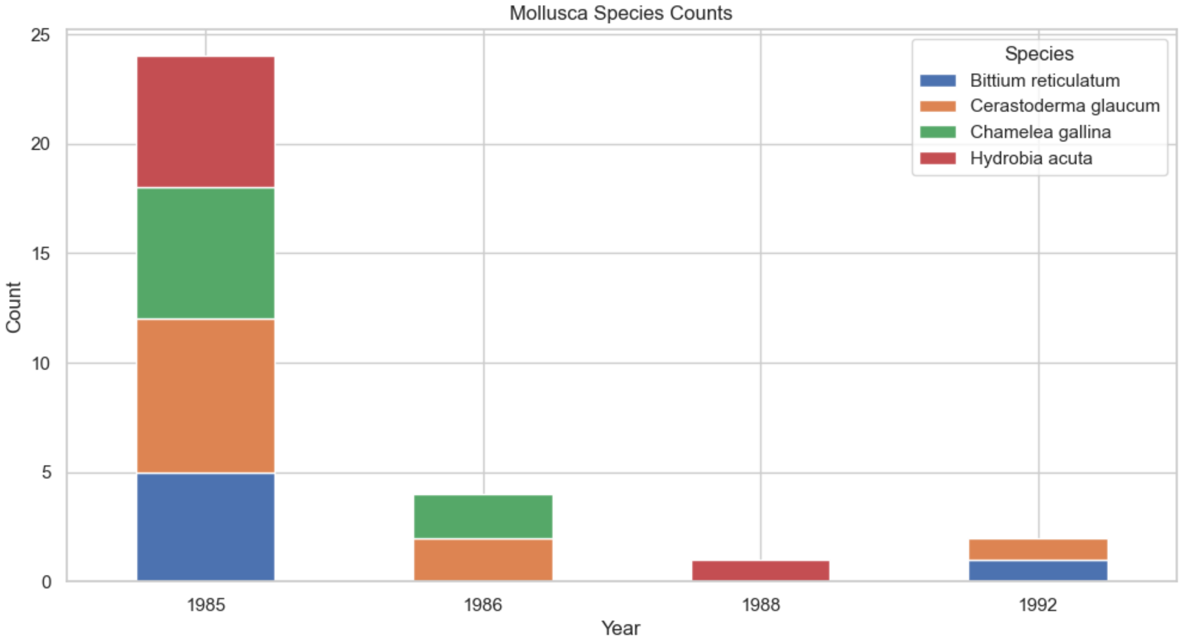
In [163…

```
#Mollusca
# Filter the DataFrame for rows where 'Phylum' is 'Mollusca'
mollusca_data = df[df['phylum'] == 'Mollusca']

# Count the occurrences of each unique scientific name within the 'Mollusca
scientificname_counts = mollusca_data['scientificname'].value_counts().reset
scientificname_counts.columns = ['Scientific Name', 'Count']


scientificname_counts = scientificname_counts[scientificname_counts['Count']


scientificname_counts = scientificname_counts.sort_values(by='Count', ascend


plt.figure(figsize=(12, 6))
sns.barplot(x='Scientific Name', y='Count', data=scientificname_counts, pale
plt.xlabel('Scientific Name')
plt.ylabel('Count')
plt.title('Scientific Names within Mollusca Phylum')
plt.xticks(rotation=0)
plt.show()
```



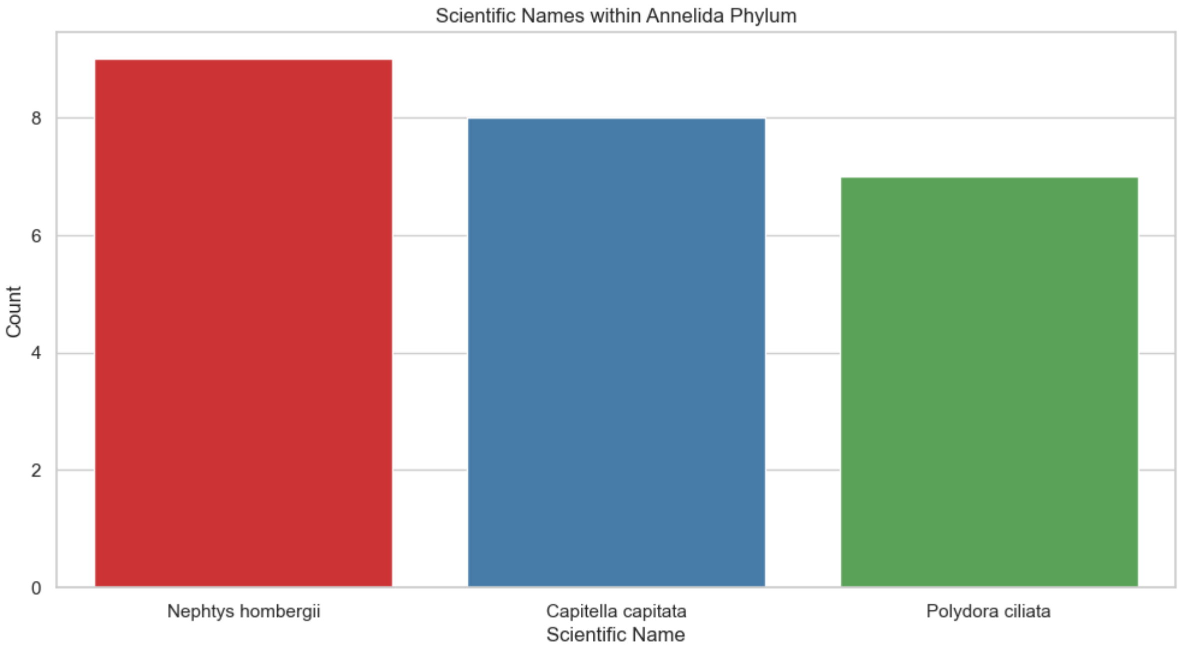
In [166…

```
#Mollusca Count over years


years_to_analyze = [1985, 1986, 1988, 1992]

species_to_plot = ['Cerastoderma glaucum', 'Chamelea gallina', 'Hydrobia acu

# Filter the DataFrame for the selected species and years
filtered_data = df[df['yearcollected'].isin(years_to_analyze) & df['scientif

# Group the data by species and year, and count the occurrences
species_counts = filtered_data.groupby(['yearcollected', 'scientificname']).


species_counts.plot(kind='bar', stacked=True, figsize=(12, 6))
plt.xlabel('Year')
plt.ylabel('Count')
plt.title('Mollusca Species Counts')
plt.xticks(rotation=0)
plt.legend(title='Species')
plt.savefig("Mollusca_Black_over_year.pdf", format="pdf")
plt.show()
```



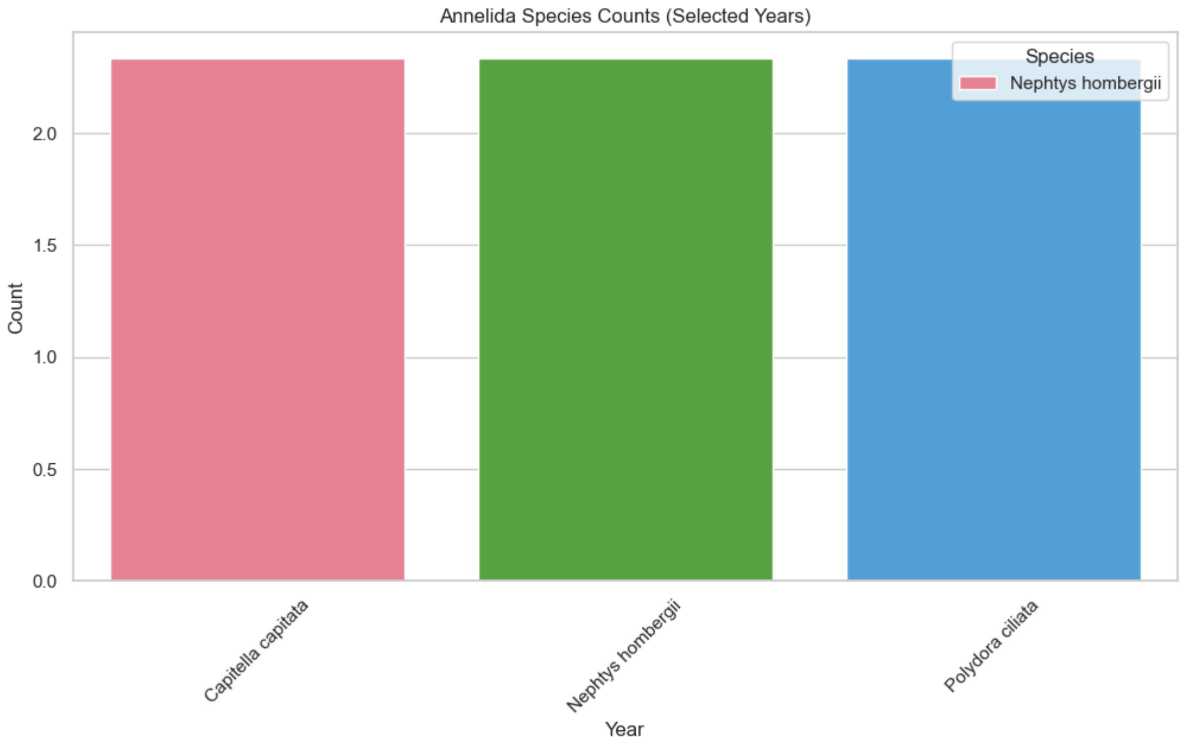
In [164…

```
#Annelida
# Filter the DataFrame for rows where 'Phylum' is 'Annelida'
annelida_data = df[df['phylum'] == 'Annelida']

# Count the occurrences of each unique scientific name within the 'Annelida
scientificname_counts = annelida_data['scientificname'].value_counts().reset
scientificname_counts.columns = ['Scientific Name', 'Count']


scientificname_counts = scientificname_counts[scientificname_counts['Count']


scientificname_counts = scientificname_counts.sort_values(by='Count', ascend


plt.figure(figsize=(12, 6))
sns.barplot(x='Scientific Name', y='Count', data=scientificname_counts, pale
plt.xlabel('Scientific Name')
plt.ylabel('Count')
plt.title('Scientific Names within Annelida Phylum')
plt.xticks(rotation=0)
plt.show()
```



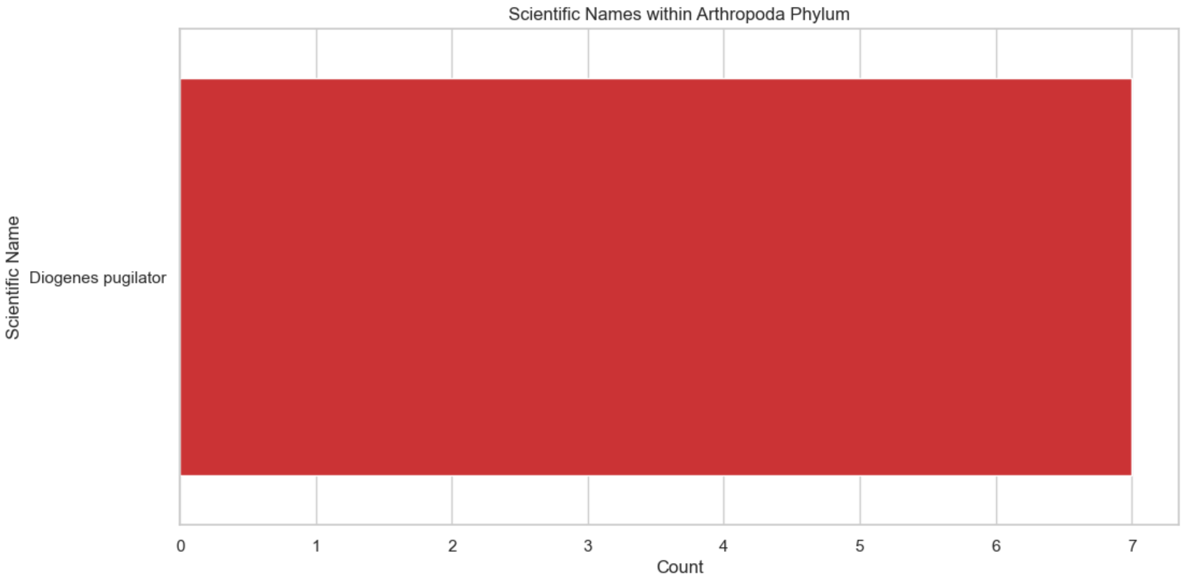
In [167…

```
#Annelida count over years


years_to_analyze = [1985, 1986, 1988, 1992]

species_to_plot = ['Nephtys hombergii', 'Polydora ciliata', 'Capitella capit


filtered_data = df[df['yearcollected'].isin(years_to_analyze) & df['scientif


species_counts = filtered_data.groupby(['yearcollected', 'scientificname']).


plt.figure(figsize=(12, 6))
sns.set_theme(style="whitegrid")
ax = sns.barplot(data=species_counts, ci=None, palette="husl", dodge=False)
ax.set_xlabel('Year')
ax.set_ylabel('Count')
ax.set_title('Annelida Species Counts (Selected Years)')
ax.set_xticklabels(ax.get_xticklabels(), rotation=45)
ax.legend(title='Species', labels=species_to_plot)
plt.show()
```



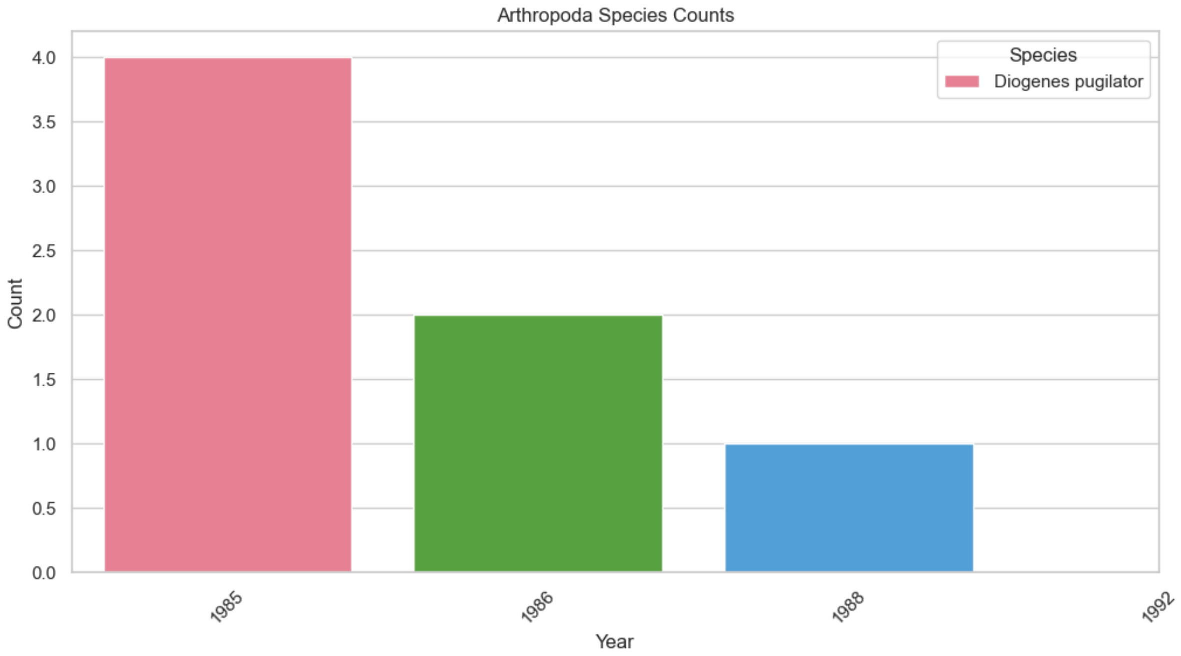
In [165…

```
#Anthropoda

# Filter the DataFrame for rows where 'Phylum' is 'Arthropoda'
arthropoda_data = df[df['phylum'] == 'Arthropoda']

# Count the occurrences of each unique scientific name within the 'Arthropod
scientificname_counts = arthropoda_data['scientificname'].value_counts().res
scientificname_counts.columns = ['Scientific Name', 'Count']


scientificname_counts = scientificname_counts[scientificname_counts['Count']


scientificname_counts = scientificname_counts.sort_values(by='Count', ascend


plt.figure(figsize=(12, 6))
sns.barplot(x='Count', y='Scientific Name', data=scientificname_counts, pale
plt.xlabel('Count')
plt.ylabel('Scientific Name')
plt.title('Scientific Names within Arthropoda Phylum')
plt.show()
```



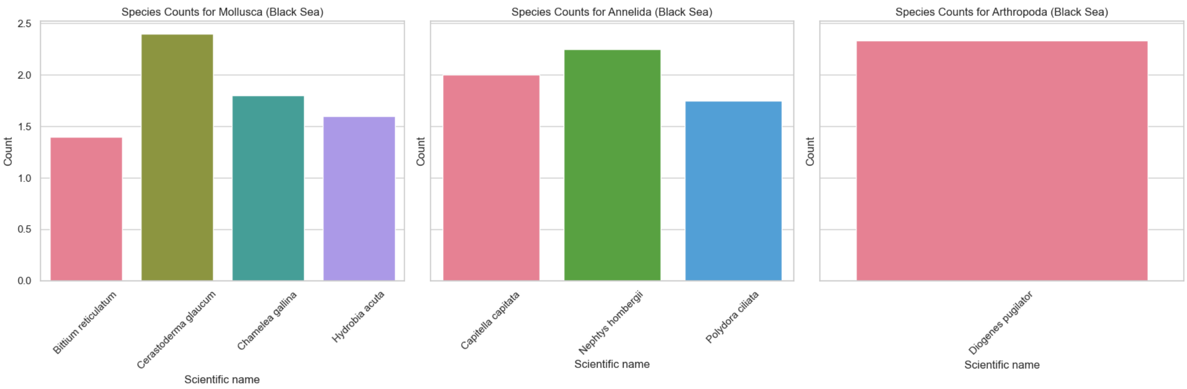
In [169…

```
years_to_analyze = [1985, 1986, 1988, 1992]

species_to_plot = ['Diogenes pugilator']


filtered_data = df[df['yearcollected'].isin(years_to_analyze) & df['scientif


species_counts = filtered_data.groupby(['yearcollected', 'scientificname']).


plt.figure(figsize=(12, 6))
sns.set_palette("Set1")
ax = sns.barplot(x=species_counts.index, y=species_counts.sum(axis=1), ci=No
ax.set_xlabel('Year')
ax.set_ylabel('Count')
ax.set_title('Arthropoda Species Counts')
ax.set_xticks(range(len(years_to_analyze)))
ax.set_xticklabels(years_to_analyze)
ax.legend(title='Species', labels=species_to_plot)
plt.xticks(rotation=45)
plt.savefig("Anthropoda_black_over_years.pdf", format="pdf")
plt.show()
```



In [189…

```
# Define the specific species for each phylum
mollusca_black_sea_species = ['Cerastoderma glaucum', 'Chamelea gallina', 'H
annelida_black_sea_species = ['Nephtys hombergii', 'Capitella capitata', 'Po
arthropoda_black_sea_species = ['Diogenes pugilator']


fig, axes = plt.subplots(1, 3, figsize=(18, 6), sharey=True)


for i, (phylum, species) in enumerate(zip(['Mollusca', 'Annelida', 'Arthropo
    phylum_data = df[(df['phylum'] == phylum) & (df['scientificname'].isin(s

    species_counts = phylum_data.groupby(['yearcollected', 'scientificname']

    ax = sns.barplot(data=species_counts, ci=None, palette="husl", dodge=Fal
    ax.set_xlabel('Scientific name')
    ax.set_ylabel('Count')
    ax.set_title(f'Species Counts for {phylum} (Black Sea)')
    ax.set_xticklabels(ax.get_xticklabels(), rotation=45)

plt.tight_layout()
plt.savefig("species_counts_plot_Black_Sea.pdf", format="pdf")
plt.show()
```



In [170…

```
import pandas as pd




species_to_count = [
    'Cerastoderma glaucum',
    'Chamelea gallina',
    'Hydrobia acuta',
    'Bittium reticulatum',
    'Nephtys hombergii',
    'Polydora ciliata',
    'Capitella capitata',
    'Diogenes pugilator'
]

# Filter the DataFrame for the selected species
filtered_data = df[df['scientificname'].isin(species_to_count)]

# Count the occurrences of each species
species_counts = filtered_data['scientificname'].value_counts()


for species, count in species_counts.items():
    print(f"Species: {species}, Count: {count}")
```

```
Species: Cerastoderma glaucum, Count: 12
Species: Chamelea gallina, Count: 9
Species: Nephtys hombergii, Count: 9
Species: Capitella capitata, Count: 8
Species: Hydrobia acuta, Count: 8
Species: Diogenes pugilator, Count: 7
Species: Polydora ciliata, Count: 7
Species: Bittium reticulatum, Count: 7
```

In [171…

```
import math


species_counts = {
    'Cerastoderma glaucum': 12,
    'Chamelea gallina': 9,
    'Nephtys hombergii': 9,
    'Capitella capitata': 8,
    'Hydrobia acuta': 8,
    'Diogenes pugilator': 7,
    'Polydora ciliata': 7,
    'Bittium reticulatum': 7
}

# Calculate the total abundance in the sample
total_abundance = sum(species_counts.values())

# Calculate the relative abundance (Pi) for each species
relative_abundance = {species: count / total_abundance for species, count in

# Calculate the natural logarithm (ln) of each Pi value
ln_pi_values = {species: math.log(pi) for species, pi in relative_abundance.

# Calculate Pi * ln(Pi) for each species
pi_ln_values = {species: pi * ln_pi for species, pi, ln_pi in zip(relative_a

# Calculate the Shannon Diversity Index (H) for this sample
shannon_index = -sum(pi_ln_values.values())


print(f"Shannon Diversity Index (H): {shannon_index:.3f}")
```

```
Shannon Diversity Index (H): 2.063
```

In [172…

```
import pandas as pd

df_train = pd.read_csv('Black_sea.csv')


selected_columns = df_train[['seasoncollected', 'phylum', 'yearcollected']]


output_csv_file = 'black_model_train.csv'


selected_columns.to_csv(output_csv_file, index=False)
```

In [179…

```
season_mapping = {"spring": 1, "summer": 0, "winter":2}


df['seasoncollected'] = df['seasoncollected'].map(season_mapping)

print(season_mapping)
```

```
{'spring': 1, 'summer': 0, 'winter': 2}
```

In [ ]:

```

```

In [178…

```python
df_m = pd.read_csv('black_model_train.csv')
df_m.head(3)

print(df_m.columns)
```

```
Index(['seasoncollected', 'phylum', 'yearcollected'], dtype='object')
```

In [180…

```python
phylum_mapping = {'Annelida': 0, 'Anthropoda': 1, 'Mollusca': 2}

# Map the 'phylum' column to binary values and create a new 'phylum_binary'
df_m['phylum_binary'] = df_m['phylum'].map(phylum_mapping)


print(df_m.head())
```

```
  seasoncollected      phylum  yearcollected  phylum_binary
0          summer    Mollusca           1986            2.0
1          summer  Arthropoda           1986            NaN
2          summer  Arthropoda           1986            NaN
3          summer  Arthropoda           1986            NaN
4          summer  Arthropoda           1986            NaN
```

In [185…

```python
# Drop rows with NaN values in the 'phylum_binary' column
df_m = df_m.dropna(subset=['phylum_binary'])

# Map 'seasoncollected' values to 0 for 'spring' and 1 for 'summer'
season_mapping = {'spring': 0, 'summer': 1}
df_m['SC'] = df_m['seasoncollected'].map(season_mapping)

# Convert 'phylum_binary' column to integers
df_m['phylum_binary'] = df_m['phylum_binary'].astype(int)


print(df_m.head())
```

```
   seasoncollected    phylum  yearcollected  phylum_binary  SC
0           summer  Mollusca           1986              2   1
5           summer  Annelida           1986              0   1
9           summer  Annelida           1986              0   1
10          summer  Mollusca           1986              2   1
11          summer  Annelida           1986              0   1
```

In [186…

```python
selected_phyla = ['Mollusca', 'Annelida', 'Anthropoda']
df_m = df_m[df_m['phylum'].isin(selected_phyla)]
df_m.drop(columns=['seasoncollected', 'phylum'], inplace=True)
df_m.head()
```

Out[186]:

	yearcollected	phylum_binary	SC
0	1986	2	1
5	1986	0	1
9	1986	0	1
10	1986	2	1
11	1986	0	1

In [187…

```python
from sklearn.svm import SVC
from sklearn.model_selection import train_test_split
```

```
# Separate the target variable from the features
X = df_m.drop(columns=['yearcollected'])
y = df_m['yearcollected']

# 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, rar

# Create and train the SVM model
clf = SVC(kernel='linear', C=1.0)
clf.fit(X_train, y_train)

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


from sklearn.metrics import accuracy_score
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)
```

```
Accuracy: 0.59375
```

In [188…

```
# Calculate the Pearson correlation coefficient and the p-value
correlation, p_value = pearsonr(df_m['phylum_binary'], df_m['yearcollected']

print(f"Pearson Correlation: {correlation:.2f}")
print(f"P-Value: {p_value:.2f}")
```

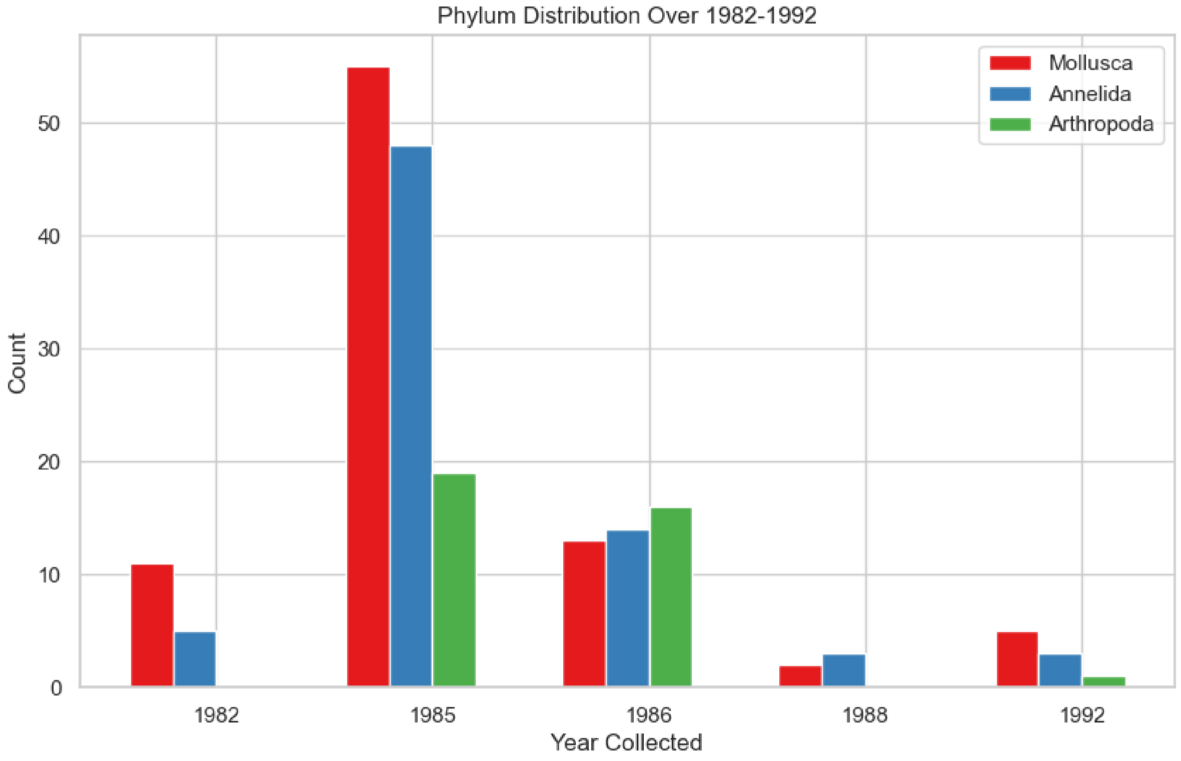
```
Pearson Correlation: -0.04
P-Value: 0.62
```

In [190…

```
import pandas as pd


tkc = pd.read_csv('Black_revised.csv')

# Filter the dataset for 'Phylum' values of 'Mollusca,' 'Annelida,' and 'Art
selected_phyla = ['Mollusca', 'Annelida', 'Arthropoda']
filtered_df =tkc[tkc['phylum'].isin(selected_phyla)]


selected_years = [1982, 1985, 1986, 1988, 1992]
filtered_df = filtered_df[filtered_df['yearcollected'].isin(selected_years)]
```

In [191…

```
import numpy as np


filtered_df['phylum'] = filtered_df['phylum'].str.strip()

# Group the data by 'Year Collected' and 'Phylum' and calculate the count
grouped_data = filtered_df.groupby(['yearcollected', 'phylum']).size().unsta


years = grouped_data.index.astype(str)


plt.figure(figsize=(10, 6))
bar_width = 0.2
for i, phylum in enumerate(selected_phyla):
    count = grouped_data[phylum]
    x_positions = np.arange(len(years)) + i * bar_width
    plt.bar(x_positions, count, width=bar_width, label=phylum)

plt.title('Phylum Distribution Over 1982-1992')
plt.xlabel('Year Collected')
plt.ylabel('Count')
plt.xticks(np.arange(len(years)) + (bar_width * len(selected_phyla)) / 2, ye
plt.legend()

plt.show()
```



In [ ]:

In [ ]:

In [ ]: