Biodiversity Project

Introduction

You are a biodiversity analyst working for the National Parks Service. You're going to help them analyze some data about species at various national parks.

Note: The data that you'll be working with for this project is *inspired* by real data, but is mostly fictional.

Step 1

Import the modules that you'll be using in this assignment:

- `from matplotlib import pyplot as plt`
- `import pandas as pd`

In [1]:

```
from matplotlib import pyplot as plt
import pandas as pd
```

Step 2

You have been given two CSV files. `species_info.csv` with data about different species in our National Parks, including:

- The scientific name of each species
- The common names of each species
- The species conservation status

Load the dataset and inspect it:

- Load `species_info.csv` into a DataFrame called `species`

In [2]:

```
species = pd.read_csv("species_info.csv")
```

Inspect each DataFrame using `.head()`.

In [3]:

```
species.head()
```

Out[3]:

	category	scientific_name	common_names	conservation_status
0	Mammal	Clethrionomys gapperi gapperi	Gapper's Red-Backed Vole	NaN

	category	scientific_name	common_names	conservation_status
1	Mammal	Bos bison	American Bison, Bison	NaN
2	Mammal	Bos taurus	Aurochs, Aurochs, Domestic Cattle (Feral), Dom...	NaN
3	Mammal	Ovis aries	Domestic Sheep, Mouflon, Red Sheep, Sheep (Feral)	NaN
4	Mammal	Cervus elaphus	Wapiti Or Elk	NaN

Step 3

Let's start by learning a bit more about our data. Answer each of the following questions.

How many different species are in the `species` DataFrame?

In [4]:

```
#using len() on .unique() returns the length of the unique array
len(species.scientific_name.unique())
```

Out[4]:

```
5541
```

In [5]:

```
#df.info() returns a concise dataframe summary
species.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 5824 entries, 0 to 5823
Data columns (total 4 columns):
 #   Column               Non-Null Count  Dtype 
---  ------               --------------  ----- 
 0   category             5824 non-null   object
 1   scientific_name      5824 non-null   object
 2   common_names         5824 non-null   object
 3   conservation_status  191 non-null    object
dtypes: object(4)
memory usage: 182.1+ KB
```

What are the different values of `category` in `species` ?

In [6]:

```
#df.columnname.unique() returns an array of unique column names
species.category.unique()
```

Out[6]:

```
array(['Mammal', 'Bird', 'Reptile', 'Amphibian', 'Fish', 'Vascular Plant',
       'Nonvascular Plant'], dtype=object)
```

In [7]:

```
#df.columnname.value_counts() returns counts of unique rows
species.category.value_counts()
```

Out[7]:

```
Vascular Plant       4470
Bird                  521
Nonvascular Plant     333
Mammal                214
Fish                  127
Amphibian              80
```

```
Reptile                79
Name: category, dtype: int64
```

What are the different values of `conservation_status` ?

In [8]:
```
species.conservation_status.unique()
```

Out[8]:
```
array([nan, 'Species of Concern', 'Endangered', 'Threatened',
       'In Recovery'], dtype=object)
```

In [9]:
```
species.conservation_status.value_counts()
```

Out[9]:
```
Species of Concern    161
Endangered             16
Threatened             10
In Recovery             4
Name: conservation_status, dtype: int64
```

Step 4

Let's start doing some analysis!

The column `conservation_status` has several possible values:

- `Species of Concern` : declining or appear to be in need of conservation
- `Threatened` : vulnerable to endangerment in the near future
- `Endangered` : seriously at risk of extinction
- `In Recovery` : formerly `Endangered` , but currnetly neither in danger of extinction throughout all or a significant portion of its range

We'd like to count up how many species meet each of these criteria. Use `groupby` to count how many `scientific_name` meet each of these criteria.

In [10]:
```
#use columnname.nunique() to count distinct observations in the column
species.groupby("conservation_status").scientific_name.nunique()\
                                    .sort_values(ascending=False)\
                                                   .reset_index()
```

Out[10]:

	conservation_status	scientific_name
0	Species of Concern	151
1	Endangered	15
2	Threatened	10
3	In Recovery	4

As we saw before, there are far more than 200 species in the `species` table. Clearly, only a small number of them are categorized as needing some sort of protection. The rest have `conservation_status` equal to `None` . Because `groupby` does not include `None` , we will need to fill in the null values. We can do this using `.fillna`. We pass in however we want to fill in our `None` values as an argument.

Paste the following code and run it to see replace `None` with `No Intervention`:

```
species.fillna('No Intervention', inplace=True)
```

In [11]:
```
#use df.columnname.fillna() to fill NA/NaN values in the column
species.conservation_status.fillna("No Intervention", inplace=True)
```

Great! Now run the same `groupby` as before to see how many species require `No Intervention`.

In [12]:
```
species.groupby("conservation_status").scientific_name.nunique()\
                                    .sort_values(ascending=False)\
                                    .reset_index()
```

Out[12]:

	conservation_status	scientific_name
0	No Intervention	5363
1	Species of Concern	151
2	Endangered	15
3	Threatened	10
4	In Recovery	4

Let's use `plt.bar` to create a bar chart. First, let's sort the columns by how many species are in each categories. We can do this using `.sort_values`. We use the the keyword `by` to indicate which column we want to sort by.

Paste the following code and run it to create a new DataFrame called `protection_counts`, which is sorted by `scientific_name`:

```
protection_counts = species.groupby('conservation_status')\
    .scientific_name.nunique().reset_index()\
    .sort_values(by='scientific_name')
```

In [13]:
```
protection_counts = species.groupby('conservation_status')\
                   .scientific_name.nunique().reset_index()\
                   .sort_values(by='scientific_name')
protection_counts.head()
```

Out[13]:

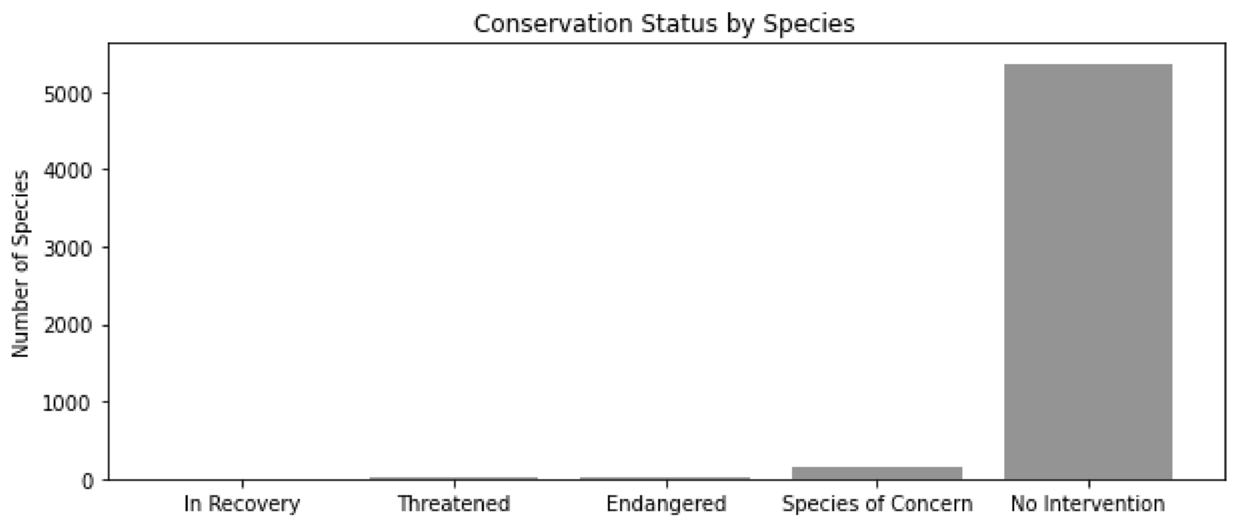
	conservation_status	scientific_name
1	In Recovery	4
4	Threatened	10
0	Endangered	15
3	Species of Concern	151

	conservation_status	scientific_name
2	No Intervention	5363

Now let's create a bar chart!

1. Start by creating a wide figure with `figsize=(10, 4)`
2. Start by creating an axes object called `ax` using `plt.subplot`.
3. Create a bar chart whose heights are equal to `scientific_name` column of `protection_counts`.
4. Create an x-tick for each of the bars.
5. Label each x-tick with the label from `conservation_status` in `protection_counts`
6. Label the y-axis `Number of Species`
7. Title the graph `Conservation Status by Species`
8. Plot the grap using `plt.show()`

In [14]:
```
plt.figure(figsize=(10, 4))
ax = plt.subplot()
plt.bar(range(len(protection_counts)),\
        protection_counts.scientific_name.values,\
        color="#949494")
ax.set_xticks(range(len(protection_counts)))
ax.set_xticklabels(protection_counts.conservation_status.values)
plt.ylabel("Number of Species")
plt.title("Conservation Status by Species")
plt.show()
plt.savefig("conservation_status_by_species.png")
```



```
<Figure size 432x288 with 0 Axes>
```

Step 4

Are certain types of species more likely to be endangered?

Let's create a new column in `species` called `is_protected`, which is `True` if `conservation_status` is not equal to `No Intervention`, and `False` otherwise.

```
In [15]: species["is_protected"] = species.conservation_status\
                                       != "No Intervention"
```

Let's group the `species` data frame by the `category` and `is_protected` columns and count the unique `scientific_name` s in each grouping.

Save your results to `category_counts` .

```
In [16]: category_counts = species.groupby(["category", "is_protected"])\
                         .scientific_name.nunique().reset_index()\
                         .sort_values(by="scientific_name")
```

Examine `category_counts` using `head()` .

```
In [17]: category_counts.head()
```

Out[17]:

	category	is_protected	scientific_name
9	Nonvascular Plant	True	5
11	Reptile	True	5
1	Amphibian	True	7
5	Fish	True	11
7	Mammal	True	30

It's going to be easier to view this data if we pivot it. Using `pivot` , rearange `category_counts` so that:

- `columns` is `is_protected`
- `index` is `category`
- `values` is `scientific_name`

Save your pivoted data to `category_pivot` . Remember to `reset_index()` at the end.

```
In [18]: category_pivot = category_counts.pivot(columns="is_protected",\
                                                index="category",\
                                                values="scientific_name")\
                                                .reset_index()
```

Examine `category_pivot` .

```
In [19]: category_pivot
```

Out[19]:

is_protected	category	False	True
0	Amphibian	72	7
1	Bird	413	75
2	Fish	115	11

is_protected	category	False	True
3	Mammal	146	30
4	Nonvascular Plant	328	5
5	Reptile	73	5
6	Vascular Plant	4216	46

Use the `.columns` property to rename the categories `True` and `False` to something more description:

- `Leave category as category`
- `Rename False to not_protected`
- `Rename True to protected`

In [20]:
```
category_pivot.columns = ["category", "not_protected", "protected"]
```

Let's create a new column of `category_pivot` called `percent_protected`, which is equal to `protected` (the number of species that are protected) divided by `protected` plus `not_protected` (the total number of species).

In [21]:
```
category_pivot["percent_protected"] = category_pivot.protected /\
                                      (category_pivot.protected +\
                                      category_pivot.not_protected)
category_pivot = category_pivot.sort_values(by="percent_protected")
```

Examine `category_pivot`.

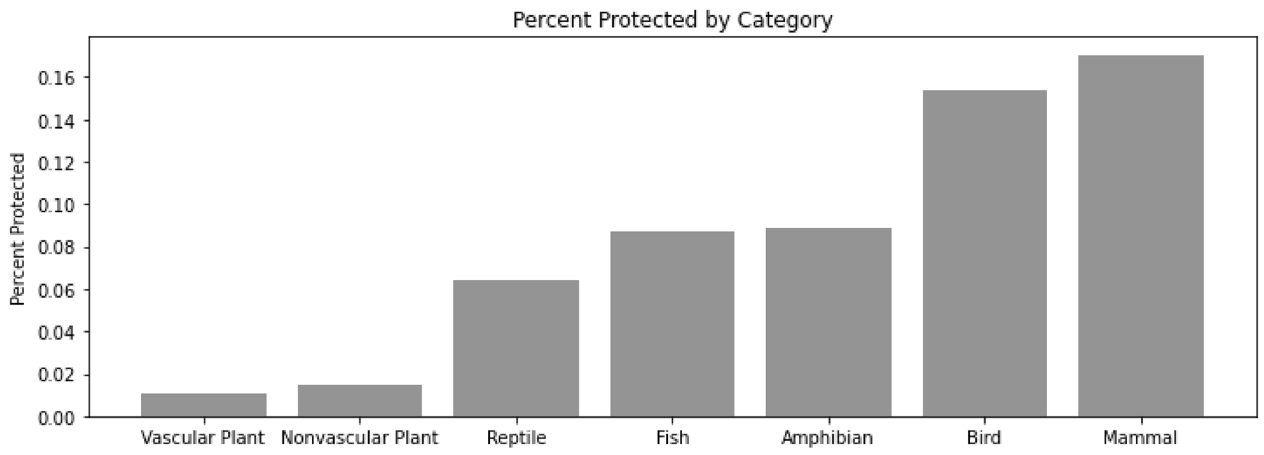
In [22]:
```
category_pivot
```

Out[22]:

	category	not_protected	protected	percent_protected
6	Vascular Plant	4216	46	0.010793
4	Nonvascular Plant	328	5	0.015015
5	Reptile	73	5	0.064103
2	Fish	115	11	0.087302
0	Amphibian	72	7	0.088608
1	Bird	413	75	0.153689
3	Mammal	146	30	0.170455

In [23]:
```
plt.figure(figsize=(12, 4))
ax = plt.subplot()
plt.bar(range(len(category_pivot)),\
        category_pivot.percent_protected.values,\
        color="#949494")
ax.set_xticks(range(len(category_pivot)))
ax.set_xticklabels(category_pivot.category.values)
```

```
plt.ylabel("Percent Protected")
plt.title("Percent Protected by Category")
plt.show()
plt.savefig("percent_protected_by_category.png")
```



```
<Figure size 432x288 with 0 Axes>
```

It looks like species in category `Mammal` are more likely to be endangered than species in `Bird`. We're going to do a significance test to see if this statement is true. Before you do the significance test, consider the following questions:

- Is the data numerical or categorical?
- How many pieces of data are you comparing?

Based on those answers, you should choose to do a *chi squared test*. In order to run a chi squared test, we'll need to create a contingency table. Our contingency table should look like this:

	protected	not protected
Mammal	?	?
Bird	?	?

Create a table called `contingency` and fill it in with the correct numbers

In [24]:
```
contingency = [[30, 146], [75, 413]]
```

In order to perform our chi square test, we'll need to import the correct function from scipy. Past the following code and run it:

```
from scipy.stats import chi2_contingency
```

In [25]:
```
from scipy.stats import chi2_contingency
```

Now run `chi2_contingency` with `contingency`.

In [26]:
```
_, pval, _, _, = chi2_contingency(contingency)
if pval < .05:
    print(pval)
    print('Significant!')
else:
    print(pval)
    print('Not significant!')
```

```
0.6875948096661336
Not significant!
```

It looks like this difference isn't significant!

Let's test another. Is the difference between `Reptile` and `Mammal` significant?

In [27]:

```
contingency = [[30, 146], [5, 73]]
_, pval, _, _ = chi2_contingency(contingency)
if pval < .05:
    print(pval)
    print('Significant!')
else:
    print(pval)
    print('Not significant!')
```

```
0.03835559022969898
Significant!
```

Yes! It looks like there is a significant difference between `Reptile` and `Mammal` !

Step 5

Conservationists have been recording sightings of different species at several national parks for the past 7 days. They've sent you their observations in a file called `observations.csv` . Load `observations.csv` into a variable called `observations` , then use `head` to view the data.

In [28]:

```
observations = pd.read_csv("observations.csv")
observations.head()
```

Out[28]:

	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

Some scientists are studying the number of sheep sightings at different national parks. There are several different scientific names for different types of sheep. We'd like to know which rows of `species` are referring to sheep. Notice that the following code will tell us whether or not a word occurs in a string:

In [29]:

```
# Does "Sheep" occur in this string?
str1 = 'This string contains Sheep'
'Sheep' in str1
```

Out[29]:

```
True
```

In [30]:
```
# Does "Sheep" occur in this string?
str2 = 'This string contains Cows'
'Sheep' in str2
```

Out[30]:
```
False
```

Use `apply` and a `lambda` function to create a new column in `species` called `is_sheep` which is `True` if the `common_names` contains `'Sheep'`, and `False` otherwise.

In [31]:
```
species["is_sheep"] = species.common_names.apply(lambda x:"Sheep" in x)
```

Select the rows of `species` where `is_sheep` is `True` and examine the results.

In [32]:
```
species[species.is_sheep]
```

Out[32]:

	category	scientific_name	common_names	conservation_status	is_protected	is_sheep
3	Mammal	Ovis aries	Domestic Sheep, Mouflon, Red Sheep, Sheep (Feral)	No Intervention	False	True
1139	Vascular Plant	Rumex acetosella	Sheep Sorrel, Sheep Sorrell	No Intervention	False	True
2233	Vascular Plant	Festuca filiformis	Fineleaf Sheep Fescue	No Intervention	False	True
3014	Mammal	Ovis canadensis	Bighorn Sheep, Bighorn Sheep	Species of Concern	True	True
3758	Vascular Plant	Rumex acetosella	Common Sheep Sorrel, Field Sorrel, Red Sorrel,...	No Intervention	False	True
3761	Vascular Plant	Rumex paucifolius	Alpine Sheep Sorrel, Fewleaved Dock, Meadow Dock	No Intervention	False	True
4091	Vascular Plant	Carex illota	Sheep Sedge, Smallhead Sedge	No Intervention	False	True
4383	Vascular Plant	Potentilla ovina var. ovina	Sheep Cinquefoil	No Intervention	False	True
4446	Mammal	Ovis canadensis sierrae	Sierra Nevada Bighorn Sheep	Endangered	True	True

Many of the results are actually plants. Select the rows of `species` where `is_sheep` is `True` and `category` is `Mammal`. Save the results to the variable `sheep_species`.

In [33]:
```
sheep_species = species[(species.is_sheep) & (species.category \
                                                 == "Mammal")]
sheep_species
```

Out[33]:

	category	scientific_name	common_names	conservation_status	is_protected	is_sheep

	category	scientific_name	common_names	conservation_status	is_protected	is_sheep
3	Mammal	Ovis aries	Domestic Sheep, Mouflon, Red Sheep, Sheep (Feral)	No Intervention	False	True
3014	Mammal	Ovis canadensis	Bighorn Sheep, Bighorn Sheep	Species of Concern	True	True
4446	Mammal	Ovis canadensis sierrae	Sierra Nevada Bighorn Sheep	Endangered	True	True

Now merge `sheep_species` with `observations` to get a DataFrame with observations of sheep. Save this DataFrame as `sheep_observations`.

In [34]:
```
sheep_observations = observations.merge(sheep_species)
sheep_observations.head()
```

Out[34]:

	scientific_name	park_name	observations	category	common_names	conservation_status	is_protecte
0	Ovis canadensis	Yellowstone National Park	219	Mammal	Bighorn Sheep, Bighorn Sheep	Species of Concern	Tru
1	Ovis canadensis	Bryce National Park	109	Mammal	Bighorn Sheep, Bighorn Sheep	Species of Concern	Tru
2	Ovis canadensis	Yosemite National Park	117	Mammal	Bighorn Sheep, Bighorn Sheep	Species of Concern	Tru
3	Ovis canadensis	Great Smoky Mountains National Park	48	Mammal	Bighorn Sheep, Bighorn Sheep	Species of Concern	Tru
4	Ovis canadensis sierrae	Yellowstone National Park	67	Mammal	Sierra Nevada Bighorn Sheep	Endangered	Tru

How many total sheep observations (across all three species) were made at each national park? Use `groupby` to get the `sum` of `observations` for each `park_name`. Save your answer to `obs_by_park`.

This is the total number of sheep observed in each park over the past 7 days.

In [35]:
```
obs_by_park = sheep_observations.groupby("park_name")\
                    .observations.sum().reset_index()\
                    .sort_values(by="observations")
obs_by_park
```

Out[35]:

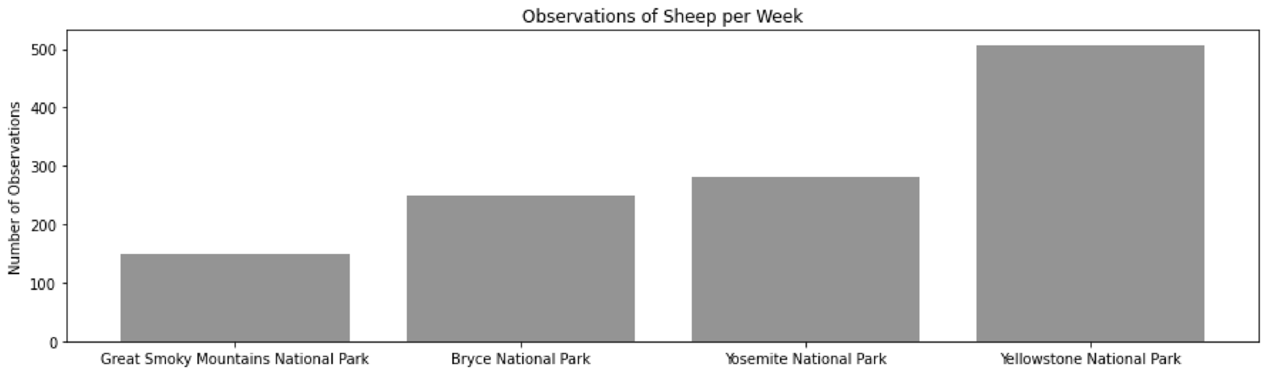
	park_name	observations

	park_name	observations
1	Great Smoky Mountains National Park	149
0	Bryce National Park	250
3	Yosemite National Park	282
2	Yellowstone National Park	507

Create a bar chart showing the different number of observations per week at each park.

1. Start by creating a wide figure with `figsize=(16, 4)`
2. Start by creating an axes object called `ax` using `plt.subplot`.
3. Create a bar chart whose heights are equal to `observations` column of `obs_by_park`.
4. Create an x-tick for each of the bars.
5. Label each x-tick with the label from `park_name` in `obs_by_park`
6. Label the y-axis `Number of Observations`
7. Title the graph `Observations of Sheep per Week`
8. Plot the grap using `plt.show()`

In [36]:
```
plt.figure(figsize=(15, 4))
ax = plt.subplot()
plt.bar(range(len(obs_by_park)),\
        obs_by_park.observations.values,\
        color="#949494")
ax.set_xticks(range(len(obs_by_park)))
ax.set_xticklabels(obs_by_park.park_name.values)
plt.ylabel("Number of Observations")
plt.title("Observations of Sheep per Week")
plt.show()
plt.savefig("observations_of_sheep_per_week.png")
```



```
<Figure size 432x288 with 0 Axes>
```

Our scientists know that 15% of sheep at Bryce National Park have foot and mouth disease. Park rangers at Yellowstone National Park have been running a program to reduce the rate of foot and mouth disease at that park. The scientists want to test whether or not this program is working. They want to be able to detect reductions of at least 5 percentage points. For instance, if 10% of sheep in Yellowstone have foot and mouth disease, they'd like to be able to know this, with confidence.

Use Codecademy's sample size calculator to calculate the number of sheep that they would need to observe from each park. Use the default level of significance (90%).

Remember that "Minimum Detectable Effect" is a percent of the baseline.

```
In [37]: baseline_conversion_rate = 15
```

```
In [38]: statistical_significance = 90
```

```
In [39]: minimum_detectable_effect = 100 * 5 / 15
         minimum_detectable_effect
```

```
Out[39]: 33.333333333333336
```

```
In [40]: sample_size_per_park = 870
```

How many weeks would you need to observe sheep at Bryce National Park in order to observe enough sheep? How many weeks would you need to observe at Yellowstone National Park to observe enough sheep?

```
In [41]: weeks_at_bryce = sample_size_per_park / 250
         weeks_at_bryce
         #About 3.5 weeks at Bryce
```

```
Out[41]: 3.48
```

```
In [42]: weeks_at_yellowstone = sample_size_per_park / 507
         weeks_at_yellowstone
         #About 1.5 weeks at Yellowstone
```

```
Out[42]: 1.7159763313609468
```