biodiversity project

June 21, 2024

1 Biodiversity in National Parks

[1]:

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
```

[2]:

```
spec = pd.read_csv('species_info.csv')
spec.head()
```

[2]:

```
  category                  scientific_name  \
0   Mammal  Clethrionomys gapperi gapperi
1   Mammal                        Bos bison
2   Mammal                       Bos taurus
3   Mammal                       Ovis aries
4   Mammal                   Cervus elaphus

                                        common_names conservation_status
0                           Gapper's Red-Backed Vole                 NaN
1                              American Bison, Bison                 NaN
2  Aurochs, Aurochs, Domestic Cattle (Feral), Dom…                 NaN
3  Domestic Sheep, Mouflon, Red Sheep, Sheep (Feral)                 NaN
4                                      Wapiti Or Elk                 NaN
```

[3]:

```
obs = pd.read_csv('observations.csv')
obs.head()
```

[3]:

```
            scientific_name                            park_name  observations
0        Vicia benghalensis  Great Smoky Mountains National Park            68
1            Neovison vison  Great Smoky Mountains National Park            77
2         Prunus subcordata               Yosemite National Park           138
3      Abutilon theophrasti                  Bryce National Park            84
4  Githopsis specularioides  Great Smoky Mountains National Park            85
```

2 Data Cleaning

[4]:

```
#check for null values
spec.isna().sum()
```

[4]:

```
category                 0
scientific_name          0
common_names             0
conservation_status   5633
dtype: int64
```

[5]:

```
spec.conservation_status.value_counts()
```

[5]:

```
conservation_status
Species of Concern    161
Endangered             16
Threatened             10
In Recovery             4
Name: count, dtype: int64
```

Majority of species has null values. Based on titles in conservation_status we see the null values most likely refers to animal species not in danger. However, it could also be missing data. for now I will change to unknown.

[6]:

```
spec = spec.fillna('Unknown')
```

[7]:

```
#for for duplicates
spec.duplicated().sum()
```

[7]:

```
0
```

[8]:

```
spec.category.value_counts()
```

[8]:

```
category
Vascular Plant       4470
Bird                  521
Nonvascular Plant     333
Mammal                214
Fish                  127
Amphibian              80
Reptile                79
Name: count, dtype: int64
```

[9]:

```
#storing known species in another df for future analysis
known_spec = spec[spec.conservation_status != 'Unknown'].reset_index().
 ↪drop('index',axis=1)
```

[10]:

```
obs.isna().sum()
```

[10]:
```
scientific_name    0
park_name          0
observations       0
dtype: int64
```

[11]:
```
obs.duplicated().sum()
```

[11]:
```
15
```

[12]:
```
#drop duplicates
obs = obs.drop_duplicates()
```

[13]:
```
obs
```

[13]:
```
                                   scientific_name  \
0                              Vicia benghalensis
1                                  Neovison vison
2                               Prunus subcordata
3                            Abutilon theophrasti
4                        Githopsis specularioides
…                                               …
23291                         Croton monanthogynus
23292                       Otospermophilus beecheyi
23293  Heterotheca sessiliflora ssp. echioides
23294                          Dicranella rufescens
23295                                Cucurbita pepo

                                park_name  observations
0      Great Smoky Mountains National Park            68
1      Great Smoky Mountains National Park            77
2                   Yosemite National Park           138
3                      Bryce National Park            84
4      Great Smoky Mountains National Park            85
…                                      …            …
23291               Yosemite National Park           173
23292                  Bryce National Park           130
23293                  Bryce National Park           140
23294               Yosemite National Park           171
23295               Yosemite National Park           164

[23281 rows x 3 columns]
```

[103]:
```
#combine into one df
model = obs.merge(spec, how='left', on='scientific_name')
```

[104]:
```
model.head()
```

[104]:

```
            scientific_name                            park_name  \
0        Vicia benghalensis  Great Smoky Mountains National Park
1            Neovison vison  Great Smoky Mountains National Park
2         Prunus subcordata               Yosemite National Park
3      Abutilon theophrasti                  Bryce National Park
4  Githopsis specularioides  Great Smoky Mountains National Park

   observations        category                        common_names  \
0            68  Vascular Plant  Purple Vetch, Reddish Tufted Vetch
1            77          Mammal                       American Mink
2           138  Vascular Plant                        Klamath Plum
3            84  Vascular Plant                          Velvetleaf
4            85  Vascular Plant                      Common Bluecup

  conservation_status
0             Unknown
1             Unknown
2             Unknown
3             Unknown
4             Unknown
```

Data is clean and ready for exploration

3 EDA

Lets explore data and answer following questions:
1. most popular categories 2. do categories differ on number of average observations 3. explore relationships between parks and observations as whole and for each category 4. explore relationships between conservation status and observations and category

3.1 Category Analysis

[16]:

```
#group category by sum and average
cat = model.groupby('category').agg(total = ('observations','sum'), average =␣
 ↪('observations','mean')).reset_index().sort_values('total', ascending=False)
```

[17]:

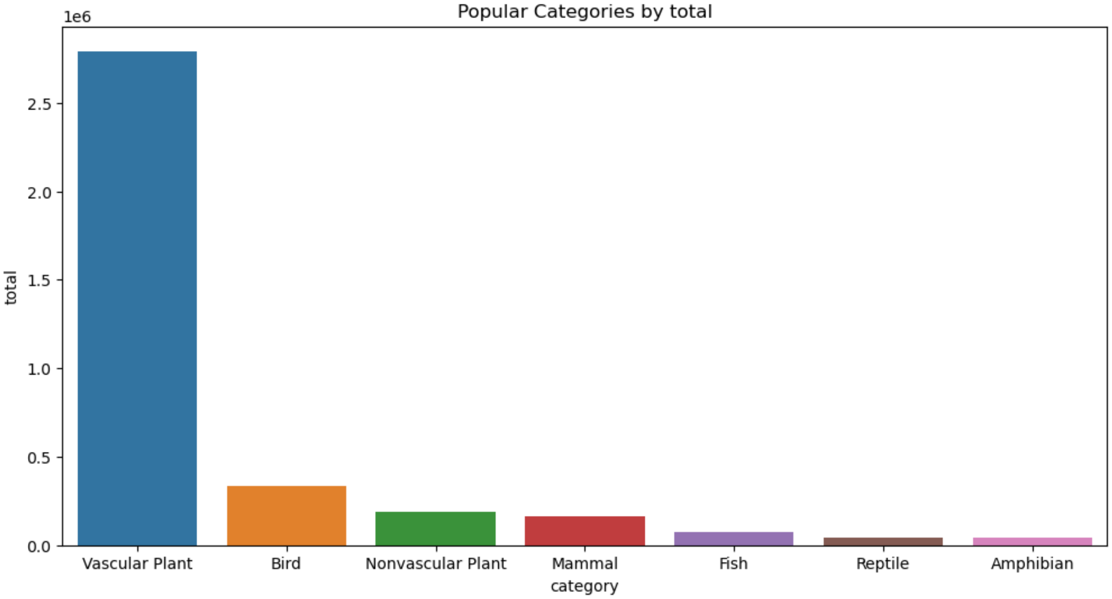
```
cat
```

[17]:

```
            category    total     average
6     Vascular Plant  2791714  142.915634
1               Bird   331606  140.451504
4  Nonvascular Plant   190653  143.132883
3             Mammal   162608  135.732888
2               Fish    72901  139.124046
5            Reptile    45822  141.425926
0          Amphibian    45068  137.402439
```

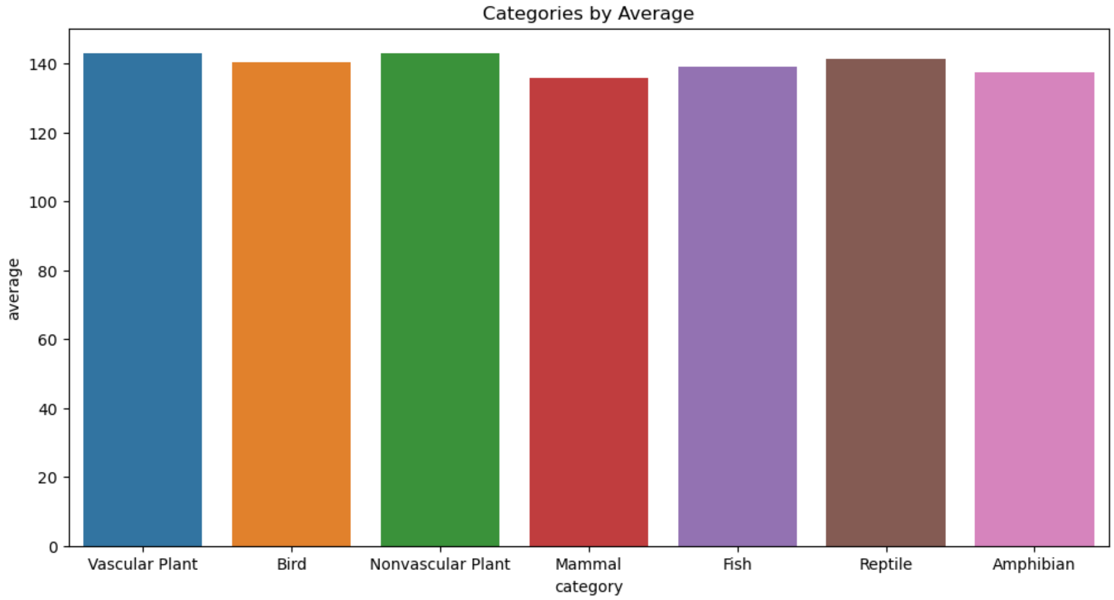
[18]:

```
#barplot of no. of observations for each category
plt.figure(figsize=(12,6))
sns.barplot(x = 'category', y='total',data=cat)
plt.title('Popular Categories by total')
plt.show()
```



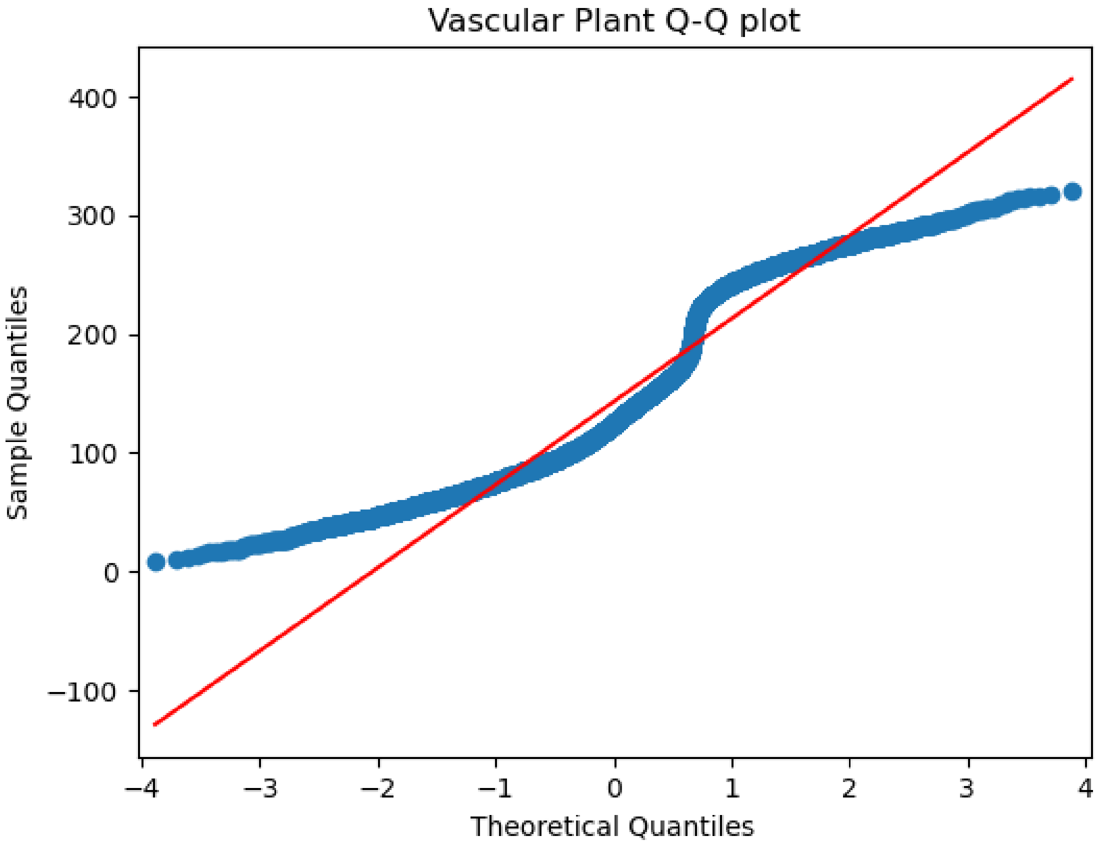
[19]:

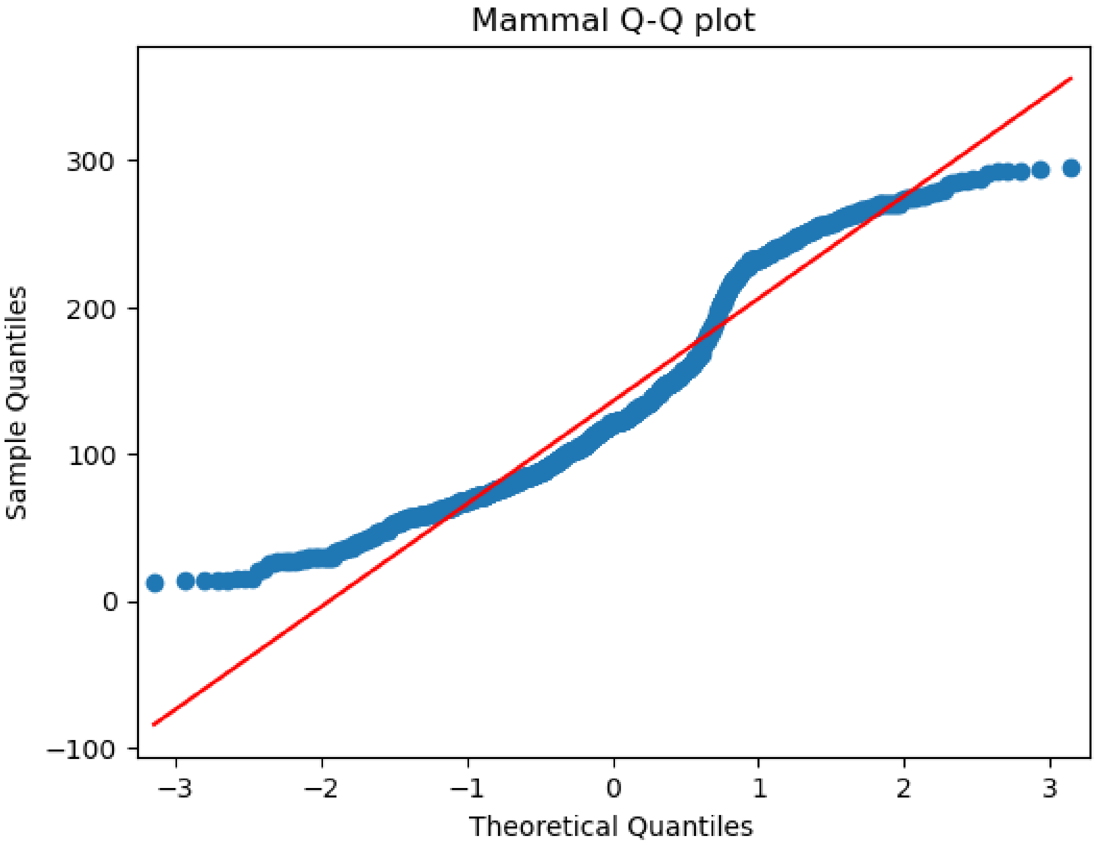
```
#barplot of average for each category
plt.figure(figsize=(12,6))
sns.barplot(x = 'category', y='average',data=cat)
plt.title('Categories by Average')
plt.show()
```

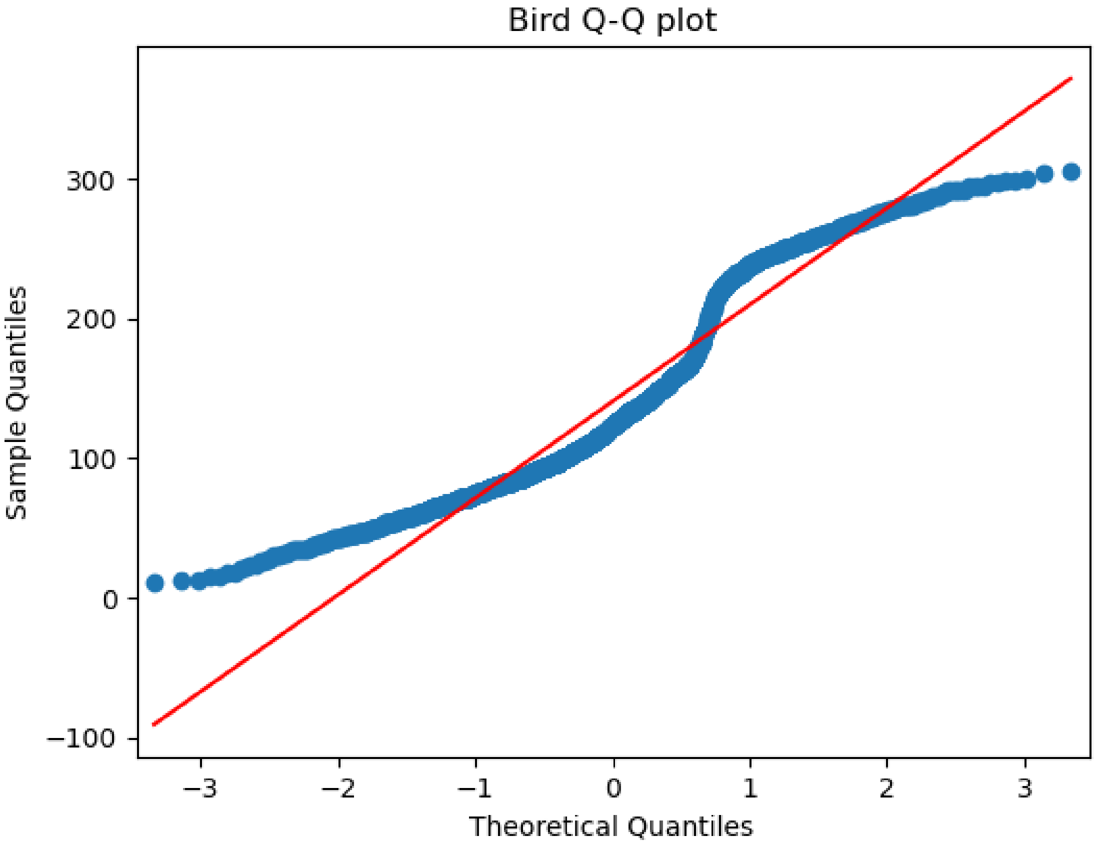


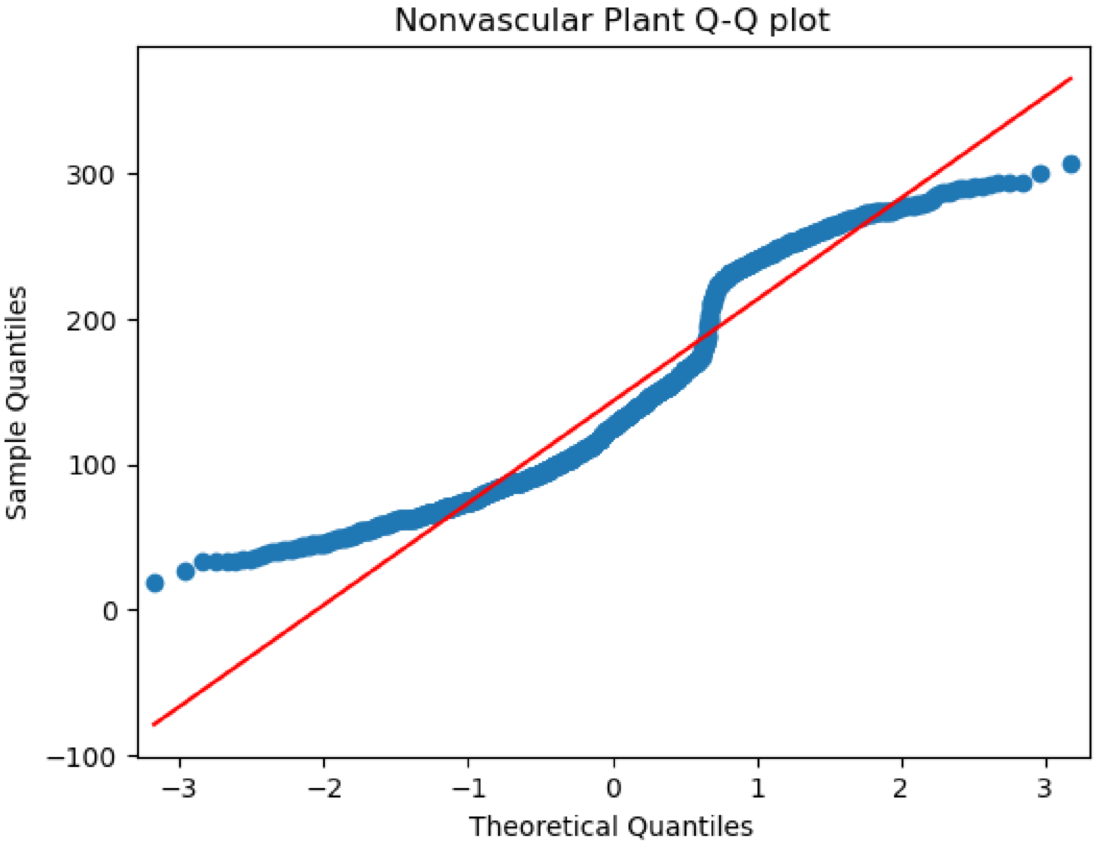
```
[20]: import statsmodels.api as sm
```

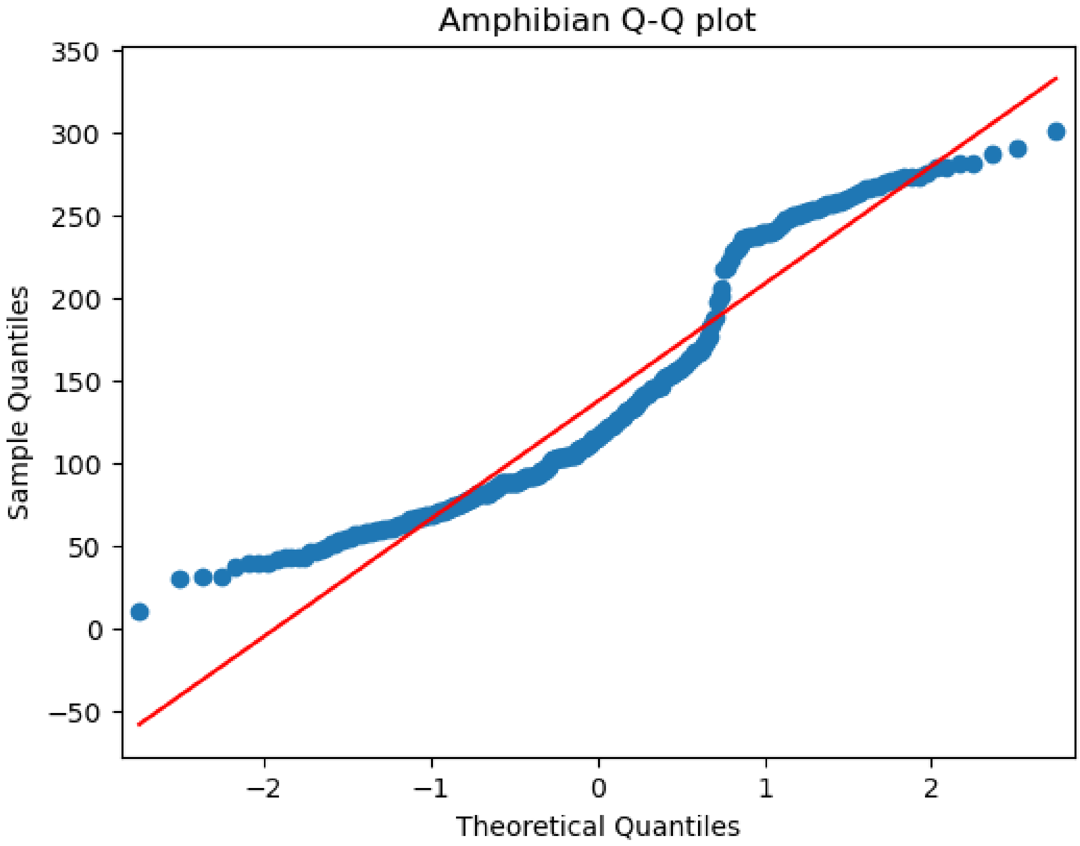
```
[21]: # test to each if category variables are normally distributed
      unique = model['category'].unique()
      for category in unique:
          pop = model[model.category == category]['observations']
          sm.qqplot(pop, line='s')
          plt.title(f'{category} Q-Q plot')
          plt.show()
```

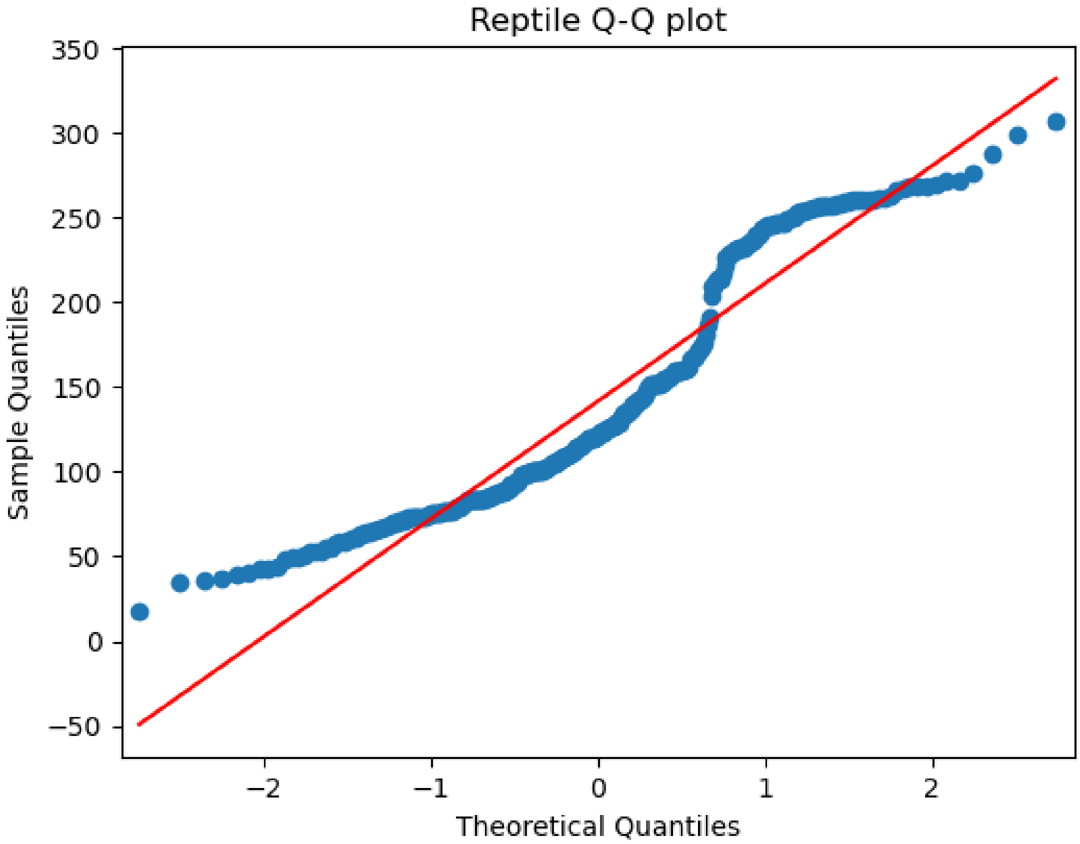

Vascular Plant Q-Q plot
Sample Quantiles
400
300
200
100
0
−100
Theoretical Quantiles
−4
−3
−2
−1
0
1
2
3
4

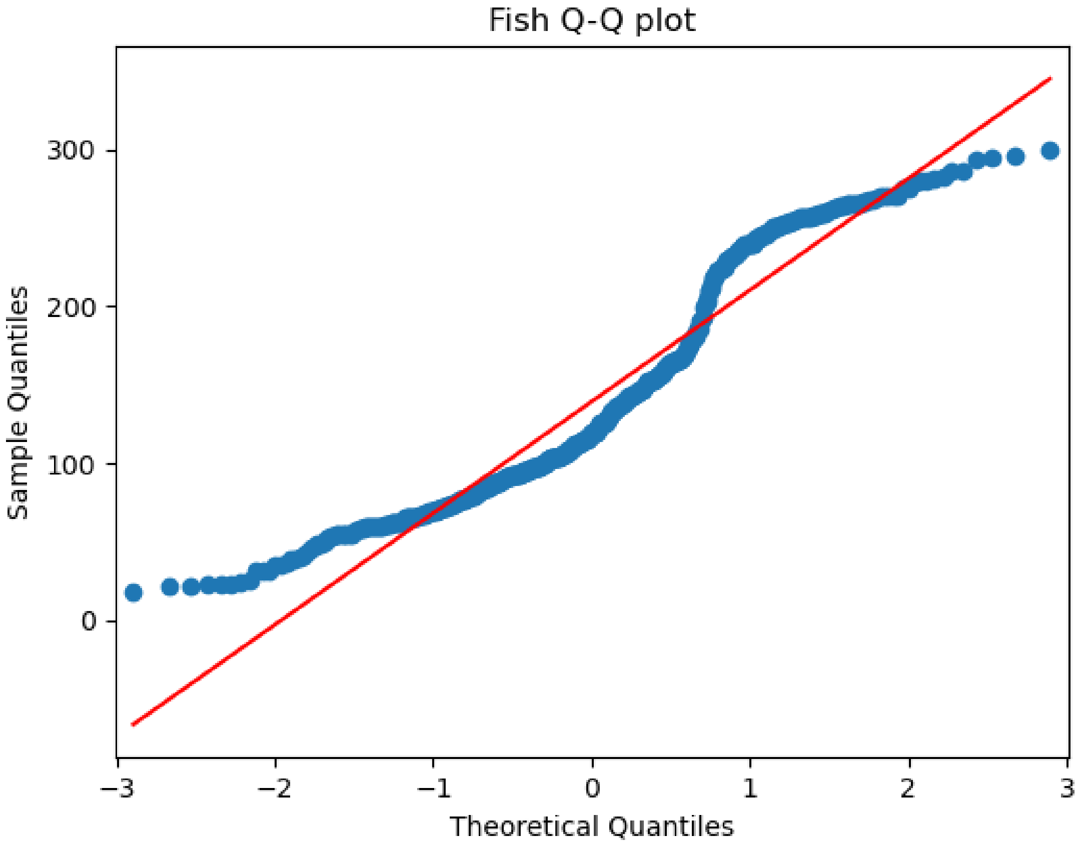

Mammal Q-Q plot
Sample Quantiles
300
200
100
0
−100
−3
−2
−1
0
1
2
3
Theoretical Quantiles


Bird Q-Q plot
Sample Quantiles
300
200
100
0
−100
−3
−2
−1
0
1
2
3
Theoretical Quantiles


Nonvascular Plant Q-Q plot
Sample Quantiles
300
200
100
0
−100
Theoretical Quantiles
−3
−2
−1
0
1
2
3


Amphibian Q-Q plot
350
300
250
200
150
100
50
0
−50
Sample Quantiles
−2
−1
0
1
2
Theoretical Quantiles


Reptile Q-Q plot
Sample Quantiles
Theoretical Quantiles
350
300
250
200
150
100
50
0
−50
−2
−1
0
1
2



[22]:

```
#Perform Anova test to compare to see if there is a difference in averages
from statsmodels.formula.api import ols
from statsmodels.stats.multicomp import pairwise_tukeyhsd
#turn time column into category for anova



# Fit ANOVA model
anova = ols('observations ~ C(category)', data=model).fit()

# Perform ANOVA (Type 1)
anova_table = sm.stats.anova_lm(anova, typ=1)
anova_table
```

[22]:

```
                  df        sum_sq       mean_sq         F    PR(>F)
C(category)      6.0  8.118702e+04  13531.169752  2.770437  0.010792
Residual     25594.0  1.250044e+08   4884.128104       NaN       NaN
```

Anova table shows there is a difference in means so we will do post ad hoc test

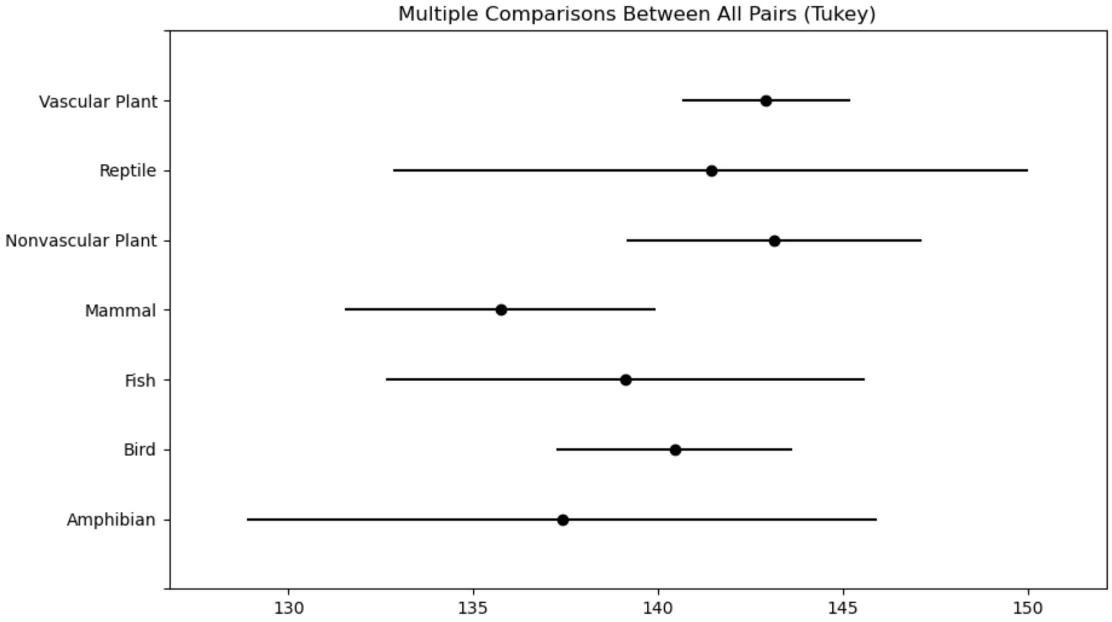
[23]:

```
# Perform the Tukey's HSD post hoc test eg, sub your groups in
tukey_results = pairwise_tukeyhsd(endog=model['observations'],␣
 ↪groups=model['category'], alpha=0.05)

print(tukey_results)

#show plot of results
tukey_results.plot_simultaneous()
plt.show()
```

```
            Multiple Comparison of Means - Tukey HSD, FWER=0.05
===========================================================================
      group1            group2      meandiff p-adj   lower    upper  reject
---------------------------------------------------------------------------
        Amphibian              Bird   3.0491 0.9901  -9.0936 15.1917  False
        Amphibian              Fish   1.7216 0.9999 -12.7868   16.23  False
        Amphibian            Mammal  -1.6696 0.9998  -14.511 11.1719  False
        Amphibian Nonvascular Plant   5.7304 0.8379  -6.9714 18.4323  False
        Amphibian           Reptile   4.0235 0.9904  -12.117  20.164  False
        Amphibian    Vascular Plant   5.5132 0.7929  -5.9599 16.9863  False
             Bird              Fish  -1.3275 0.9997 -11.2784  8.6234  False
             Bird            Mammal  -4.7186  0.478 -12.0282  2.5909  False
             Bird Nonvascular Plant   2.6814 0.9223    -4.38  9.7428  False
             Bird           Reptile   0.9744    1.0 -11.2339 13.1827  False
             Bird    Vascular Plant   2.4641 0.6705  -2.0257   6.954  False
             Fish            Mammal  -3.3912 0.9684 -14.1837  7.4014  False
             Fish Nonvascular Plant   4.0088 0.9246  -6.6173 14.6349  False
             Fish           Reptile   2.3019 0.9992 -12.2615 16.8653  False
             Fish    Vascular Plant   3.7916 0.8844  -5.3303 12.9135  False
           Mammal Nonvascular Plant      7.4 0.1088  -0.8051 15.6051  False
           Mammal           Reptile    5.693 0.8518  -7.2105 18.5966  False
           Mammal    Vascular Plant   7.1827   0.01   1.0494 13.3161   True
Nonvascular Plant           Reptile   -1.707 0.9997 -14.4716 11.0577  False
Nonvascular Plant    Vascular Plant  -0.2172    1.0  -6.0527  5.6182  False
          Reptile    Vascular Plant   1.4897 0.9998 -10.0529 13.0323  False
---------------------------------------------------------------------------
```



Tukey test shows mammals and Vascular plants have different means, vascular is higher. Otherwise every other mean is not statistically different.

Analysis of categories shows vascular plants had highest observations, but on average all the same except for mammals and vascularr plants, vascular plants has higher mean.

3.2 Location Analysis

[24]:
```
model.head()
```

[24]:
```
            scientific_name                            park_name  \
0        Vicia benghalensis  Great Smoky Mountains National Park
1            Neovison vison  Great Smoky Mountains National Park
2         Prunus subcordata               Yosemite National Park
3      Abutilon theophrasti                  Bryce National Park
4  Githopsis specularioides  Great Smoky Mountains National Park

   observations        category                        common_names  \
0            68  Vascular Plant  Purple Vetch, Reddish Tufted Vetch
1            77          Mammal                       American Mink
2           138  Vascular Plant                        Klamath Plum
3            84  Vascular Plant                          Velvetleaf
4            85  Vascular Plant                      Common Bluecup

  conservation_status
0             Unknown
1             Unknown
```

```
2              Unknown
3              Unknown
4              Unknown
```

[25]:

```
park = model.groupby('park_name').
 ↪agg(total=('observations','sum'),average=('observations','mean')).
 ↪reset_index().sort_values('total',ascending=False)
```

[26]:

```
park = park.reset_index().drop('index',axis=1)
```

[27]:

```
park
```

[27]:

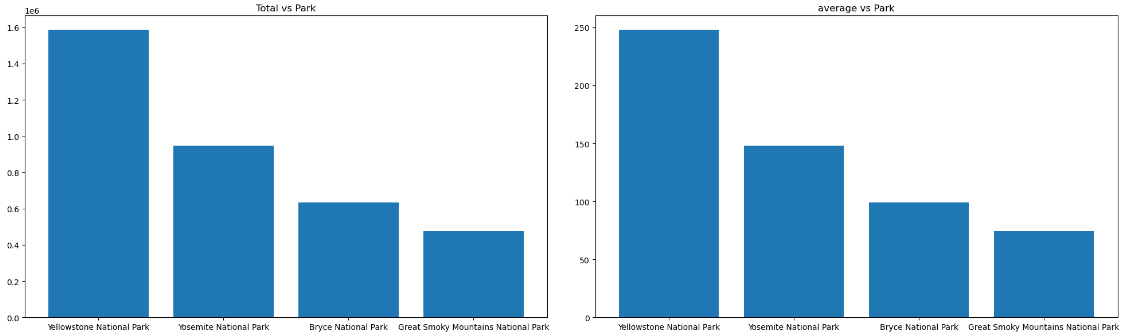
```
                             park_name    total     average
0             Yellowstone National Park  1584890  247.755198
1                Yosemite National Park   948460  148.150578
2                   Bryce National Park   633043   98.820325
3  Great Smoky Mountains National Park   473979   74.105535
```

[28]:

```
#create bar plots for total and average
fig, axs = plt.subplots(1,2,figsize=(20,6))
axs[0].bar(park.park_name,park.total)
axs[0].set_title('Total vs Park')

axs[1].bar(park.park_name, park.average)
axs[1].set_title('average vs Park')

plt.tight_layout()
plt.show()
```



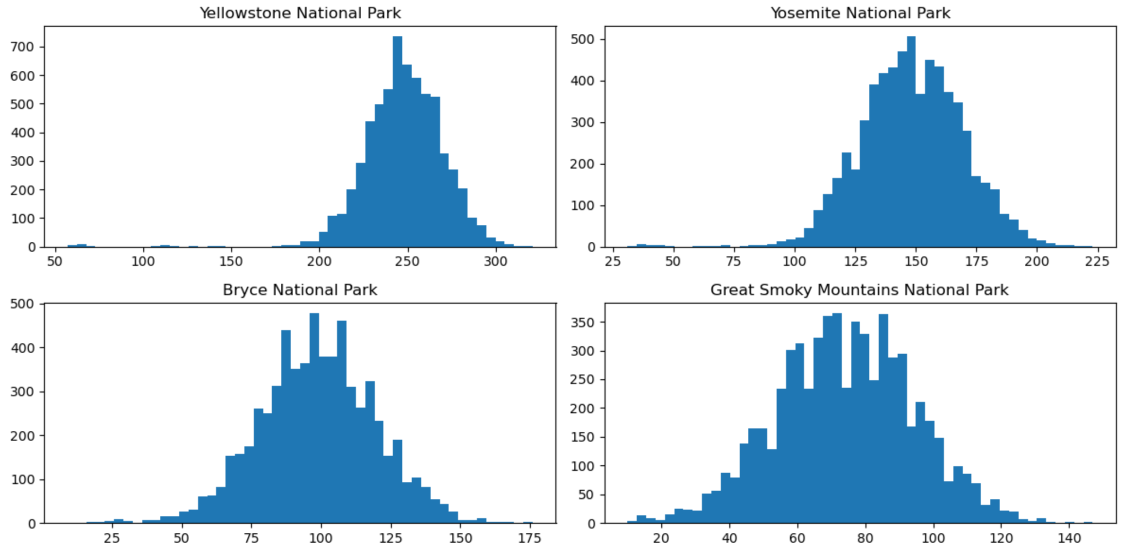
[29]:

```
#create hist plots for each park
fig, axs = plt.subplots(2,2,figsize=(12,6))
axs[0,0].hist(model[model['park_name']== 'Yellowstone National␣
 ↪Park']['observations'], bins = 50)
axs[0,0].set_title('Yellowstone National Park')
```

```
axs[0,1].hist(model[model['park_name']== 'Yosemite National␣
 ↪Park']['observations'], bins = 50)
axs[0,1].set_title('Yosemite National Park')

axs[1,0].hist(model[model['park_name']== 'Bryce National␣
 ↪Park']['observations'], bins = 50)
axs[1,0].set_title('Bryce National Park')

axs[1,1].hist(model[model['park_name']== 'Great Smoky Mountains National␣
 ↪Park']['observations'], bins = 50)
axs[1,1].set_title('Great Smoky Mountains National Park')
plt.tight_layout()
plt.show()
```



histplots show data appears to be normally distributed so we can do anova test now.

[30]:
```
# Fit ANOVA model
anova = ols('observations ~ C(park_name)', data=model).fit()

# Perform ANOVA (Type 1)
anova_table = sm.stats.anova_lm(anova, typ=1)
anova_table
```

[30]:
```
                    df        sum_sq       mean_sq             F  PR(>F)
C(park_name)       3.0  1.132135e+08  3.773785e+07  81365.742825     0.0
Residual       25597.0  1.187202e+07  4.638051e+02           NaN     NaN
```

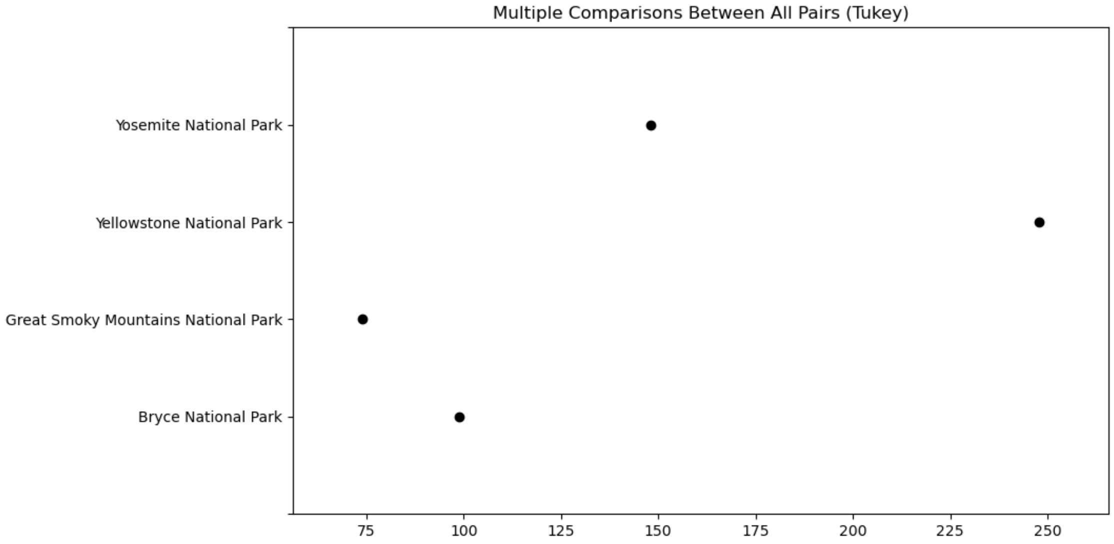
[31]:

```
# Perform the Tukey's HSD post hoc test since p-value < 0.05 for anova
tukey_results = pairwise_tukeyhsd(endog=model['observations'],␣
 ↪groups=model['park_name'], alpha=0.05)

print(tukey_results)

#show plot of results
tukey_results.plot_simultaneous()
plt.show()
```

```
                              Multiple Comparison of Means - Tukey HSD,
FWER=0.05
================================================================================
================================
               group1                              group2               meandiff
p-adj   lower    upper   reject
--------------------------------------------------------------------------------
--------------------------------
                Bryce National Park Great Smoky Mountains National Park -24.7148
0.0  -25.6928 -23.7367   True
                Bryce National Park           Yellowstone National Park 148.9349
0.0  147.9569 149.9129   True
                Bryce National Park              Yosemite National Park  49.3303
0.0   48.3524  50.3081   True
Great Smoky Mountains National Park           Yellowstone National Park 173.6497
0.0  172.6713  174.628   True
Great Smoky Mountains National Park              Yosemite National Park   74.045
0.0   73.0668  75.0232   True
          Yellowstone National Park              Yosemite National Park -99.6046
0.0 -100.5828 -98.6265   True
--------------------------------------------------------------------------------
--------------------------------
```



Tukey test shows to reject all nulls, hence all means are different. Yellowstone, Yosemite, Great Smoky and Bryce is descending order of means. Shows which parks are most popular.

3.3 Category and Park Analysis

```
[32]: cat_pat = model.groupby(['category','park_name'])['observations'].sum().
        ↪reset_index()
```

```
[33]: cat_pat
```

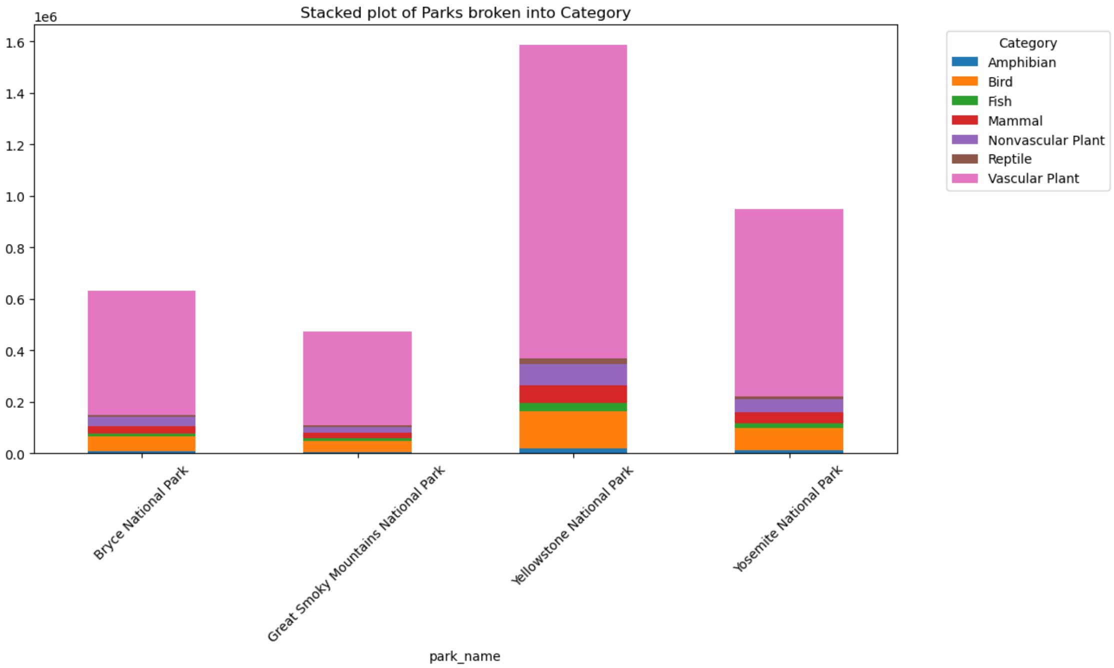
```
[33]:             category                            park_name  observations
      0          Amphibian                  Bryce National Park          7542
      1          Amphibian  Great Smoky Mountains National Park          5876
      2          Amphibian            Yellowstone National Park         19937
      3          Amphibian               Yosemite National Park         11713
      4               Bird                  Bryce National Park         58590
      5               Bird  Great Smoky Mountains National Park         42869
      6               Bird            Yellowstone National Park        143535
      7               Bird               Yosemite National Park         86612
      8               Fish                  Bryce National Park         12823
      9               Fish  Great Smoky Mountains National Park          9482
      10              Fish            Yellowstone National Park         31459
      11              Fish               Yosemite National Park         19137
      12            Mammal                  Bryce National Park         28830
      13            Mammal  Great Smoky Mountains National Park         21056
      14            Mammal            Yellowstone National Park         70189
      15            Mammal               Yosemite National Park         42533
      16  Nonvascular Plant                  Bryce National Park         32992
      17  Nonvascular Plant  Great Smoky Mountains National Park         24857
```

```
18  Nonvascular Plant           Yellowstone National Park        83021
19  Nonvascular Plant              Yosemite National Park        49783
20            Reptile                 Bryce National Park         8141
21            Reptile  Great Smoky Mountains National Park         5841
22            Reptile           Yellowstone National Park        20061
23            Reptile              Yosemite National Park        11779
24     Vascular Plant                 Bryce National Park       484125
25     Vascular Plant  Great Smoky Mountains National Park       363998
26     Vascular Plant           Yellowstone National Park      1216688
27     Vascular Plant              Yosemite National Park       726903
```

[34]:
```
#create pivot df to have park_name as columns
pivot = cat_pat.pivot(columns='category', index = 'park_name', values =␣
 ↪'observations')
```

[35]:
```
#create stacked bar chart
pivot.plot(kind = 'bar', stacked = True, figsize=(12,6))
plt.xticks(rotation=45)
plt.title('Stacked plot of Parks broken into Category')
plt.legend(title='Category', bbox_to_anchor=(1.05, 1), loc='upper left')

plt.show()
```



From graph can see each park has a lot of vascular plant. I will remove vascular plant so I can see a better distribution of each category as some are too tiny to view

[36]:

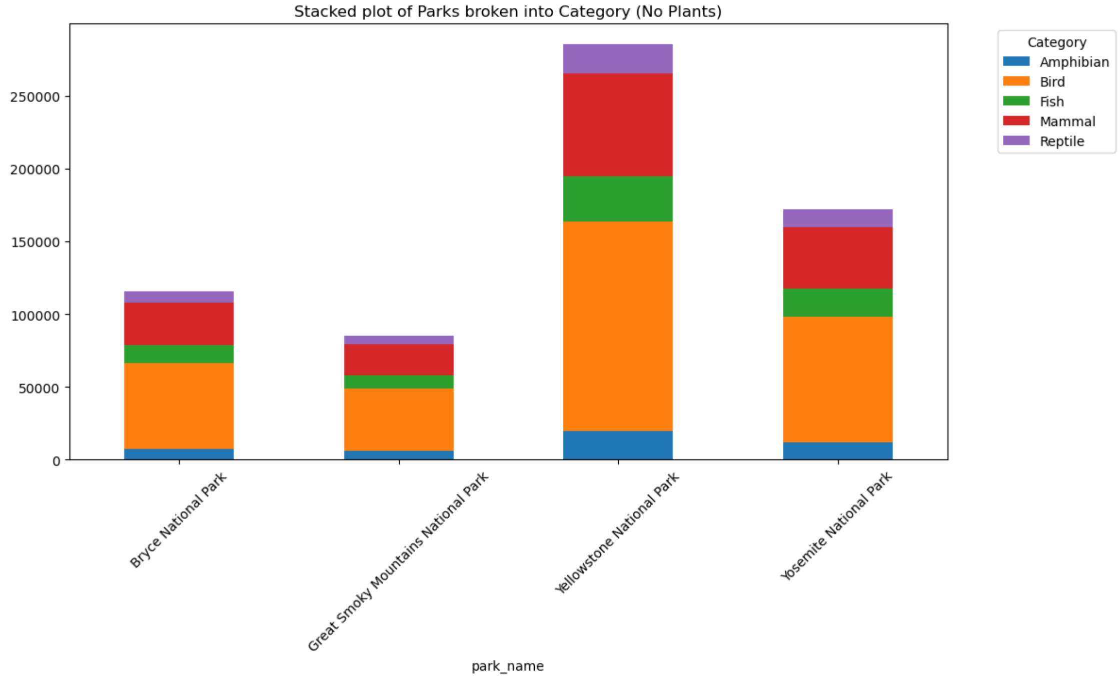
```
#remove vascular plant and nonvusclar plant
no_plant = cat_pat[(cat_pat.category != 'Vascular Plant') & (cat_pat.category !
 ↪= 'Nonvascular Plant')]
```

[37]:

```
#repeat above to get stacked chart
pivot = no_plant.pivot(columns='category', index = 'park_name', values =␣
 ↪'observations')

#create stacked bar chart
pivot.plot(kind = 'bar', stacked = True, figsize=(12,6))
plt.xticks(rotation=45)
plt.title('Stacked plot of Parks broken into Category (No Plants)')
plt.legend(title='Category', bbox_to_anchor=(1.05, 1), loc='upper left')

plt.show()
```



[38]:

```
from scipy.stats import chi2_contingency

# Create contingency table
contingency_table = pd.crosstab(cat_pat['category'],␣
 ↪cat_pat['park_name'],values=cat_pat['observations'], aggfunc='sum')

# Perform chi-square test
chi2, p, dof, expected = chi2_contingency(contingency_table)
print(f'Chi-square statistic: {chi2}, p-value: {p}')
```

```
Chi-square statistic: 77.43347812940053, p-value: 2.4006277787402894e-09
```

```
[39]: contingency_table
```

```
[39]: park_name          Bryce National Park  Great Smoky Mountains National Park  \
      category
      Amphibian                         7542                                 5876
      Bird                             58590                                42869
      Fish                             12823                                 9482
      Mammal                           28830                                21056
      Nonvascular Plant                32992                                24857
      Reptile                           8141                                 5841
      Vascular Plant                  484125                               363998

      park_name          Yellowstone National Park  Yosemite National Park
      category
      Amphibian                              19937                   11713
      Bird                                  143535                   86612
      Fish                                   31459                   19137
      Mammal                                 70189                   42533
      Nonvascular Plant                      83021                   49783
      Reptile                                20061                   11779
      Vascular Plant                       1216688                  726903
```

The null hypothesis in a chi-square test is that there is no association between the two categories based on observed frequencies. Since p-value is 0.000 (3 dp) I can reject the null and I conclude that statistically speaking the location and category will have an impact on the amount of each species present. I will repeat for no plant df to see if plant data makes an impact.

```
[40]: # Create contingency table
      contingency_table1 = pd.crosstab(no_plant['category'],␣
       ↪no_plant['park_name'],values=no_plant['observations'], aggfunc='sum')

      # Perform chi-square test
      chi2, p, dof, expected = chi2_contingency(contingency_table1)
      print(f'Chi-square statistic: {chi2}, p-value: {p}')
```

```
Chi-square statistic: 40.35780021019432, p-value: 6.270748523339204e-05
```

```
[41]: contingency_table1
```

```
[41]: park_name  Bryce National Park  Great Smoky Mountains National Park  \
      category
      Amphibian                 7542                                 5876
      Bird                     58590                                42869
      Fish                     12823                                 9482
      Mammal                   28830                                21056
      Reptile                   8141                                 5841
```

```
park_name  Yellowstone National Park  Yosemite National Park
category
Amphibian                      19937                   11713
Bird                          143535                   86612
Fish                           31459                   19137
Mammal                         70189                   42533
Reptile                        20061                   11779
```

Same results as above, 0.000 p-value. Hence, there is an association between park and all species.

[42]:

```
#mearue correlation between each categorical data

# Number of observations
n = contingency_table.sum().sum()

# Calculate Cramer's V
cramers_v = np.sqrt(chi2 / (n * (min(contingency_table.shape) - 1)))

print(f'Cramer\'s V: {cramers_v}')
```

```
Cramer's V: 0.0019223401335661508
```

Cramer's V test of 0.00266 shows a very weak association between category and park names

[43]:

```
#mearue correlation between each categorical data for animals

# Number of observations
n = contingency_table1.sum().sum()

# Calculate Cramer's V
cramers_v = np.sqrt(chi2 / (n * (min(contingency_table1.shape) - 1)))

print(f'Cramer\'s V: {cramers_v}')
```

```
Cramer's V: 0.004521562296818128
```

Slightly stronger association between park and animals, but still very weak.

These findings suggest that while there is a statistically significant association between the categories of species and the national parks, the strength of this association is minimal. This could imply that other unmeasured factors may play a more substantial role in determining the distribution of species across different parks.

3.4 Conservation Status analysis

[44]:

```
model.head()
```

[44]:

```
          scientific_name                            park_name  \
0      Vicia benghalensis  Great Smoky Mountains National Park
1          Neovison vison  Great Smoky Mountains National Park
```

```
2         Prunus subcordata              Yosemite National Park
3      Abutilon theophrasti                 Bryce National Park
4  Githopsis specularioides  Great Smoky Mountains National Park

   observations        category                        common_names  \
0            68  Vascular Plant  Purple Vetch, Reddish Tufted Vetch
1            77          Mammal                       American Mink
2           138  Vascular Plant                        Klamath Plum
3            84  Vascular Plant                          Velvetleaf
4            85  Vascular Plant                      Common Bluecup

  conservation_status
0             Unknown
1             Unknown
2             Unknown
3             Unknown
4             Unknown
```

[45]:

```
model.conservation_status.value_counts()
```

[45]:

```
conservation_status
Unknown               24721
Species of Concern      732
Endangered               80
Threatened               44
In Recovery              24
Name: count, dtype: int64
```

[46]:

```
boot =model[model.conservation_status != 'Unknown'].reset_index()
```

Too many unknown values, therefore I will bootstrap to get proper analysis

[47]:

```
# Specify sample size
sample_size = 25000

# Perform bootstrap sampling on selected columns
bootstrap_samples = boot.sample(n=sample_size, replace=True)

# Create a DataFrame with synthetic samples
df_synthetic = pd.DataFrame(bootstrap_samples)

# Concatenate with original known data if needed
df_extended = pd.concat([boot, df_synthetic], ignore_index=True)
```

[48]:

```
df_extended.head()
```

[48]:

```
   index                    scientific_name  \
0     26                   Zizia trifoliata
```

```
1     41          Camissonia sierrae ssp. alticola
2     79                          Tofieldia glabra
3    105                        Accipiter cooperii
4    130  Dichanthelium acuminatum var. acuminatum

                             park_name  observations        category  \
0               Yosemite National Park           135  Vascular Plant
1                  Bryce National Park            84  Vascular Plant
2  Great Smoky Mountains National Park            75  Vascular Plant
3                  Bryce National Park            95            Bird
4               Yosemite National Park           123  Vascular Plant

                                        common_names conservation_status
0  Meadow Alexanders, Three-Leaved Golden Alexanders  Species of Concern
1  Mono Hot Springs Evening Primrose, Mono Hot Sp…  Species of Concern
2              Smooth Bog-Asphodel, Smooth Tofieldia  Species of Concern
3                                      Cooper's Hawk  Species of Concern
4                              Tapered Rosette Grass  Species of Concern
```

[49]:

```
df_extended.conservation_status.value_counts()
```

[49]:

```
conservation_status
Species of Concern    21431
Endangered             2375
Threatened             1329
In Recovery             745
Name: count, dtype: int64
```

3.4.1 Consevation vs Category

Now we have a df similar size to original with all conservation status filled

[143]:

```
#category vs conservation status
cat_con = df_extended.
 ↪groupby(['category','conservation_status'])['observations'].sum().
 ↪reset_index(name='count').sort_values('count').reset_index().
 ↪drop('index',axis=1)
```

[144]:

```
cat_con
```

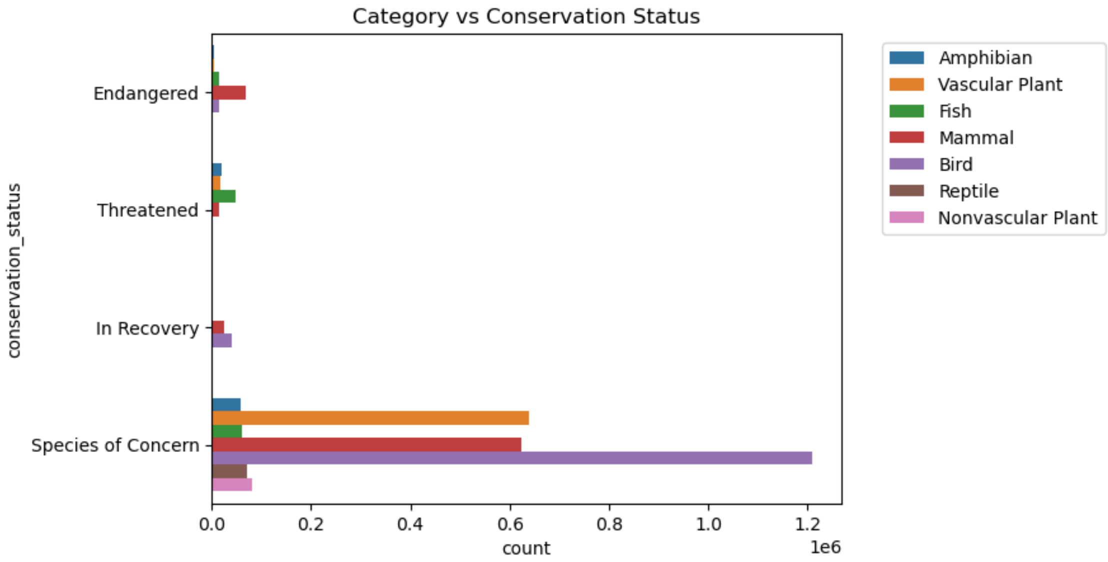
[144]:

```
             category conservation_status    count
0           Amphibian          Endangered     4744
1      Vascular Plant          Endangered     4820
2                Fish          Endangered    13604
3              Mammal          Threatened    15251
4                Bird          Endangered    15488
5      Vascular Plant          Threatened    18175
6           Amphibian          Threatened    18449
```

```
7               Mammal         In Recovery    24158
8                 Bird         In Recovery    39558
9                 Fish          Threatened    48731
10           Amphibian  Species of Concern    57809
11                Fish  Species of Concern    59567
12              Mammal          Endangered    67105
13             Reptile  Species of Concern    72140
14    Nonvascular Plant  Species of Concern    79856
15              Mammal  Species of Concern   622905
16      Vascular Plant  Species of Concern   639872
17                Bird  Species of Concern  1208549
```

[145]:

```
#bar plot of category vs conservation
sns.barplot(x='count', y= 'conservation_status', hue='category',data=cat_con)
plt.legend(bbox_to_anchor = (1.05,1),loc='upper left')
plt.title('Category vs Conservation Status')
plt.show()
```



It seems mammals are the most endangered species by a large margin. That is something I will look into later.

[146]:

```
#test to see if there is a  relationship between category and conservation␣
 ↪status
# Create contingency table
contingency_table2 = pd.crosstab(cat_con['category'],␣
 ↪cat_con['conservation_status'],values=cat_con['count'], aggfunc='sum').
 ↪fillna(0)
```

```
# Perform chi-square test
chi2, p, dof, expected = chi2_contingency(contingency_table2)
print(f'Chi-square statistic: {chi2}, p-value: {p}')
```

```
Chi-square statistic: 829000.120030483, p-value: 0.0
```

[147]:

```
#mearue correlation between each categorical data

# Number of observations
n = contingency_table2.sum().sum()

# Calculate Cramer's V
cramers_v = np.sqrt(chi2 / (n * (min(contingency_table2.shape) - 1)))

print(f'Cramer\'s V: {cramers_v}')
```

```
Cramer's V: 0.30295427555504316
```

I see there is a moderate relationship between category and conservation status. This indicates species plays a role in determining the conservation status. I will use a poisson regression to see if it is an appropriate fit to predict observations based on category and conservation status. I use poisson as I want to ensure positive values for count.

[148]:

```
import statsmodels.api as sm
import statsmodels.formula.api as smf



# Define the formula for the Poisson regression
formula = 'count ~ category + conservation_status'

# Fit the model
model = smf.poisson(formula=formula, data=cat_con).fit()

# Print the summary of the model
model.summary()
```

```
Optimization terminated successfully.
         Current function value: 8569.971873
         Iterations 8
```

[148]:

Dep. Variable:	count	**No. Observations:**	18
Model:	Poisson	**Df Residuals:**	8
Method:	MLE	**Df Model:**	9
Date:	Fri, 21 Jun 2024	**Pseudo R-squ.:**	0.9543
Time:	01:22:38	**Log-Likelihood:**	-1.5426e+05
converged:	True	**LL-Null:**	-3.3773e+06
Covariance Type:	nonrobust	**LLR p-value:**	0.000

	coef	**std err**	**z**	**P>|z|**	**[0.025**	**0.975]**
Intercept	7.9984	0.005	1726.056	0.000	7.989	8.007
category[T.Bird]	2.7801	0.004	765.294	0.000	2.773	2.787
category[T.Fish]	0.4087	0.005	90.169	0.000	0.400	0.418
category[T.Mammal]	2.1666	0.004	584.682	0.000	2.159	2.174
category[T.Nonvascular Plant]	0.0919	0.005	18.406	0.000	0.082	0.102
category[T.Reptile]	-0.0097	0.005	-1.896	0.058	-0.020	0.000
category[T.Vascular Plant]	2.1021	0.004	564.763	0.000	2.095	2.109
conservation_status[T.In Recovery]	-0.1490	0.005	-29.618	0.000	-0.159	-0.139
conservation_status[T.Species of Concern]	3.1977	0.003	1019.318	0.000	3.192	3.204
conservation_status[T.Threatened]	0.5545	0.004	124.934	0.000	0.546	0.563

[149]:

```
from sklearn.metrics import mean_squared_error, mean_absolute_error


# Predict the observations for the current data
predicted_values = model.predict(cat_con[['category', 'conservation_status']])


# Calculate the Mean Squared Error (MSE) and Mean Absolute Error (MAE)
mse = mean_squared_error(cat_con['count'], predicted_values)
mae = mean_absolute_error(cat_con['count'], predicted_values)

print("Mean Squared Error (MSE):", mse)
print("Mean Absolute Error (MAE):", mae)

# Create a DataFrame to compare actual and predicted values
comparison_df = pd.DataFrame({
    'Actual': cat_con['count'],
    'Predicted': predicted_values
})

comparison_df
```

```
Mean Squared Error (MSE): 697015058.1280621
Mean Absolute Error (MAE): 20669.209596058066
```

[149]:

```
   Actual     Predicted
0    4744  2.976054e+03
1    4820  2.435406e+04
2   13604  4.478740e+03
3   15251  4.522625e+04
4   15488  4.797523e+04
5   18175  4.240083e+04
6   18449  5.181359e+03
7   24158  2.238130e+04
8   39558  4.133470e+04
```

```
9      48731  7.797562e+03
10     57809  7.284459e+04
11     59567  1.096257e+05
12     67105  2.597692e+04
13     72140  7.214000e+04
14     79856  7.985600e+04
15    622905  6.358345e+05
16    639872  5.961121e+05
17   1208549  1.174285e+06
```

Even thought the possion regression was significant and had a high R2 value of 0.95, I see mse and mae are very high and I can see the predicted values are far off. I conclude category alone is not enough. I will now examine parks.

3.4.2 Conservation vs Park

[150]:

```
#category vs conservation status
park_con = df_extended.
 ↪groupby(['park_name','conservation_status'])['observations'].sum().
 ↪reset_index(name='count').sort_values('count').reset_index().
 ↪drop('index',axis=1)
```

[151]:

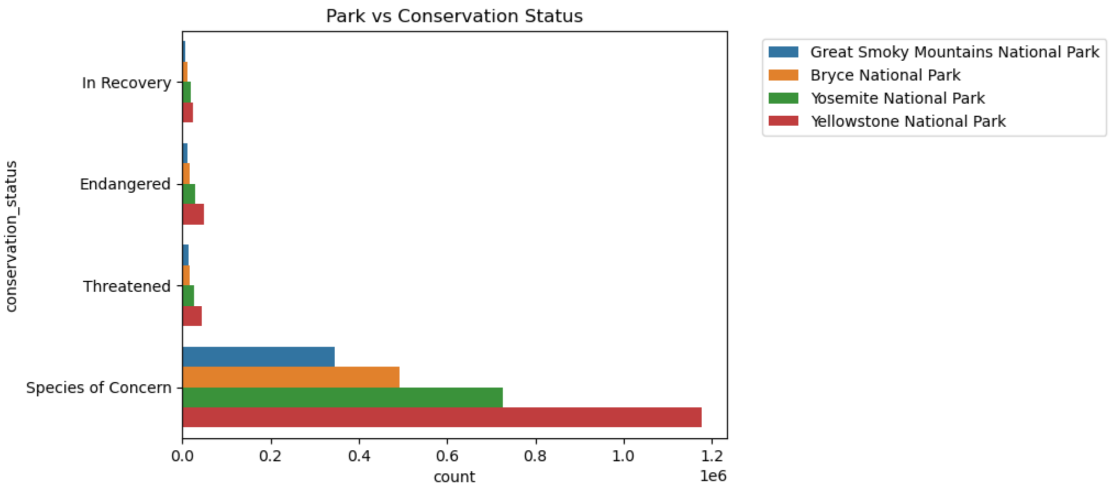
```
park_con
```

[151]:

```
                              park_name conservation_status    count
0   Great Smoky Mountains National Park         In Recovery     7335
1                 Bryce National Park         In Recovery    11483
2   Great Smoky Mountains National Park          Endangered    12316
3   Great Smoky Mountains National Park          Threatened    13608
4                 Bryce National Park          Threatened    16656
5                 Bryce National Park          Endangered    17262
6              Yosemite National Park         In Recovery    19539
7           Yellowstone National Park         In Recovery    25359
8              Yosemite National Park          Threatened    25619
9              Yosemite National Park          Endangered    28041
10          Yellowstone National Park          Threatened    44723
11          Yellowstone National Park          Endangered    48142
12  Great Smoky Mountains National Park  Species of Concern   345375
13                Bryce National Park  Species of Concern   491829
14             Yosemite National Park  Species of Concern   727316
15          Yellowstone National Park  Species of Concern  1176178
```

[152]:

```
#bar plot of category vs conservation
sns.barplot(x='count', y= 'conservation_status', hue='park_name',data=park_con)
plt.legend(bbox_to_anchor = (1.05,1),loc='upper left')
plt.title('Park vs Conservation Status')
plt.show()
```



First observation is distribution of conservation status for each type is similar across each park.

[153]:

```
#test to see if there is a  relationship between category and conservation␣
↪status
# Create contingency table
contingency_table3 = pd.crosstab(park_con['park_name'],␣
↪park_con['conservation_status'],values=park_con['count'], aggfunc='sum').
↪fillna(0)

# Perform chi-square test
chi2, p, dof, expected = chi2_contingency(contingency_table3)
print(f'Chi-square statistic: {chi2}, p-value: {p}')
```

```
Chi-square statistic: 1262.7010532813238, p-value: 3.51287936237 25e-266
```

[154]:

```
# Number of observations
n = contingency_table3.sum().sum()

# Calculate Cramer's V
cramers_v = np.sqrt(chi2 / (n * (min(contingency_table3.shape) - 1)))

print(f'Cramer\'s V: {cramers_v}')
```

```
Cramer's V: 0.011823609033910621
```

Chi-sqaure test for independence shows there is an assocaiton between parks and conservation status, however, Crammer's V shows its a very weak one.

3.5 Mammal Endangered Analysis

```
[114]: mammal = df_extended[df_extended.category=='Mammal']
       mammal.head()
```

```
[114]:     index         scientific_name                               park_name  \
       12    286  Lasiurus blossevillii                    Bryce National Park
       29    670  Lasiurus blossevillii  Great Smoky Mountains National Park
       35   1046             Canis rufus                    Bryce National Park
       39   1179     Myotis californicus                Yosemite National Park
       40   1180     Myotis californicus                Yosemite National Park

           observations category                                      common_names  \
       12           113   Mammal                                  Western Red Bat
       29            70   Mammal                                  Western Red Bat
       35            30   Mammal                                         Red Wolf
       39           148   Mammal  California Myotis, California Myotis, Californ…
       40           148   Mammal                                California Myotis

          conservation_status
       12  Species of Concern
       29  Species of Concern
       35          Endangered
       39  Species of Concern
       40  Species of Concern
```

```
[155]: mammal_end = mammal.
         ↪groupby(['common_names','conservation_status'])['observations'].sum().
         ↪reset_index().sort_values('conservation_status', ascending = True).
         ↪reset_index()
```

```
[156]: mammal_end
```

```
[156]:     index                                     common_names  \
       0      17              Indiana Bat, Indiana Or Social Myotis
       1      14                                    Gray Wolf, Wolf
       2      30                          Sierra Nevada Bighorn Sheep
       3      13                                          Gray Wolf
       4       8  Carolina Northern Flying Squirrel, Northern Fl…
       5      28                                           Red Wolf
       6      12                                        Gray Myotis
       7      15                                    Gray Wolf, Wolf
       8       0                             American Badger, Badger
       9      23              Long-Legged Myotis, Long-Legged Myotis
       10     24                        Malheur Shrew, Preble's Shrew
       11     27                             Pallid Bat, Pallid Bat
       12     22                Long-Eared Myotis, Long-Eared Myotis
       13     29                                           Ringtail
```

```
14     31                     Sierra Nevada Mountain Beaver
15     32                       Sierra Nevada Snowshoe Hare
16     33                                 Silver-Haired Bat
17     34              Silver-Haired Bat, Silver-Haired Bat
18     35                          Spotted Bat, Spotted Bat
19     25           Mississippi Myotis, Southeastern Myotis
20     21                               Little Brown Myotis
21     18                                     Keen's Myotis
22     19             Little Brown Bat, Little Brown Myotis
23     36                                   Western Red Bat
24     11                    Fringed Myotis, Fringed Myotis
25     10  Eastern Small-Footed Bat, Eastern Small-Footed…
26      9                                            Coyote
27      7  California Myotis, California Myotis, Californ…
28      6                                 California Myotis
29      5                                      Brush Rabbit
30      4                      Bighorn Sheep, Bighorn Sheep
31      3                      Big Brown Bat, Big Brown Bat
32      2                                     Big Brown Bat
33      1                                            Badger
34     20  Little Brown Bat, Little Brown Myotis, Little …
35     37                          Yuma Myotis, Yuma Myotis
36     16                                      Grizzly Bear
37     26          Northern Long-Eared Bat, Northern Myotis

   conservation_status  observations
0           Endangered          4205
1           Endangered         21405
2           Endangered          4594
3           Endangered         24159
4           Endangered          4106
5           Endangered          3387
6           Endangered          5249
7          In Recovery         24158
8   Species of Concern         25272
9   Species of Concern         14701
10  Species of Concern         14687
11  Species of Concern         14595
12  Species of Concern         16958
13  Species of Concern         15344
14  Species of Concern         13358
15  Species of Concern         13721
16  Species of Concern         29929
17  Species of Concern         34182
18  Species of Concern         15558
19  Species of Concern         11600
20  Species of Concern         47446
```

```
21  Species of Concern         15799
22  Species of Concern         40342
23  Species of Concern         15940
24  Species of Concern         17480
25  Species of Concern         16709
26  Species of Concern         13227
27  Species of Concern         34903
28  Species of Concern         30300
29  Species of Concern         12472
30  Species of Concern         11917
31  Species of Concern         29082
32  Species of Concern         28476
33  Species of Concern         29379
34  Species of Concern         44593
35  Species of Concern         14935
36          Threatened          8248
37          Threatened          7003
```

I can see the red wolf is the most endangered mammal as it has the lowest observations.

4 Building a predictive model

```
[71]: df_extended.head()
```

```
[71]:    index                           scientific_name  \
      0     26                          Zizia trifoliata
      1     41          Camissonia sierrae ssp. alticola
      2     79                          Tofieldia glabra
      3    105                        Accipiter cooperii
      4    130  Dichanthelium acuminatum var. acuminatum

                                   park_name  observations        category  \
      0               Yosemite National Park           135  Vascular Plant
      1                  Bryce National Park            84  Vascular Plant
      2  Great Smoky Mountains National Park            75  Vascular Plant
      3                  Bryce National Park            95            Bird
      4               Yosemite National Park           123  Vascular Plant

                                              common_names conservation_status
      0  Meadow Alexanders, Three-Leaved Golden Alexanders  Species of Concern
      1    Mono Hot Springs Evening Primrose, Mono Hot Sp…  Species of Concern
      2              Smooth Bog-Asphodel, Smooth Tofieldia  Species of Concern
      3                                      Cooper's Hawk  Species of Concern
      4                              Tapered Rosette Grass  Species of Concern
```

```
[73]: df2 = df_extended.copy()
```

[74]:
```
df2.conservation_status = np.where(df_extended.conservation_status ==␣
↪'Endangered', 1, 0)
```

[75]:
```
df2.head()
```

[75]:
```
   index                            scientific_name  \
0     26                           Zizia trifoliata
1     41         Camissonia sierrae ssp. alticola
2     79                           Tofieldia glabra
3    105                          Accipiter cooperii
4    130  Dichanthelium acuminatum var. acuminatum

                             park_name  observations        category  \
0                Yosemite National Park           135  Vascular Plant
1                   Bryce National Park            84  Vascular Plant
2  Great Smoky Mountains National Park            75  Vascular Plant
3                   Bryce National Park            95            Bird
4                Yosemite National Park           123  Vascular Plant

                                      common_names  conservation_status
0  Meadow Alexanders, Three-Leaved Golden Alexanders                    0
1  Mono Hot Springs Evening Primrose, Mono Hot Sp…                    0
2              Smooth Bog-Asphodel, Smooth Tofieldia                    0
3                                      Cooper's Hawk                    0
4                              Tapered Rosette Grass                    0
```

[76]:
```
pred_model = df2[['park_name', 'observations', 'category',␣
↪'conservation_status']]
```

[79]:
```
#building a predictive model to see if i can predict if a species is endangered␣
↪1 = endgandered, 0 = not endangered
pred_model.head()
```

[79]:
```
                             park_name  observations        category  \
0                Yosemite National Park           135  Vascular Plant
1                   Bryce National Park            84  Vascular Plant
2  Great Smoky Mountains National Park            75  Vascular Plant
3                   Bryce National Park            95            Bird
4                Yosemite National Park           123  Vascular Plant

   conservation_status
0                    0
1                    0
2                    0
3                    0
4                    0
```

[80]:

```python
final_pred_model = pd.get_dummies(pred_model, dtype=int)
```

[89]:

```python
y = final_pred_model['conservation_status']
X = final_pred_model.drop('conservation_status', axis=1)
```

[90]:

```python
# Importing necessary libraries
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, classification_report

# Splitting 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)

# Initializing the Random Forest classifier
rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)

# Training the classifier on the training data
rf_classifier.fit(X_train, y_train)

# Making predictions on the test data
y_pred = rf_classifier.predict(X_test)

# Evaluating the classifier
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")

# Printing the classification report
print(classification_report(y_test, y_pred))
```

```
Accuracy: 0.98
              precision    recall  f1-score   support

           0       0.99      0.99      0.99      4702
           1       0.87      0.94      0.91       474

    accuracy                           0.98      5176
   macro avg       0.93      0.96      0.95      5176
weighted avg       0.98      0.98      0.98      5176
```

[91]:

```python
# Assuming rf_classifier is your trained Random Forest classifier
# and X_train is your training feature matrix

# Get feature importances
importances = rf_classifier.feature_importances_

# Get indices of features sorted by importance in descending order
```

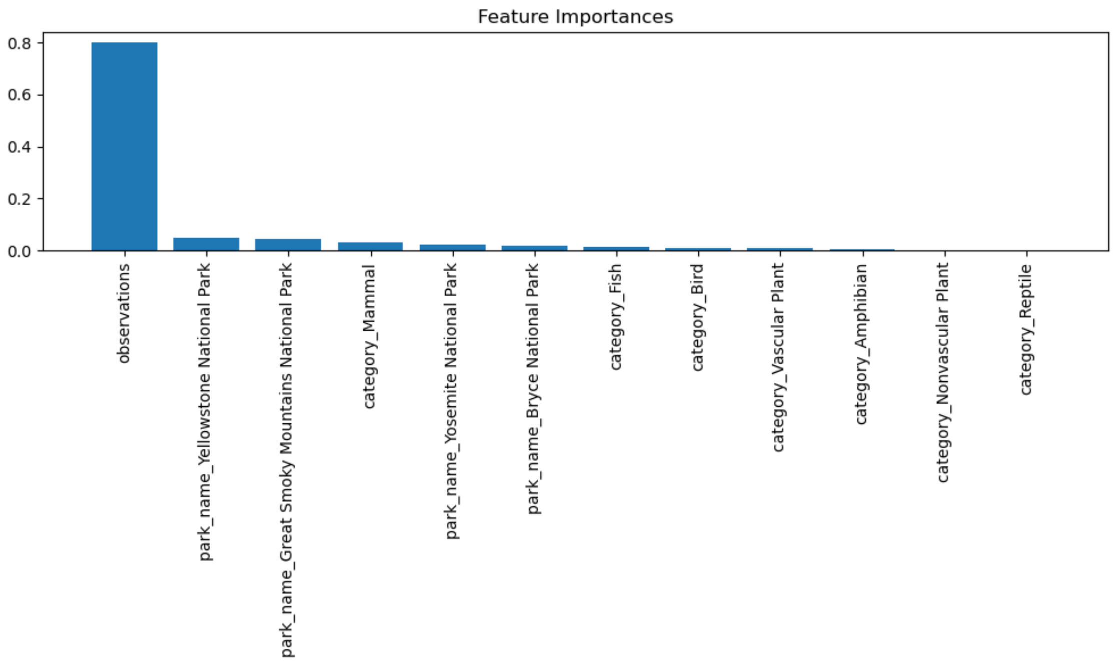
```
indices = np.argsort(importances)[::-1]

# Print the feature ranking
print("Feature ranking:")

for i, idx in enumerate(indices):
    print(f"{i + 1}. Feature {idx + 1} ({X_train.columns[idx]}):␣
  ↪{importances[idx]}")

# Plot feature importances (optional)
plt.figure(figsize=(10, 6))
plt.title("Feature Importances")
plt.bar(range(X_train.shape[1]), importances[indices], align="center")
plt.xticks(range(X_train.shape[1]), X_train.columns[indices], rotation=90)
plt.xlim([-1, X_train.shape[1]])
plt.tight_layout()
plt.show()
```

```
Feature ranking:
1. Feature 1 (observations): 0.7982827310783224
2. Feature 4 (park_name_Yellowstone National Park): 0.048731936521708256
3. Feature 3 (park_name_Great Smoky Mountains National Park):
0.04381795206828022
4. Feature 9 (category_Mammal): 0.02981702198724861
5. Feature 5 (park_name_Yosemite National Park): 0.02053078247695497
6. Feature 2 (park_name_Bryce National Park): 0.019794717336424485
7. Feature 8 (category_Fish): 0.01297195421052927
8. Feature 7 (category_Bird): 0.011093866820602045
9. Feature 12 (category_Vascular Plant): 0.008741655099975418
10. Feature 6 (category_Amphibian): 0.0038039752715443263
11. Feature 10 (category_Nonvascular Plant): 0.0013564192570319144
12. Feature 11 (category_Reptile): 0.001056987871378271
```



The random forest classifier was able to predict if a species was endangered with 87% precision. The main importance was observations. Every other feature has a significane of less than 0.05. This shows observations alone are a very good predictor of predicting if a species is endangered or not. I will now test to see if the model can predict every species type.

[92]:
```
df2.head()
```

[92]:
```
   index                            scientific_name  \
0     26                          Zizia trifoliata   
1     41          Camissonia sierrae ssp. alticola   
2     79                          Tofieldia glabra   
3    105                        Accipiter cooperii   
4    130  Dichanthelium acuminatum var. acuminatum   

                             park_name  observations        category  \
0               Yosemite National Park           135  Vascular Plant   
1                  Bryce National Park            84  Vascular Plant   
2  Great Smoky Mountains National Park            75  Vascular Plant   
3                  Bryce National Park            95            Bird   
4               Yosemite National Park           123  Vascular Plant   

                                        common_names  conservation_status  
0  Meadow Alexanders, Three-Leaved Golden Alexanders                    0  
1    Mono Hot Springs Evening Primrose, Mono Hot Sp…                    0  
2              Smooth Bog-Asphodel, Smooth Tofieldia                    0  
3                                      Cooper's Hawk                    0  
```

```
4                   Tapered Rosette Grass             0
```

[99]:

```
pred_model2 =␣
 ↪df_extended[['park_name','observations','category','conservation_status']]
```

[100]:

```
y = pred_model2['conservation_status']
x = pred_model2.drop('conservation_status',axis=1)
X = pd.get_dummies(x, dtype=int)
```

[101]:

```
# Splitting 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)

# Initializing the Random Forest classifier
rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)

# Training the classifier on the training data
rf_classifier.fit(X_train, y_train)

# Making predictions on the test data
y_pred = rf_classifier.predict(X_test)

# Evaluating the classifier
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")

# Printing the classification report
print(classification_report(y_test, y_pred))
```

```
Accuracy: 0.97
                    precision    recall  f1-score   support

        Endangered       0.83      0.99      0.91       474
       In Recovery       0.85      0.16      0.27       139
Species of Concern       0.99      0.99      0.99      4297
        Threatened       0.99      1.00      0.99       266

          accuracy                           0.97      5176
         macro avg       0.91      0.79      0.79      5176
      weighted avg       0.97      0.97      0.97      5176
```

[102]:

```
# Assuming rf_classifier is your trained Random Forest classifier
# and X_train is your training feature matrix

# Get feature importances
importances = rf_classifier.feature_importances_
```

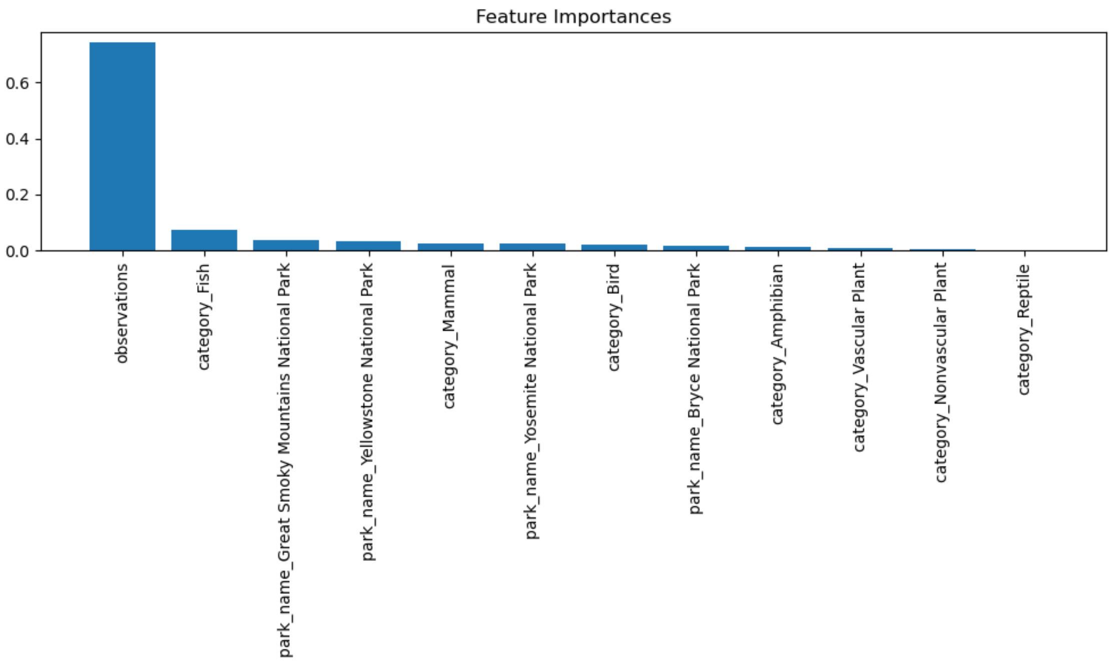
```python
# Get indices of features sorted by importance in descending order
indices = np.argsort(importances)[::-1]

# Print the feature ranking
print("Feature ranking:")

for i, idx in enumerate(indices):
    print(f"{i + 1}. Feature {idx + 1} ({X_train.columns[idx]}): {importances[idx]}")

# Plot feature importances (optional)
plt.figure(figsize=(10, 6))
plt.title("Feature Importances")
plt.bar(range(X_train.shape[1]), importances[indices], align="center")
plt.xticks(range(X_train.shape[1]), X_train.columns[indices], rotation=90)
plt.xlim([-1, X_train.shape[1]])
plt.tight_layout()
plt.show()
```

```
Feature ranking:
1. Feature 1 (observations): 0.7418508211916618
2. Feature 8 (category_Fish): 0.07271500011178288
3. Feature 3 (park_name_Great Smoky Mountains National Park):
0.03859624969588306
4. Feature 4 (park_name_Yellowstone National Park): 0.03359775823997414
5. Feature 9 (category_Mammal): 0.024746715095985562
6. Feature 5 (park_name_Yosemite National Park): 0.024073607487566494
7. Feature 7 (category_Bird): 0.01963630444802723
8. Feature 2 (park_name_Bryce National Park): 0.016759792547794538
9. Feature 6 (category_Amphibian): 0.01417961643847246
10. Feature 12 (category_Vascular Plant): 0.00954780663923113
11. Feature 10 (category_Nonvascular Plant): 0.002896353094273365
12. Feature 11 (category_Reptile): 0.0013999750093472145
```



The overall model had 97% accuracy. The model was able to predict endangered species with 83% precision, in recovery with 85% precision, species of concern with 99% precision and threatened with 99% precision. Again obseravtion was most significant feature with 0.74 importance, others having minimal impact. Overall I can conclude that observation count is a very good predictor of conservation status.

5 Summary

My findings include: 1. The mean observation across all categories was the same except for vascular plants and mammals. 2. Mean observation across all parks differed, Yellowstone park having the highest. 3. Park and category variable have a weak association. 4. Category had a moderate assosiation with conservation status. 5. There was a weak association between conservation status and parks. 6. Mammals had highest count of endangered species, with red wolf being the most endangered with lowest observations. 7. Random Forest Classifier was highly accurate in predicting a species by its conservation status with observations being the most significant feature by far.

```
[ ]:
```