

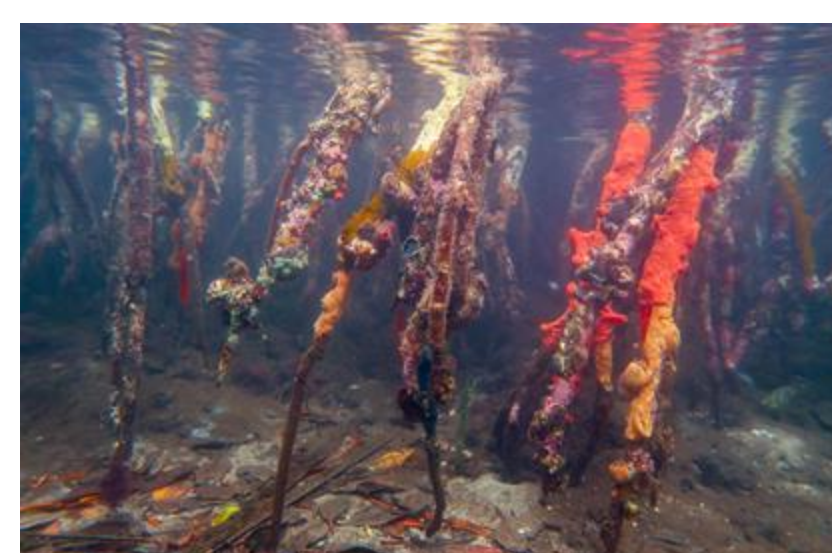
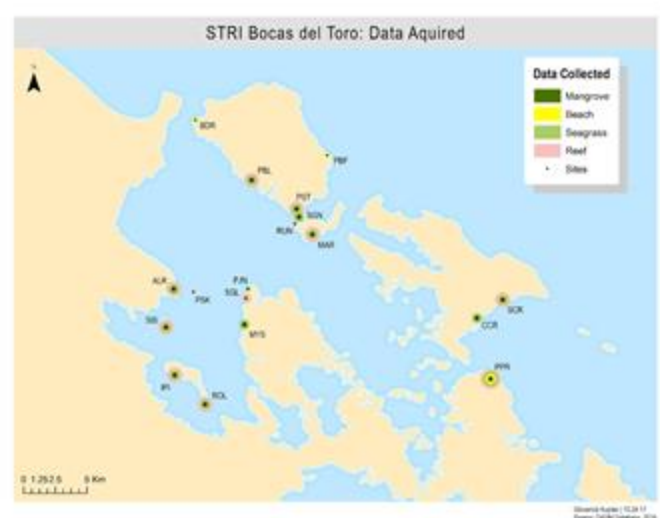
Scaling of Marine Biodiversity in Bocas del Toro, Panama

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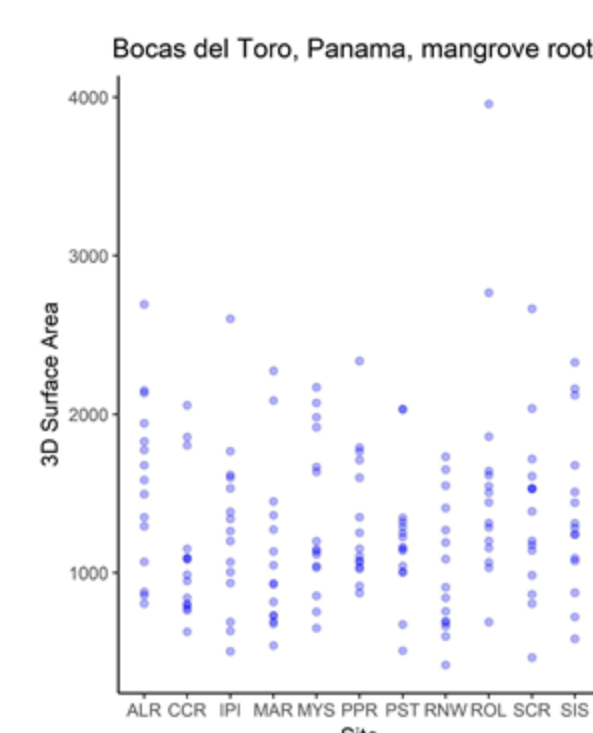
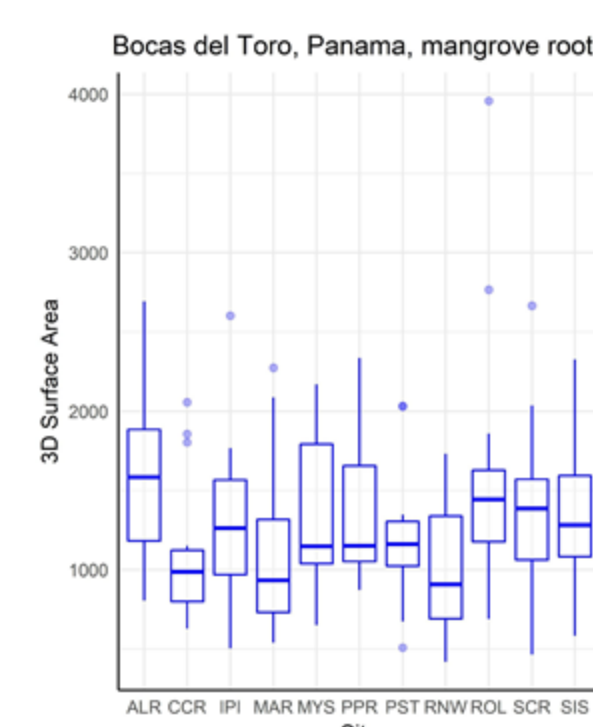
Background

- In the Summer of 2017, interns at the Smithsonian National Museum of Natural History traveled to Panama in order to learn about the contribution of four ecosystems – seagrass, mangrove roots, coral reefs, and sediment – to the marine biodiversity in Bocas del Toro, Panama. They collected samples of each and prepared them for pictures by taking off any organisms living on them.
- As part of the Honors College Smithsonian Internship, I joined the researchers at the National Museum of Natural History in the summer of 2018. My mission for the research project was to measure the surface area of mangrove roots using a scientific imaging software known as FIJI and to organize, visualize, and analyze this data using a statistical and graphical program called RStudio.
- The purpose of collecting and analyzing this data was to aid research in calculating to what extent these each of these ecosystems contribute to the marine biodiversity in the region.
- Considering my mentors could not find a research project as in-depth as this study, our research maybe one of the most comprehensive tropical marine biodiversity studies to date.



Methodology

- As I had never used Fiji nor RStudio, my co-mentor explained how to edit the perspective of an image in order to calculate the surface area of mangrove roots using FIJI. He also explained the application of RStudio in data science and taught me how to use it to manipulate and graph data sets.
- I proceeded to individually measure each section of each mangrove root and seagrass patch, totaling in 1113 mangrove data points organized into 11 groups.
- All the data was entered into an Excel file and imported into Studio. I then visualized the data by creating a scatterplot and a boxplot.
- After this, I performed a statistical analysis of the 3D surface area of the mangrove roots from each site. I also *log-transformed* the data and performed additional statistical tests on this data.



Results

Analysis of Untransformed Surface Area Data

- I first performed a Shapiro-Wilk Normality Test on the data to see whether the total surface area of each site was normally distributed
 - The majority of the sites have p-values greater than 0.05, with the exception of CCR, MAR, PPR, AND ROL. So, for the majority of the sites, we cannot reject the null hypothesis that the samples from these sites are normally distributed. For the four other sites, we can reject the null hypothesis that the samples from these sites are normally distributed. Because not all of the sites are normally distributed, the assumptions for Analysis of Variance (ANOVA) are not met; therefore, the Kruskal-Wallis One-Way Analysis of variance must be used for this set of data.
- I then performed a Kruskal-Wallis Test to see whether our data samples originate from the same distribution
 - Because the resulting p-value equals 0.05551, which is greater than 0.05, we cannot reject the null hypothesis that there is no significant difference between the sites, albeit with little confidence considering how close the p-value is to 0.05

Analysis of Log-Transformed Surface Area Data

- Using the Shapiro-Wilk Normality Test as in the previous section, I tested the normality of the log-transformed data.
 - All of the sites have p-values greater than 0.05; therefore, we cannot reject the hypothesis that the sample is normally distributed, which is an assumption necessary to perform ANOVA. Now Levene's Test must be used to test for common variances to see whether the other ANOVA assumption is met.
- Using Levene's Test for Common Variance, the p-value of the data was found to be 0.9588, which is greater than 0.05. Therefore, we cannot reject the null hypothesis that there is no significant difference between the variances of each site. ANOVA can be performed on our data.
- I performed ANOVA on the set of data to analyze the differences among group means in our sample.
 - Because the p-value equals 0.0341, which is less than 0.05, we can reject the null hypothesis that there is no significant difference between the mean value of each site; therefore, a Tukey HSD must be performed to compare the mean values of each site to each other.
- Finally I performed a Tukey HSD, which finds out which specific groups' means differ from the other group's means.
 - Because the adjusted p-values for every combination of site are greater than 0.05, we cannot reject the null hypothesis that there is no significant difference between the means of each site.

Conclusions

- After extensive statistical analysis, the mangrove root surface area data, both untransformed and log-transformed, is primed for further research in calculating the contributions of mangrove roots to the marine biodiversity of Bocas Del Toro, Panama.
- Further research interests include incorporating environmental variables, expanding analyses to other ecosystems, and incorporating and barcoding macroorganisms.

Acknowledgements

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