

## CS 506 project proposal (deliverable 0)

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### Motivation & background

All animals are an amalgamation of an animal host and the billions of microorganisms that reside within. As next-generation sequencing technology advances, we are learning more about the outsized role that these microorganisms play in the fitness of their hosts. For instance, bacteria are responsible for a person's ability to digest certain complex carbohydrates and have even been shown to help modulate social behavior in mammals. Researchers have long understood the importance of micro-algae belonging to the family Symbiodiniaceae for coral host health. These algal symbionts capitalize on abundant light penetration in oligotrophic waters to photosynthesize and share carbon with their coral hosts for building coral reef structures. More recently, the bacterial microbiome has also been implicated in regulating coral health through immune system function and nutrient cycling. Furthermore, empirical evidence indicates that these microbes interact together, potentially aiding the coral host synergistically. Unfortunately, this tripartite symbiosis is highly sensitive to a multitude of environmental stressors. However, we have yet to understand the ways in which storm disturbances, projected to intensify under climate change, impact these two important microorganismal communities living within corals. Subsequently, **the objective of my proposed project is to identify whether a significant storm disturbance, Hurricane Irma, disrupted the networks of unicellular algae and bacteria residing within two coral species in the Florida Keys.**

The data in the proposed project were generated using DNA metabarcoding, a method that amplifies specific algal & bacterial genes that can be used to determine which species are living within the coral host. Corals typically host tens to hundreds of algal species and thousands of bacterial species within a single tissue sample. Tissue samples of corals were collected from six sites across the Florida Keys before (2015), shortly after (2017), and a year after Hurricane Irma (2018). Using these data, the following objectives will be addressed:

1. Characterize the composition of coral-associated algal & bacterial communities at each of three timepoints (before, shortly after, and a year post-Irma) as co-occurrence networks both within bacteria & algae separately, as well as between these two groups.
2. Determine whether the compositions and interactions of these microorganismal communities change across the three timepoints.

I hypothesize that the corals sampled from the Hurricane Irma timepoint will display a breakdown in the connectedness of the microorganismal networks, as the stressful environmental conditions (increased turbidity, temperature swings) of the superstorm should disrupt these coral symbioses.

### Methods notes & product outcome

The sequencing data are already collected. There are established pipelines for taxonomic assignment of the gene sequences, which primarily take place in R and Unix. I have completed such analyses on previous projects (see [github.com/nicfall/moorea\\_holobiont](https://github.com/nicfall/moorea_holobiont)). I have not yet attempted network analysis, but that will be an integral component of this project to learn about. A completed product will be visualized networks of bacteria-bacteria, algal-algal, and algal-bacterial co-occurrences, from each of the three timepoints. In addition, statistical analyses will need to be undertaken to determine whether the timepoints display significant differences in these networks.