**Surgeonfish gut microbiome results section outline**

I **The surgeonfish gut microbiome possesses a great diversity of microbial communities**

1. **Data from the collection trip to the Hawaii Institute of Marine Biology 2013**
2. Prior to quality filtering, Illumina sequencing generated 12,730,293 sequences. The median sequence length was 253 base pairs.
3. there are 2,960 unique otus observed in the posterior section of the gut when 21,150 sequences are analyzed from each sample,
4. There was an observed difference in microbial community structure when different sections of the surgeonfish gut were compared
5. Taxonomic summaries of different samples from the surgeonfish gut showed a great variety of taxa, but did not show the presence of *Epulopiscium* as a genus.
6. After a correction in the taxonomic assignment of otus, the genus *Epulopiscium* could be observed in taxonomic summary graphs

**2. Data from the collection trip to the Hawaii Institute of Marine Biology 2014**

1. Prior to quality filtering, Illumina sequencing generated 11,750,346 sequences. The median sequence length was 265 base pairs.
2. There are 1,814 unique otus observed in samples taken from *Acanthurus oliveaceus* when 22,000 sequences were analyzed from each sample.

**3. Combined data from 2013 & 2014**

1. 2909.650 is the highest amount of unique otus observed from samples of any single fish in the combined analysis
2. Microbial communities in *Naso unicornis* are significantly different in community structure between certain members of the gut

**4. How can we describe the composition of the surgeonfish gut microbiome?**

1. What phyla make up the largest percentage of the surgeonfish gut?
2. What samples have the largest percentage of *Epulopiscium?*

II. **In some species of surgeonfish, *Epulopiscium* is the taxa that is in the highest proportion out of any of the observed microbial communities in certain areas of the gut.**

1. In species of surgeonfish such as *Naso lituratus*, *Epulopiscium* can make up 23 % of the bacterial community of midgut samples

IV. **Core gut microbiome of surgeonfish**

IV. **Comparisons between samples from the surgeonfish gut microbiome**

**All samples analyzed together**

a.What drives the most variation in the bacterial communities from each sample in the gut?

b. Are different sections of the surgeonfish gut significantly different from each other?

**Each individual fish analyzed by gut section**

1. Are different sections of the gut significantly different from each other?

V. **Comparison between the human gut microbiome and the surgeonfish gut microbiome**

1. How does the surgeonfish gut microbiome compare to the human gut microbiome in terms of unique otus that are observed?
2. How do the microbial communities of the surgeonfish gut microbiome compare to the human gut microbiome in terms of their phylogenetic diversity?
3. How do species estimates compare between the surgeonfish gut microbiome and the human gut microbiome?