CAPSTONE PROJECT: BIODIVERSITY OF THE NATIONAL PARKS INTRODUCTION TO DATA ANALYSIS WITH PYTHON

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code cademy / PRO





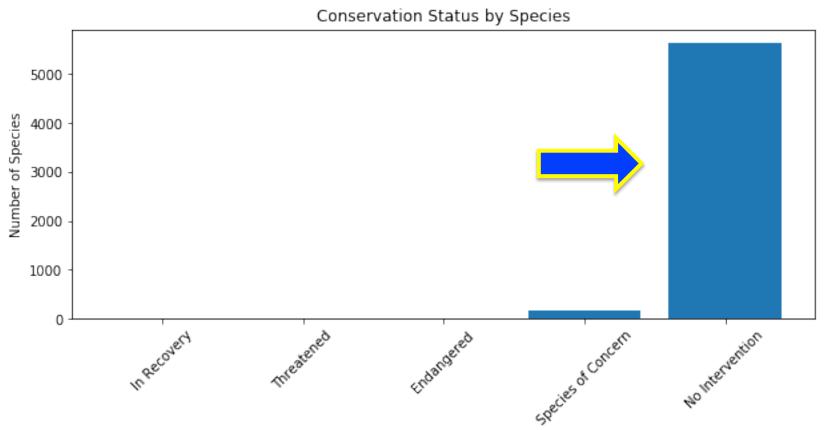




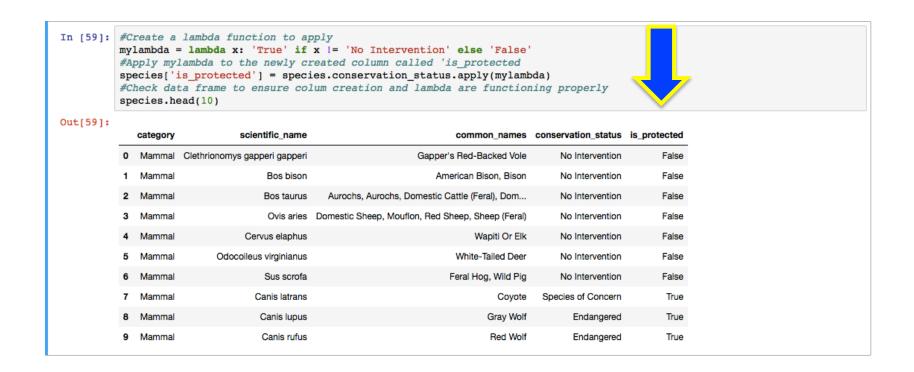
category		scientific_name	common_names	conservation_status	
0	Mammal Clethrionomys gapperi gapperi		Gapper's Red-Backed Vole	NaN	
1	Mammal	Bos bison	American Bison, Bison	NaN	
7	Mammal	Canis latrans	Coyote	Species of Concern	
8	Mammal	Canis lupus	Gray Wolf	Endangered	
9	Mammal	Canis rufus	Red Wolf	Endangered	

Our data frame contains 5,824 observations over 4 columns: Category, Scientific Name, Common Names, and Conservations status. A sampling of the data is above.

- **category** There are 7 unique categories of species: Mammal, Bird, Reptile, Amphibian, Fish, Vascular Plant, Nonvascular Plant.
- **scientific_name** There are 5,541 unique instances within this field, far too many to list and nearly 1 for every record within the data set.
- **common_names** This field contains corresponding common names for each of the scientific_names entries. This data is untidy as there are multiple values for each observation. We did not do extensive research into this column.
- **conservation_status** This field contains 5 unique values: Species of Concern, Endangered, Threatened, In Recovery, and nan.



After grouping our data by conservation status, we can see there are a large number of species on the list without intervention concerns. We plotted our data using matplotlib imported as plt, but we also used the Pandas library imported as pd to use their robust database manipulation tools.



As such, we considered only those species who are were not labeled as "No Intervention". We did so by creating a lambda function that checked the conservations status, when "No Intervention" was found, a flag of "False" was applied to a new column labeled "is_protected". In this way we were not able to quickly subset by the remaining animals.

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

After grouping the applicable data, then pivoting to make our table more legible, we created a "percent_protected" column to help us further visualize the protection status of each category of species.

SPECIES_INFO.CSV DATA SET. How confident am I with my data?

	category	not_protected	protected	percent_protected
0	Amphibian	72	7	0.088608
1 2 3	Bird	413	75	0.153689
	Fish	Fish 115 11 0.087	0.087302	
	Mammal	146	30	0.170455
4	Nonvascular Plant	328	5	0.015015
5 6	Reptile	73	5	0.064103
	Vascular Plant	4216	46	0.010793

	protected	not protected
Mammal	146	30
Bird	413	75
1	protected	not protected
Mammal	146	30
Reptiles	73	5

After importing our SciPy library, we want to test our data. In order to test the significance of our assumption, that the Mammal category is more likely to be endangered than the species in Bird, we're going to run a chi-squared test. In order to do so, we need to create a contingency table. But while we're at it, let's also compare the species in Mammal and Reptiles as well.

SPECIES_INFO.CSV DATA SET. How confident am I with my data?

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	protected	not protected
Mammal	146	30
Bird	413	75
1	protected	not protected
Mammal	146	30
Reptiles	73	5

```
chi2, pval, dof, expected = chi2_contingency(contingency)
print "The p-value of {} shows there is NOT a significant difference between Birds and Mammals".format(pval)
```

The p-value of 0.687594809666 shows there is NOT a significant difference between Birds and Mammals

```
contingency2 = [[146,30],[73,5]]
chi2, pval, dof, expected = chi2_contingency(contingency2)
print "The p-value of {} shows there IS a significant difference between Reptiles and Mammals".format(pval)
```

The p-value of 0.0383555902297 shows there IS a significant difference between Reptiles and Mammals

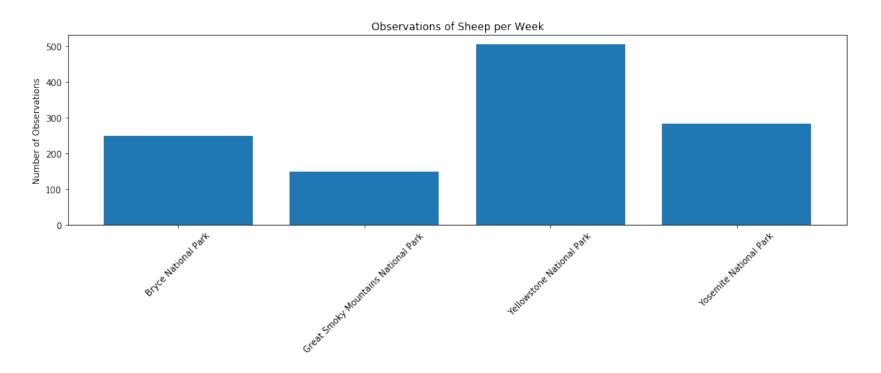
After running our two tests on our two contingency tables it's become clear, there are NOT significant differences between the Birds and Mammals species and there ARE significant differences between the Birds and Reptiles species.

SPECIES_INFO.CSV + OBSERVATIONS. Insights from the data?

	category	scientific_name	common_names	conservation_status	is_protected	is_sheep	park_name	observations
0	Mammal	Ovis aries	Domestic Sheep, Mouflon, Red Sheep, Sheep (Feral)	No Intervention	False	True	Yosemite National Park	126
1	Mammal	Ovis aries	Domestic Sheep, Mouflon, Red Sheep, Sheep (Feral)	No Intervention	False	True	Great Smoky Mountains National Park	76
2	Mammal	Ovis aries	Domestic Sheep, Mouflon, Red Sheep, Sheep (Feral)	No Intervention	False	True	Bryce National Park	119
3	Mammal	Ovis aries	Domestic Sheep, Mouflon, Red Sheep, Sheep (Feral)	No Intervention	False	True	Yellowstone National Park	221

We merged our database with another titled Observations, by amending the average number of sheep observations per week and the park they were observed.

SPECIES_INFO.CSV + OBSERVATIONS. Insights from the data?

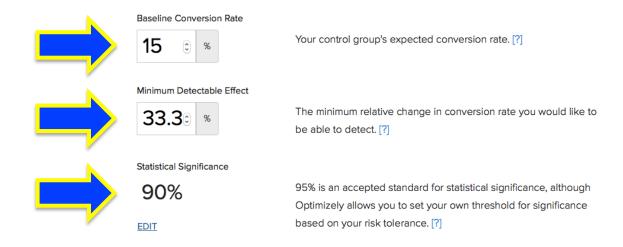


After grouping our data into observation parks, we plotted the weekly sheep sightings per location. While we didn't subset the data by sheep who were labeled as "no intervention" from those "of concern" or "endangered", we can clearly see a healthier population of sheep in the Yellowstone National Park. This could be attributed to simple volume of population, volume of observations commensurate with observers, or some other unforeseen variable. But given the large shifts in observations, I'd recommend that conservationists dig deeper into the data to ensure there aren't best practices being applied in Yellowstone that may be applicable to the other national parks.

SPECIES_INFO.CSV + OBSERVATIONS. Disease Population Sampling

A/B Test Sample Size Calculator

Powered by Optimizely's Stats Engine



Finally, we would like to acknowledge the amount of Foot and Mouth disease our sheep population at Bryce National Park have. Let's use these data to calculate whether or not our goal of reducing instances of Foot and Mouth by 5% was successful, with confidence.

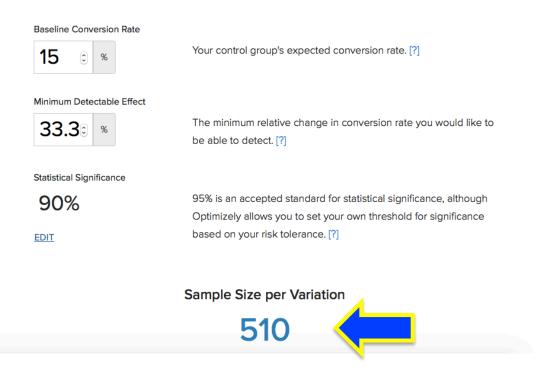
First I calculate my minimum relative change in conversion. In this case it's simply $100 \times 5\% / 15\% = 33.3\%$

Then I was provided a baseline conversions (15% of the population) and our required statistical significance (90%)

SPECIES_INFO.CSV + OBSERVATIONS. Disease Population Sampling

A/B Test Sample Size Calculator

Powered by Optimizely's Stats Engine



I use my online A/B Test Sample Size Calculator from Optimizely to determine my minimum population size required. And that number is 510!

SPECIES_INFO.CSV + OBSERVATIONS. Disease Population Sampling

A/B Test Sample Size Calculator

Powered by Optimizely's Stats Engine

Sample Size per Variation

510

print"In Bryce National Park I see an average of 250 sheeps per week, as such, I would need ~ {} weeks to complete my re

In Bryce National Park I see an average of 250 sheeps per week, as such, I would need ~ 2 weeks to complete my requir ed samples size

print"In Yellowstone National Park I see an average of 507 sheeps per week, as such, I would need ~ {} week to complete

In Yellowstone National Park I see an average of 507 sheeps per week, as such, I would need ~ 1 week to complete my r equired samples size

If I were to test that my 5% reduction was accurate at Bryce National Park, it would take me ~ 2 weeks, given I have an average of 250 observations per week.

If I were to test that my 5% reduction was accurate at Yellowstone National Park, it would take me ~ 1 weeks, given I have an average of 507 observations per week.