



Hitch a Ride on the Raft! *Turbinaria ornata* Rafts as a Novel Mode of Dispersal



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Introduction

- Globally, coral reefs are shifting from coral to algal dominance (Done 1992).
- In South Pacific reef lagoons, *T. ornata* reaches such high densities that storms dislodge and form large rafts of *T. ornata*.
- T. ornata* rafts are novel tropical ecosystems that form in shallow lagoons before transiting to open ocean environments potentially increasing connectivity among reef ecosystems.
- Algal rafts are common and important in regions like the Sargasso Sea with much work focusing on macrofauna, overlooking epibionts that live on the algal surface (Laffoley et al. 2011).
- Epibionts include an array of epiphytes, invertebrates, and other microscopic organisms. Of particular concern are ciguatoxic algae and coral pathogens (Bittick et al. 2019).

What organisms compose the epibiont community on *T. ornata* rafts and how do these communities change over time?



T. ornata raft formed after a storm on the North shore of Mo'orea.

Experimental Design

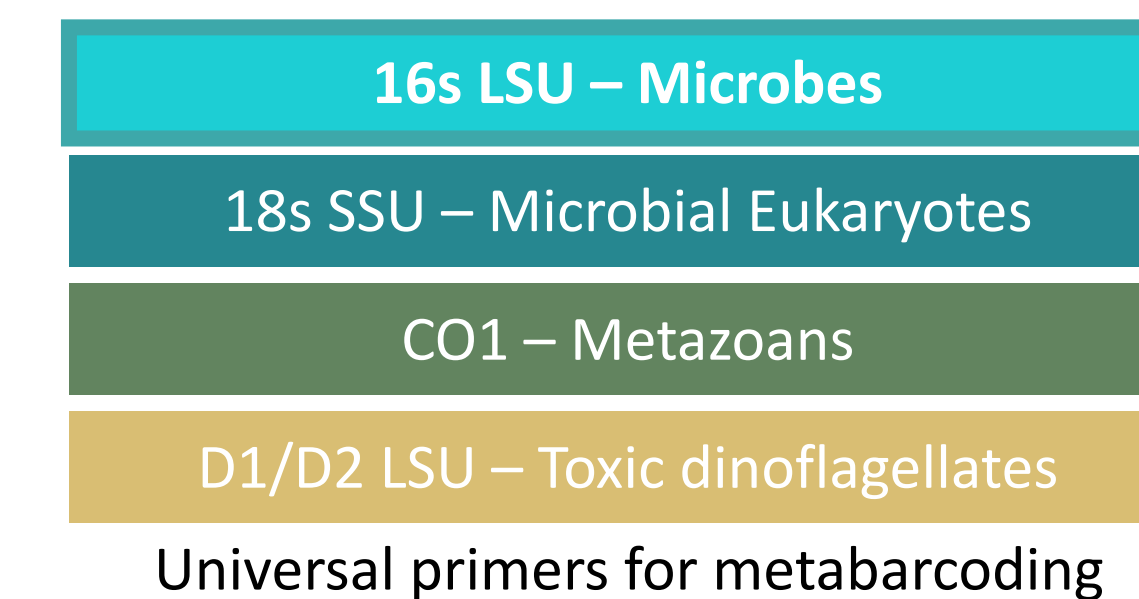
Attached <i>T. ornata</i>	Floating <i>T. ornata</i> Time Series
In situ collections	Mesocosm experiment
3 Fringing Reef sites	11 timepoints across 30 days
3 Reef Crest sites	T0=Day 0, ..., T11=Day 30

Methods

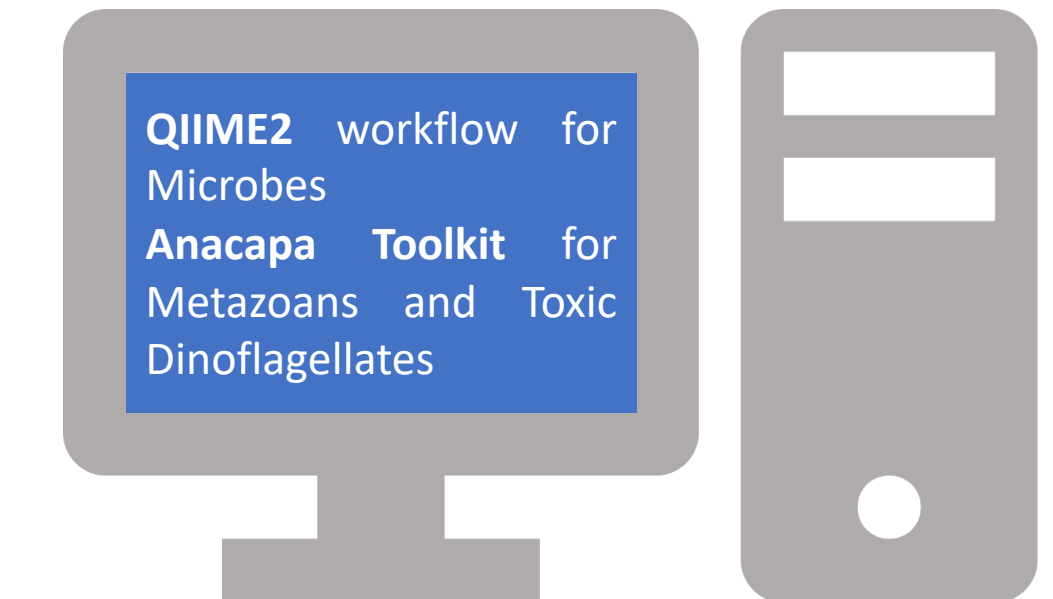


Attached *T.ornata* collection Mesocosm experiment

sample collection



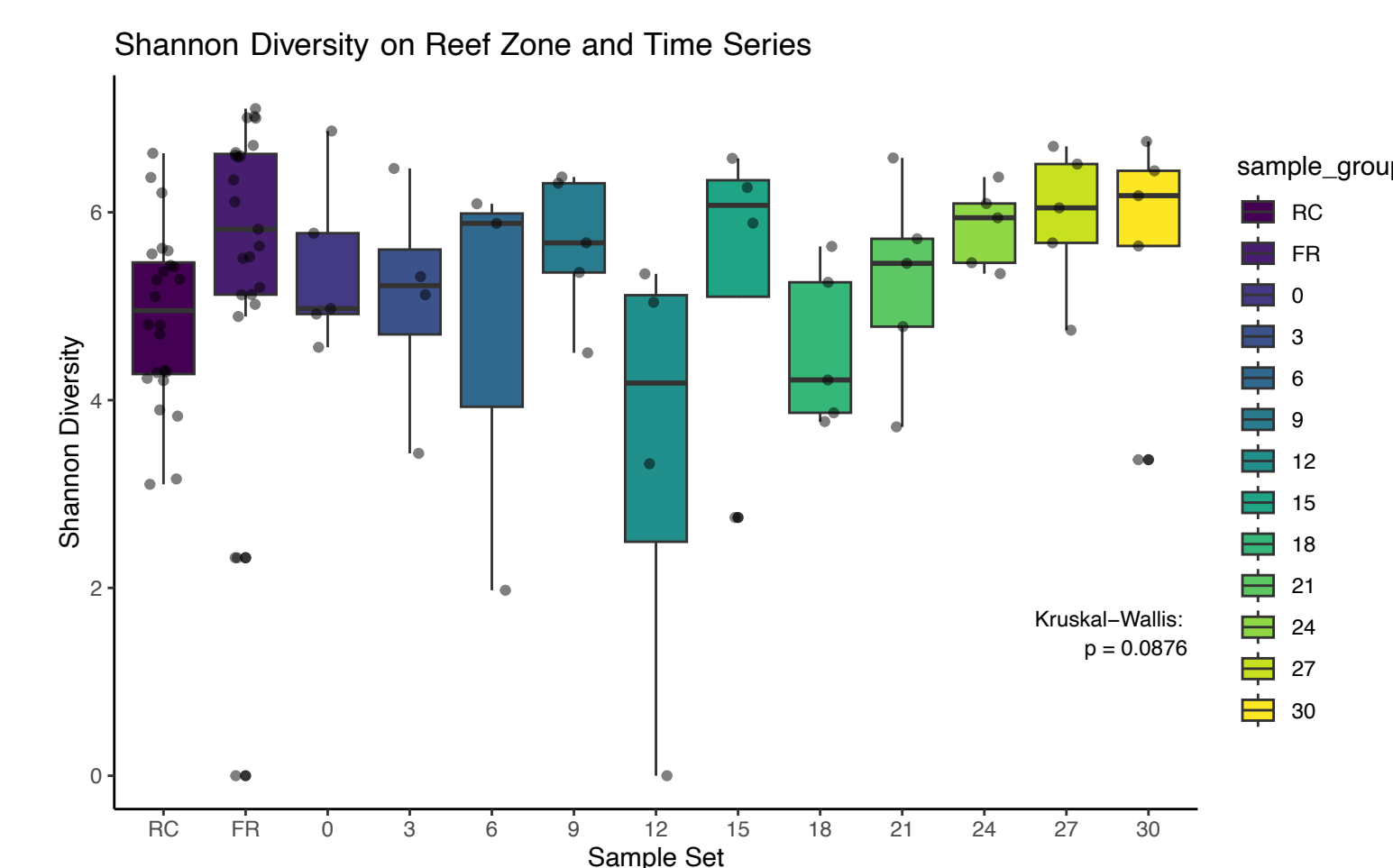
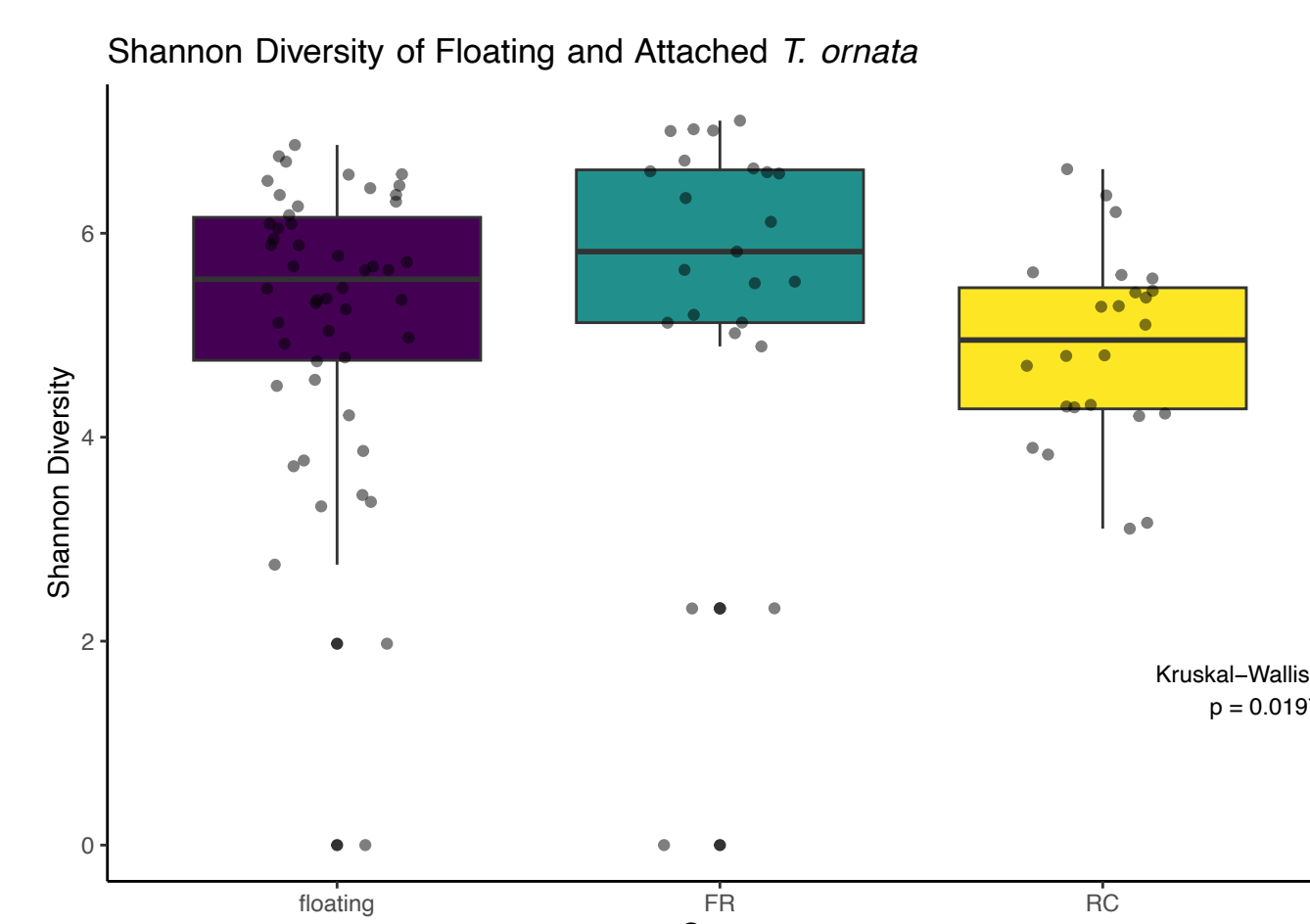
high-throughput sequencing



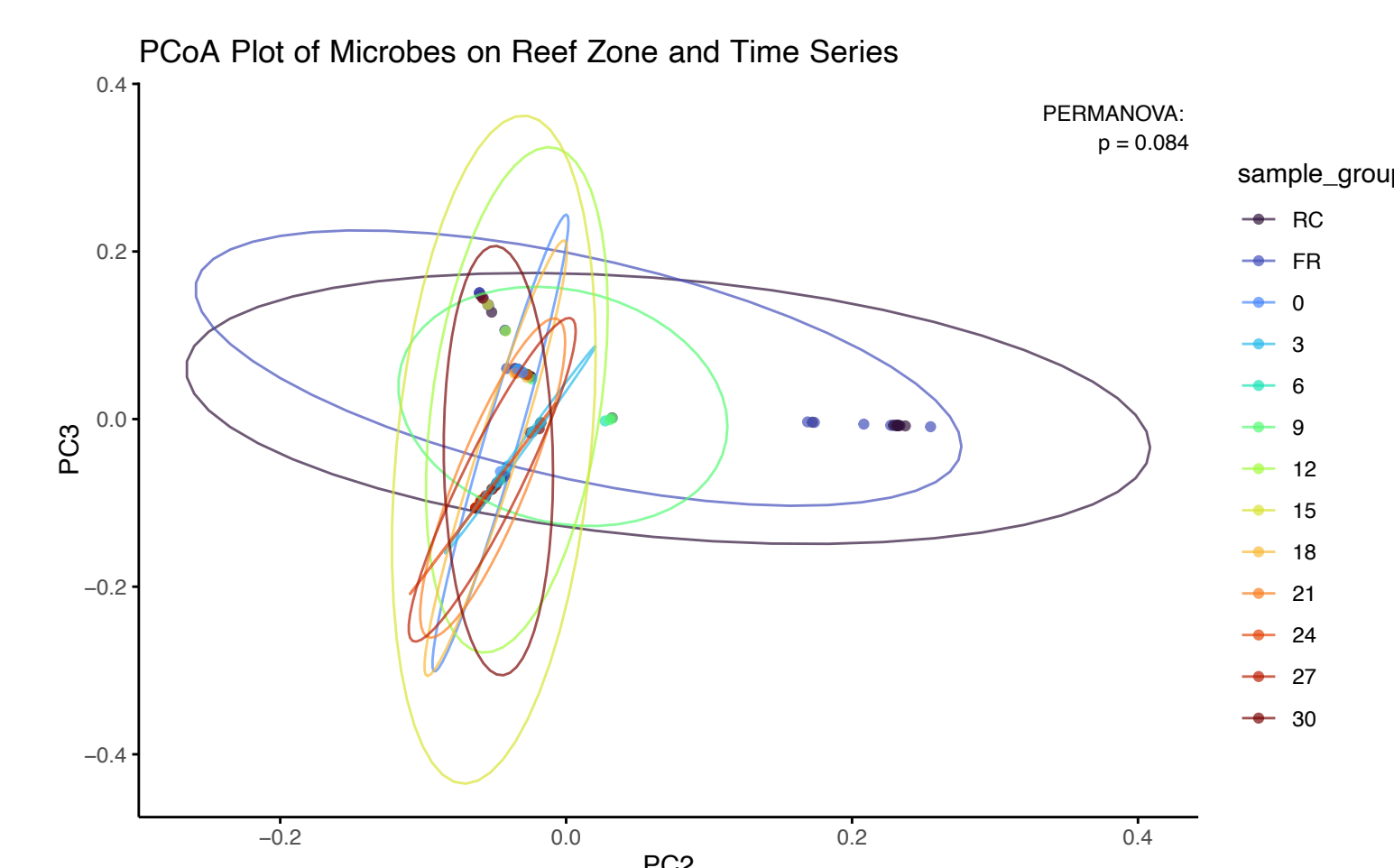
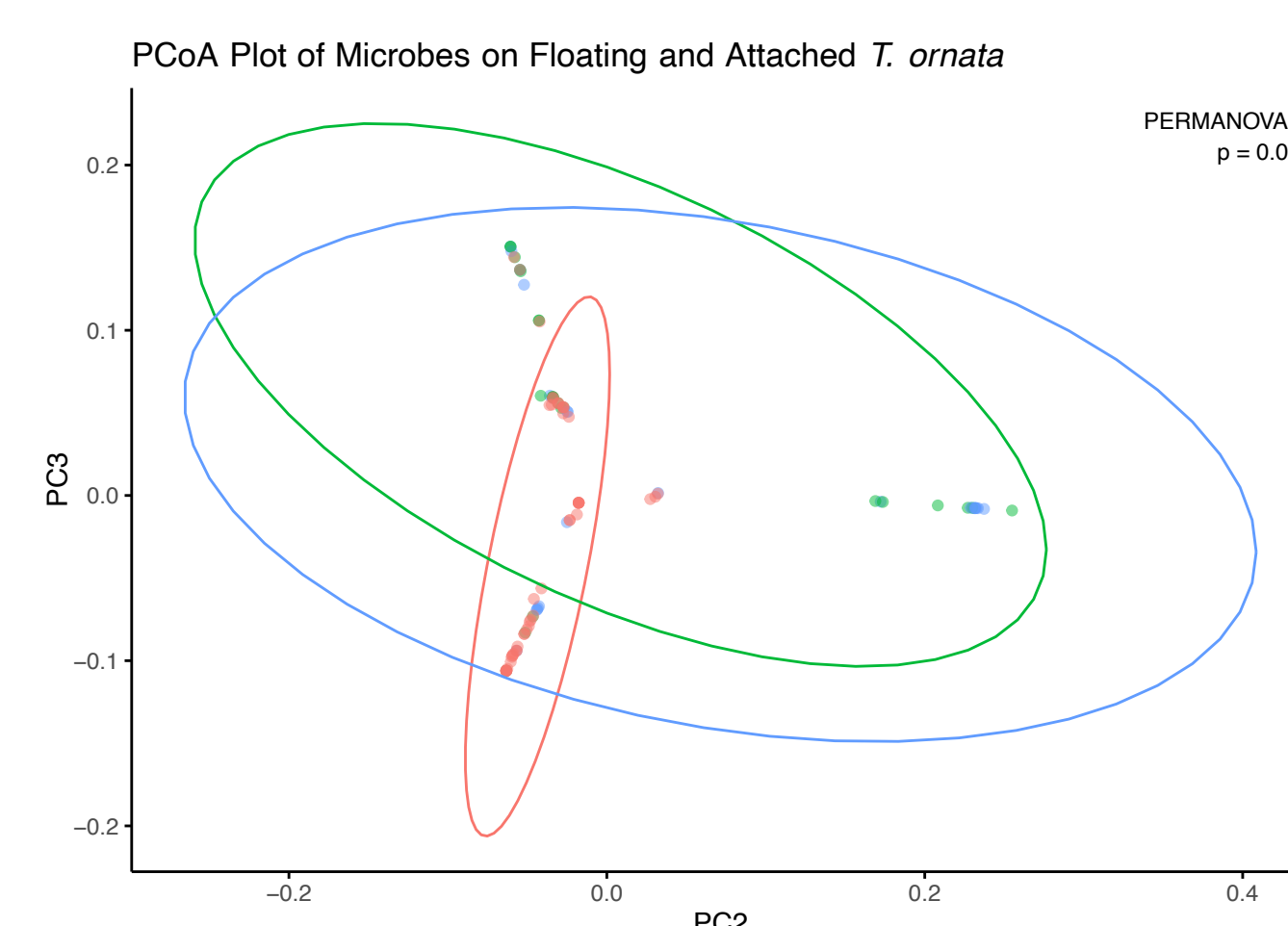
Bioinformatics

Preliminary Results

Alpha Diversity



Beta Diversity



- Takeaway 1:** Fringing reef microbial epibionts on *T. ornata* exhibited greater alpha diversity compared to microbial communities on reef crest and rafting *T. ornata*.
- Takeaway 2:** Microbial diversity and community composition on *T. ornata* rafts fluctuates over time.
- Takeaway 3:** *T. ornata* rafts host a subset of the microbial community originally seen on attached *T. ornata*.

Next Steps

- Re-sequence microbe library to improve sequencing depth.
- Identify ecologically significant microbial taxa and infer their functions.
- Process and sequence other constituent epibiont communities.
- Implement viral metagenomics to gain a clearer understanding of microbial dynamics and identify potentially harmful strains of viruses.

Bibliography

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Acknowledgements

This research was funded partly by NSF and the UC-HBCU Initiative. I acknowledge and thank the UC Berkeley Gump Research Station staff and Western Society of Naturalists. I would like to thank Erick Zerecero, Caitlin Fong, Jeanie Barber-Choi, and Nicholas Barber-Choi for their support in sample collection throughout this project. I would also like to thank my team of undergraduate mentees Amarie Strong, Mei Lin McLaughlin, Mahala Peter-Frank, and Madeleine Wright for their help in the laboratory.