Intro to Visualization Final Activity

We've made it this far, congratulations! I hope at this point that you are feeling confident in your ability to deploy python and matplotlib to create informative and attractive data visualizations! You should feel like you have a new tool in your scientific toolkit. I also hope that that this semester's activities have helped to reinforce some of your other python skills. The more you practice with things like loops, conditionals, and the various python data structures (lists, dictionaries, and dataframes) the less daunting they seem. As I've said many times, you can always look up the syntax again later, but every time you complete one of these notebooks you are building up base skills in computational thinking that I think will allow you to problem-solve in your own projects someday.

So let's give you a chance to show off! I've included a dataset in this folder called BioMar.csv. Your challenge is to summarize that data set using visualizations to create a set of figures that tell the 'story' of the data as you see it. Within the data folder I have included a an article (along with its supplementary data file) that describes this recent data

from the marine zone of Area de Conservación Guanacaste (you'll see on the first page of the paper that this is part of a special issue of the journal Biotropica

that I was involved in producing). The paper is describing the results of a new biodiversity surveying effort. The main concern is documenting previously undocumented marine species within the conservation area. Your answer should include AT LEAST one each of: pie chart histogram bar plot

and for each individual plot that you make your code should export the figure as a .pdf file named LastName Fig X.pdf where LastName is your last

- scatter plot box plot*
- heat map annotated figure multi-plot layout
- The data that I have given you is drawn from the tables in the paper and the supplementary material.

name and x is the number for each figure.

- Biomar_samples: the total organisms collected from within the particular taxonomic group
- Biomar_species: the number of unique species found in the sample
- Poss New species: species in the sample that are undescribed (new to science)
 - New_to_ACG: speciesin the sample not previously known to occur in ACG New to Costa Rica: species in the sample not previously known to occur in Costa Rica

been documented for the ACG before this effort, but you can calculate it given what you have.

- Total_species_ACG: previous species count know to occur in ACG plus 'New_to_ACG'
- Two further notes:

need that because the data on Total_species_ACG isn't broken down into subgroups. So for some comparisons you will have to use some subsets of the

rows and for other comparisons you will have to add up different subsets. I'll let you figure out how to do this, but do this subsetting within python to practice your pandas skills (in other words, don't just go into Excel and make two separate datasets -- even this would probably be the easiest thing to do).

1. You don't have all the variables that you need to plot in order to answer some obvious questions. For example, you don't know how many species had

2. There are a few rows in the data that need to be handled differently than others. For example, there is a row for the TOTAL number of Crustaceans. We

- * The box plot will be the hardest thing to figure out. For this in particular you may want to think about how you can create different values by combining the existing columns in different ways. For example, you may want to plot some variables that aren't just driven by the large differences in sample size. In [76]: ###pie chart (New to Costa Rica) import matplotlib.pyplot as plt
 - import numpy as np import pandas as pd from matplotlib.backends.backend_pdf import PdfPages final_df = pd.read_csv (r'C:\Users\renie\Downloads\6_final_project\6_final_project\data\BioMar.csv')

totals= final_df[~final_df['Taxonomic _group'].str.contains("_") | final_df['Taxonomic _group'].str.contains("TOTAL")]

#totals['Taxonomic group'] #totals['New_to_Costa_Rica']

lab= totals['Taxonomic _group'].str.replace('_TOTAL', '') colors =['red', 'orange', 'yellow', 'green', 'cyan', 'pink', 'violet', 'peru', 'khaki', 'whitesmoke', 'grey', 'indigo' , 'maroon', 'teal', 'navy', 'deeppink']

plt.pie(totals['New_to_Costa_Rica'],colors= colors, autopct= '%.1f%%', radius= 3) plt.title('Percentage of Species New to Costa Rica per Taxonomic Group', y=2) plt.legend(lab, loc='best') plt.show()

fig.savefig('Cooper_Fig_1.pdf') Percentage of Species New to Costa Rica per Taxonomic Group

7.6%

Cyanophyta Chlorophyta

> Porifera Mollusca

Annelida Nemertea

Ochrophyta Rhodophyta 8.5%

3.4%

3.4%

6.8%

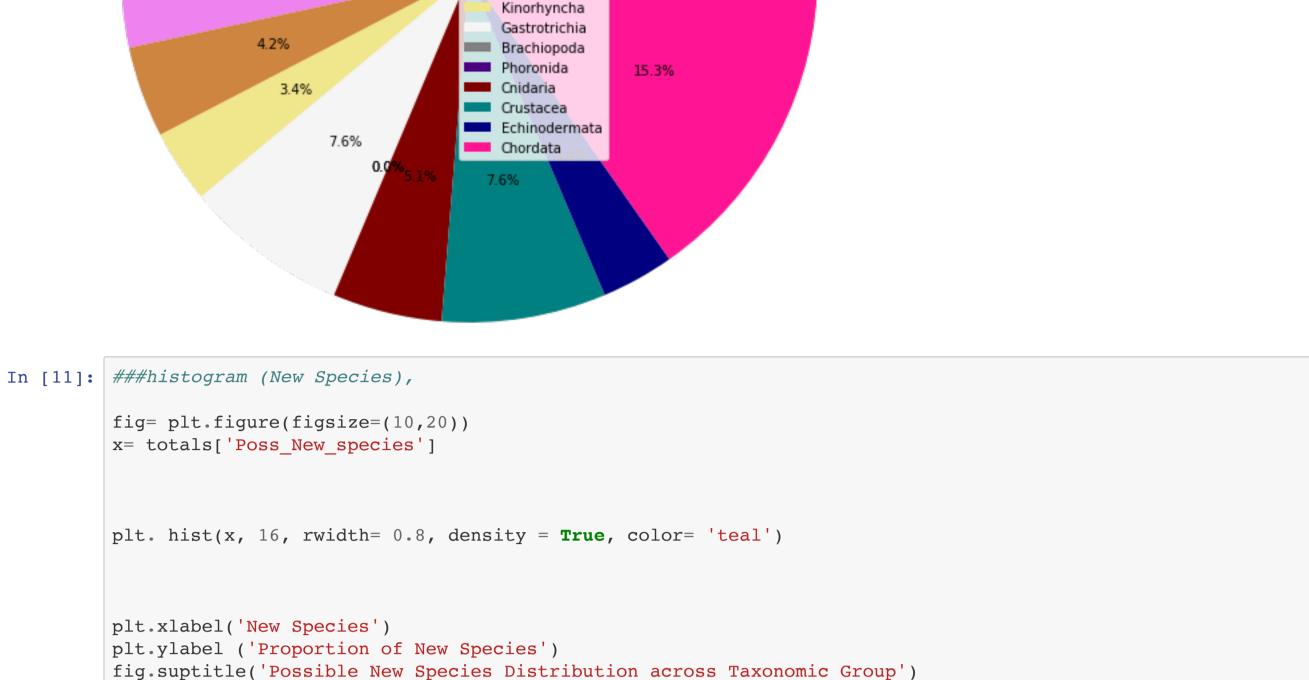
8.5%

plt.show()

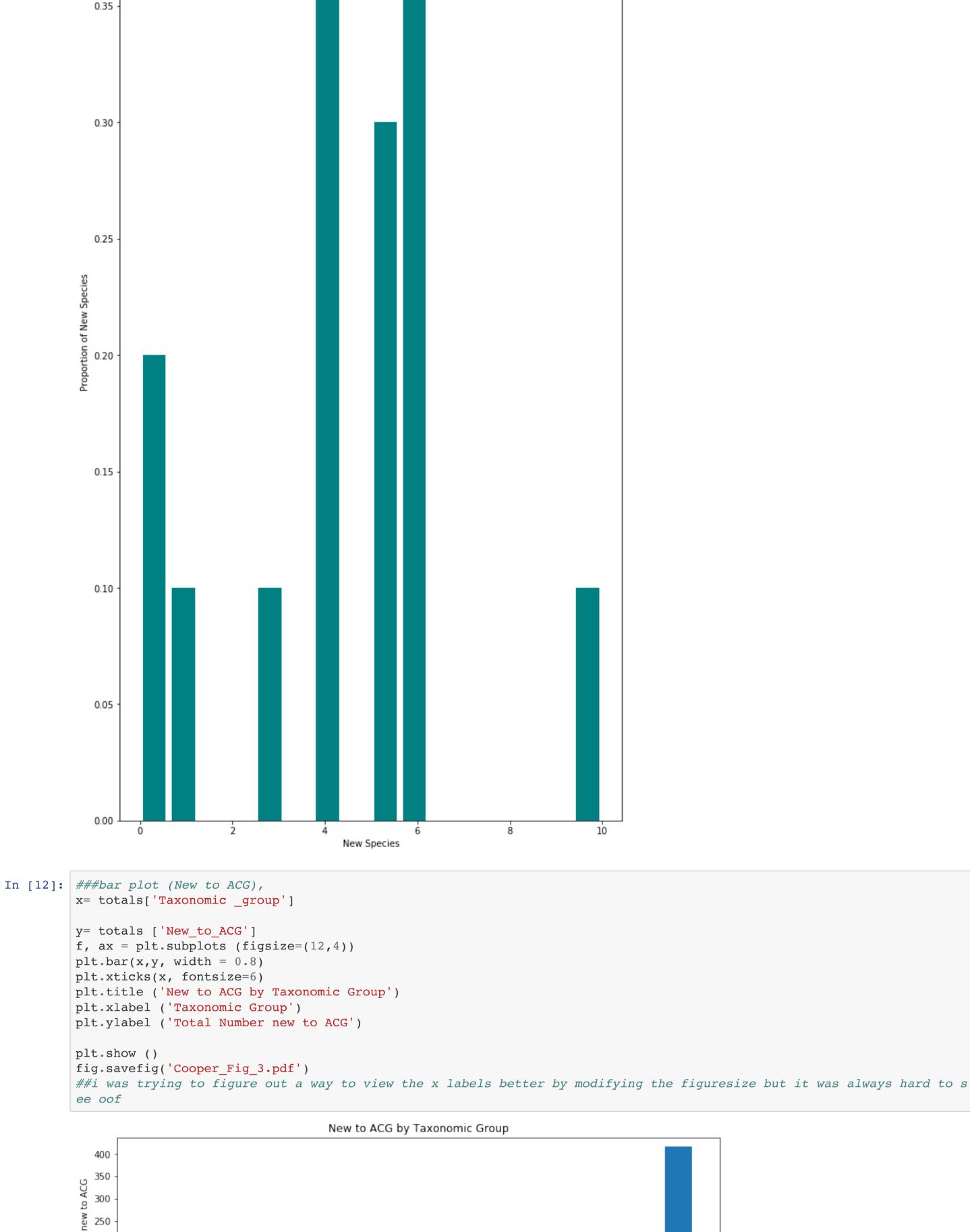
0.40

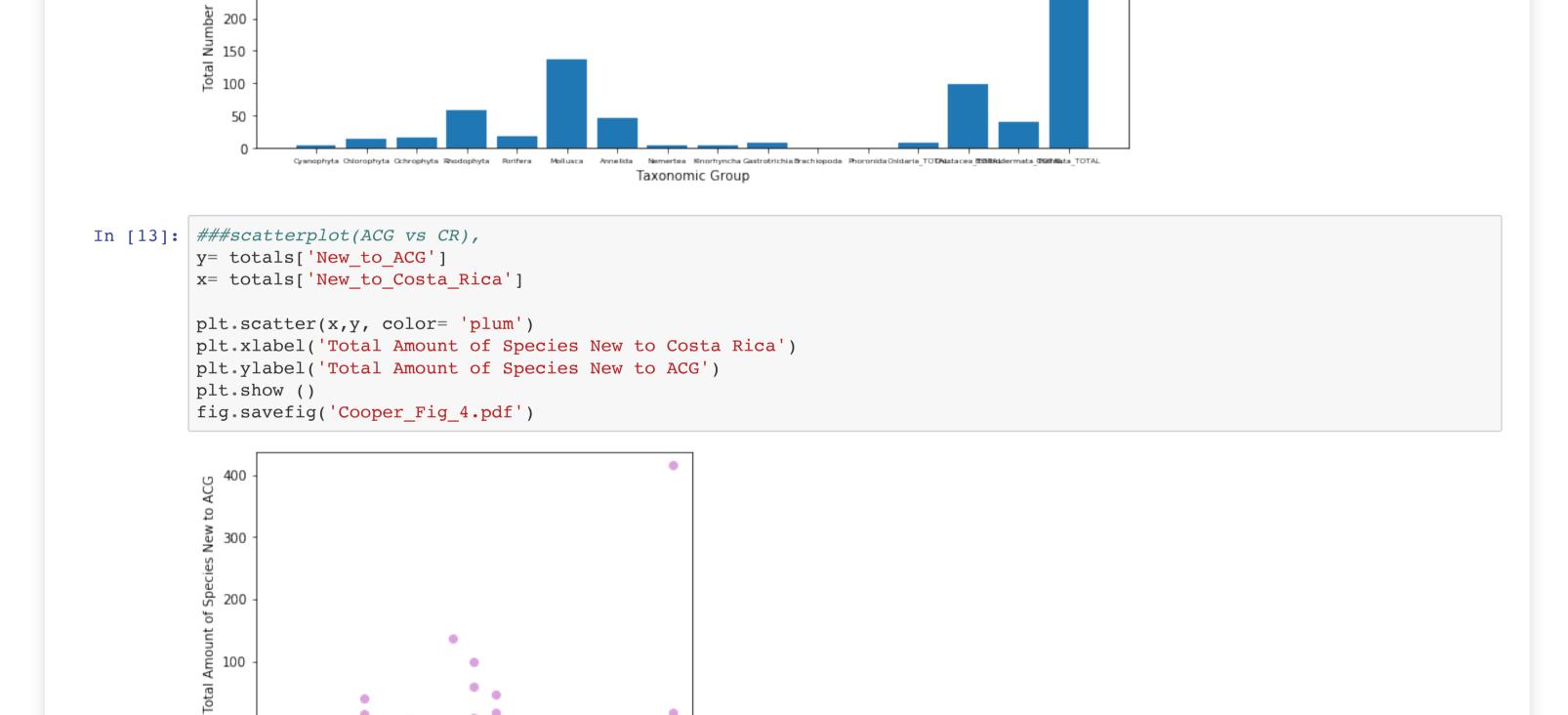
fig.savefig('Cooper_Fig_2.pdf')

15.3%



Possible New Species Distribution across Taxonomic Group







10.0

Total Amount of Species New to Costa Rica

7.5

12.5

15.0

17.5

data = [totals['Poss_New_species'], totals['New_to_ACG'], totals['New_to_Costa_Rica']]

5.0

Possible New Species New to ACG

from IPython.core.display import HTML

2.5

In [14]: ###box plot (),

In [88]: ###heatmap (),

plt.show()

29

15 -

14 -

fig.savefig('Cooper_Fig_6.pdf')

fig= plt.figure(figsize =(14,8)) ax= plt.subplot() species= totals.groupby(totals.index).mean() plt.pcolormesh(species, cmap='YlGn', edgecolor='white', alpha = 0.8) plt.colorbar() ax.spines['bottom'].set_color('white') ax.spines['left'].set_color('white') ax.spines['top'].set_color('white') ax.spines['right'].set_color('white') # i in range (len(totals[Biomar_species].index)): #for j in range(len(totals.columns)): # plt.text(j+0.2, i+ 0.4, totals.iloc[i,j]) plt.yticks(np.linspace(0.5, len(species.index)-0.5, len(species.index)), species.index, size=13) plt.xticks(np.linspace(0.5, len(species.columns)- 0.5, len(species.columns)), species.columns,size=10) plt.title('Species Count? Not sure what this reflects', size= 18)

#way I could get a heatmap to come up. I tried to drop colums like before but te code said that was coming back

2500

- 2000

1500

New to CR

28 27 26 -16 -

#as an error, and when I tried to specify colums it wouldn't let me

###gonna be honest, I'm not sure what this shows, but this code was the only

Species Count

13 -12 -11 -1000 10 4 -3 -500 2 -1 -0 -Biomar_species Biomar samples Poss_New_species New_to_ACG New_to_Costa_Rica Total_species_ACG In [81]: ###annotated figure, y= totals['New_to_ACG'] x= totals['New_to_Costa_Rica'] plt.scatter(x,y, color= 'plum') plt.xlabel('Total Amount of Species New to Costa Rica') plt.ylabel('Total Amount of Species New to ACG')

```
plt.annotate('449 New Chordata \nSpecies were found in ACG', (x[13], y[13]), xytext= (0.6, 0.8), textcoords='axes fra
ction')
plt.show()
fig.savefig('Cooper_Fig_7.pdf')
Total Amount of Species New to ACG
                                    449 New Chordata
                                    Species were found in ACG
```



5.0

7.5

10.0

Total Amount of Species New to Costa Rica

12.5

15.0

fig.savefig('Cooper_Fig_8.pdf') 2500 Total Species 1000 1000

Cyanophyta Chlorophyta Ochrophyta

500

Nemertea Kinorhyncha Gastrotrichia Brachiopoda Phoronida Chidaria_TOTALCrustacea_TOEdinodermata_TOTAL

400

Species 500 S

New

New to ACG by Taxonomic Group

Porifera

Mollusca

Rhodophyta