

Supplementary Material for Gallego et al., 2020, "Environmental DNA Metabarcoding Reveals Winners and Losers of Global Change in Coastal Waters"

The most comprehensive Supplementary Information is in the online Repository

<https://github.com/ramongallego/eDNA.and.Ocean.Acidity.Gallego.et.al.2020>

This repository contains all the code we used to generate the manuscript analysis and figures, starting from Raw Fastq files.

In this document we provide the figures mentioned in the manuscript that refer to the Supplemental Information.

Future projections of environmental conditions

Find the code that generates these simulations in the script *Manuscript.Main.Analysis.Rmd*, lines 98-135, using functions explained in the file *Future_climate_conditions.r*

Species responses Models

Find the comparisons between models and the code associated with it in the file *Supplement_ModelTesting.pdf*

Cluster analysis - San Juan Island

Figure 2 from the main manuscript refers only to the Hood Canal samples. The corresponding figure for the San Juan Islands is attached here, and the code used to generate it is on the github repository.

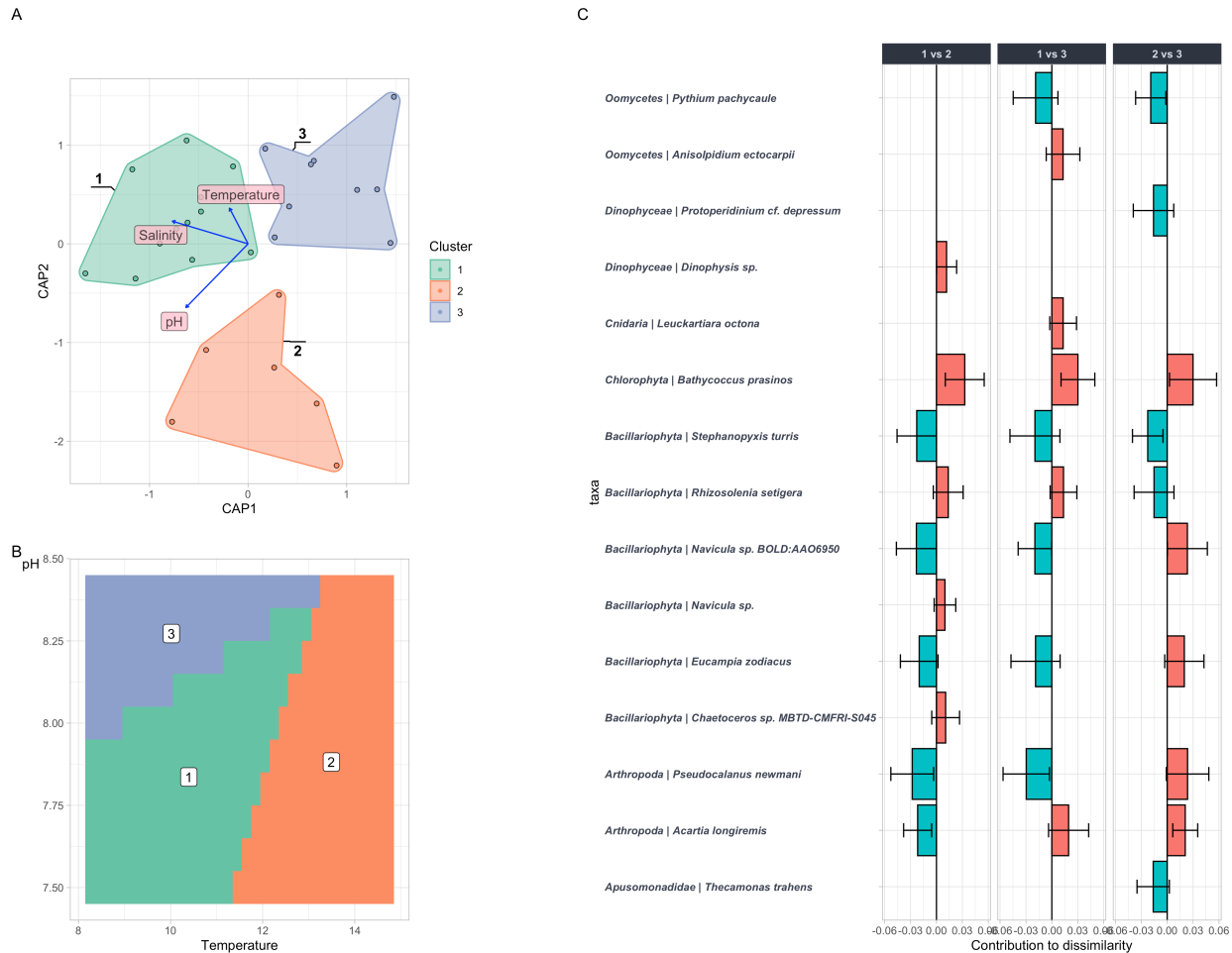


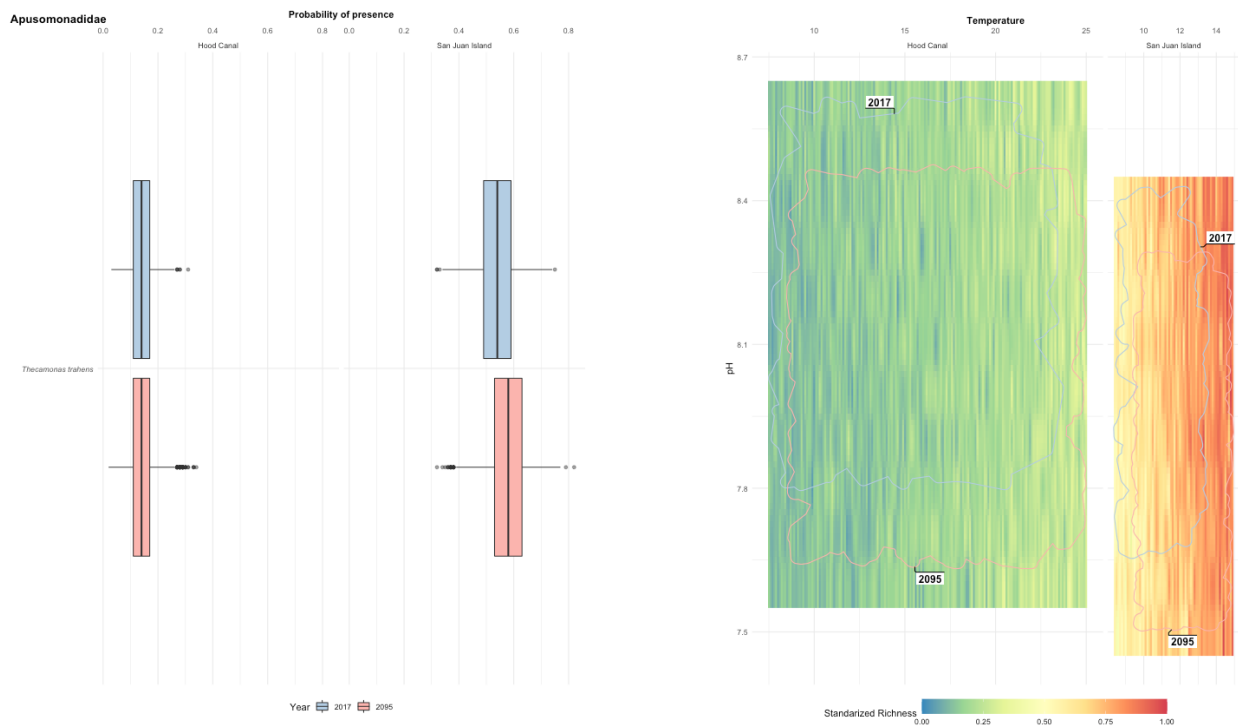
Figure 1: Biological communities and their relationship with environmental variables in San Juan Island. **A** Constrained Analysis of Principal Coordinates (CAP) of Bray-Curtis dissimilarities among biological communities, as constrained by pH, temperature and salinity (arrows). **B** Most-likely cluster as a function of temperature and pH given a multinomial logistic model (salinity was uninformative, being tightly correlated with temperature). **C** Relative abundance (eDNA index; see Kelly et al, 2019) of the taxa best distinguishing the three communities illustrated (SIMPER analysis).

Species responses, full list

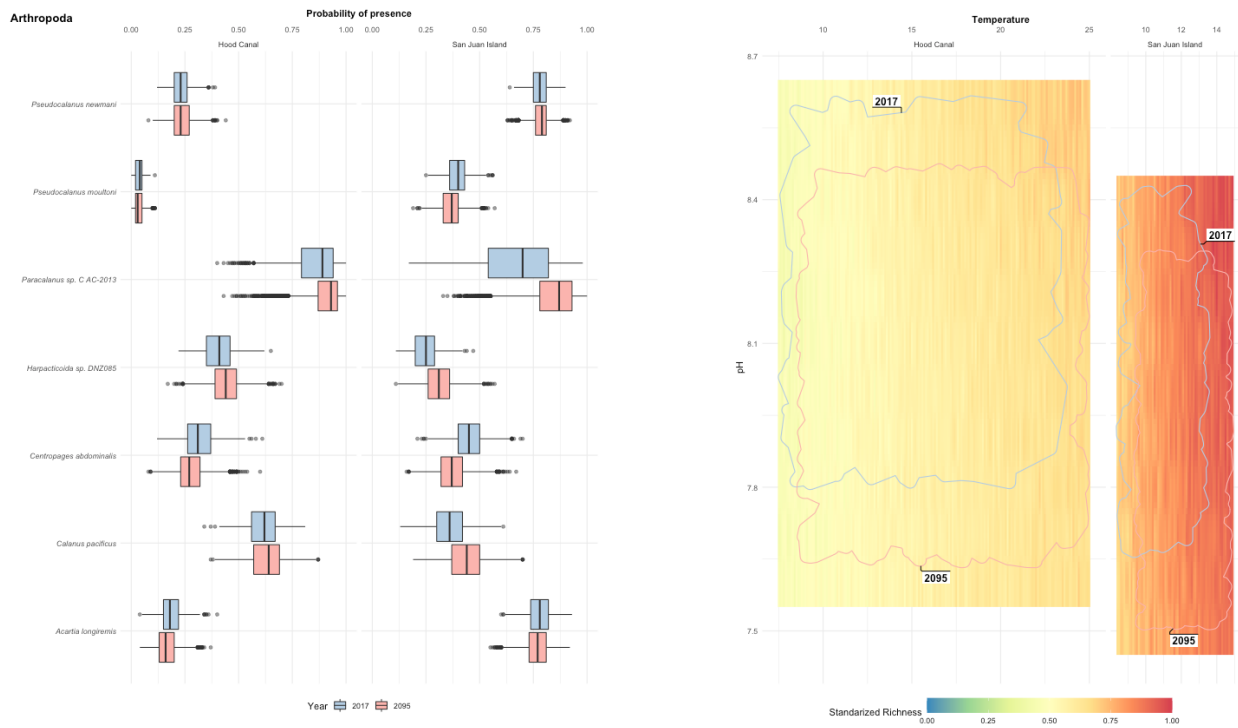
The results section reported changes in suitability and species richness for a few taxa. Find below the full set of species projections, grouped by phylum.

For each phyla, the left panel shows probability densities for the occurrence of each taxa (species- and genus-level) for 2017 (blue) and 2095 (red); data are mean probabilities over 100 model draws, and variance in probability is due to differences in underlying environmental conditions. The right panel shows relative taxon richness (raster colour, warmer colours are more taxon-rich) for each of these same higher-taxa, for plausible ranges of pH and Temperature. Envelopes of observed (2017, blue) and modelled (2095, red) annual conditions in the Salish Sea shown for reference. Hood Canal and San Juan Island plotted separately to illustrate environmental differences between them.

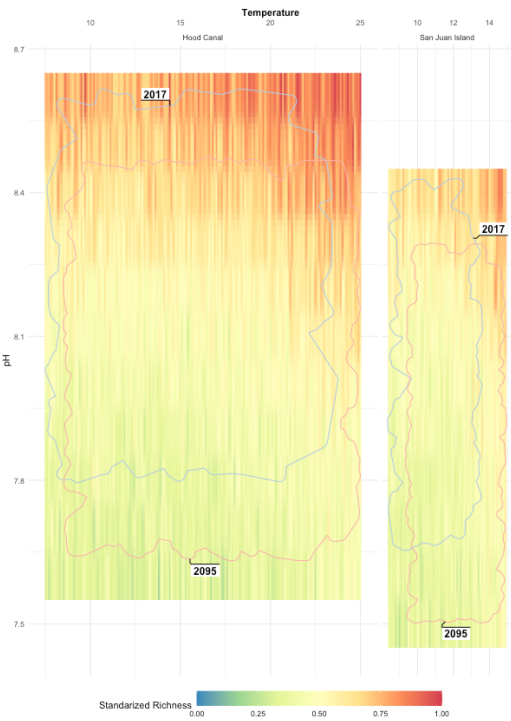
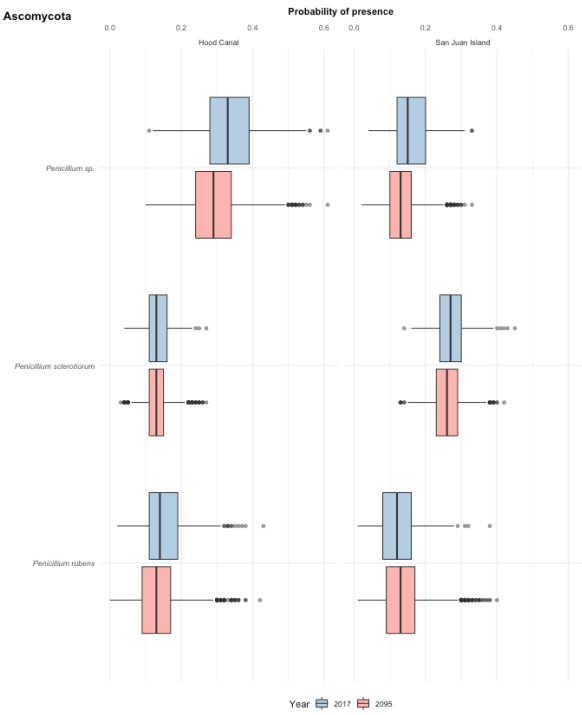
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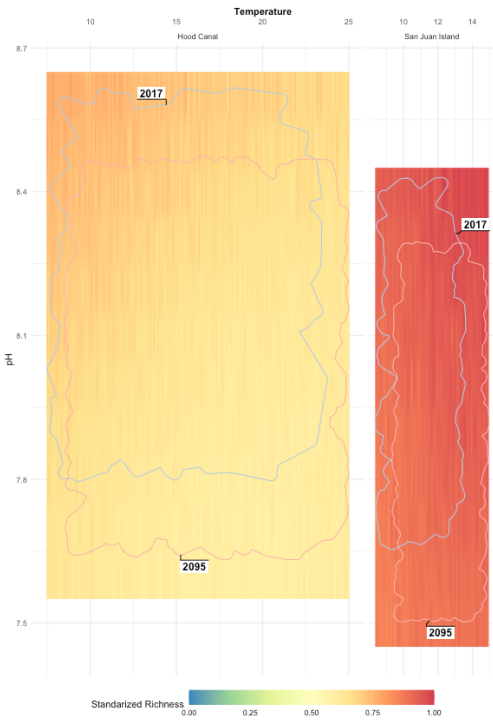
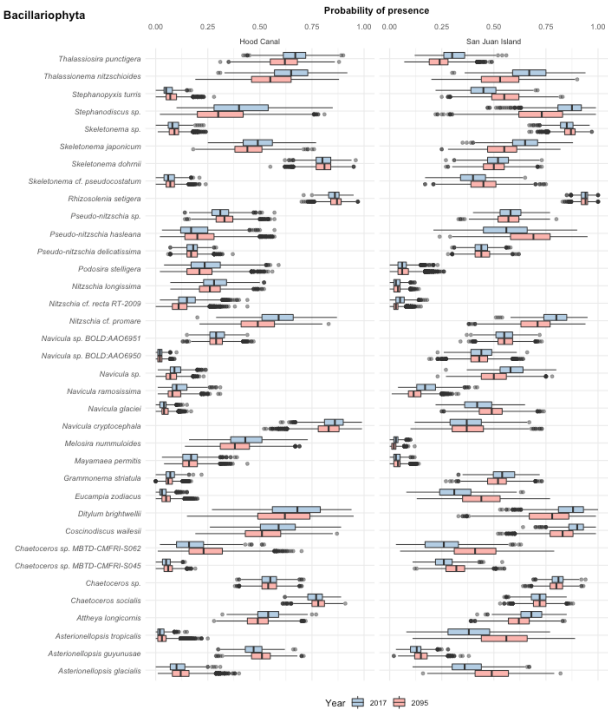
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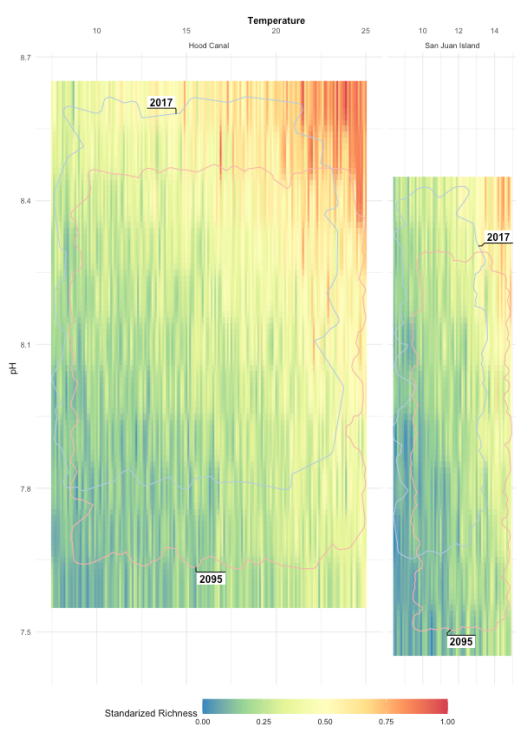
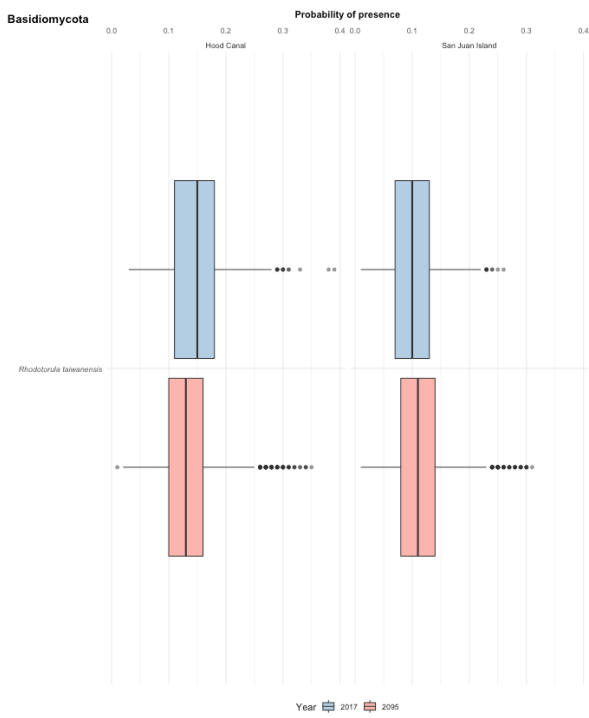
Ascomycota



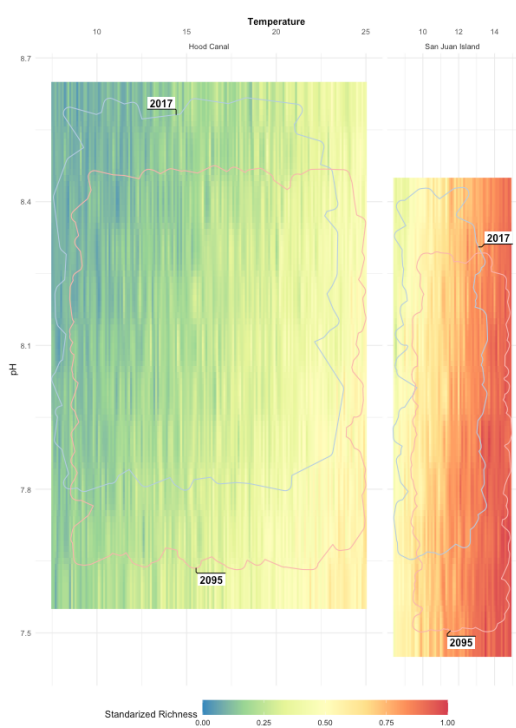
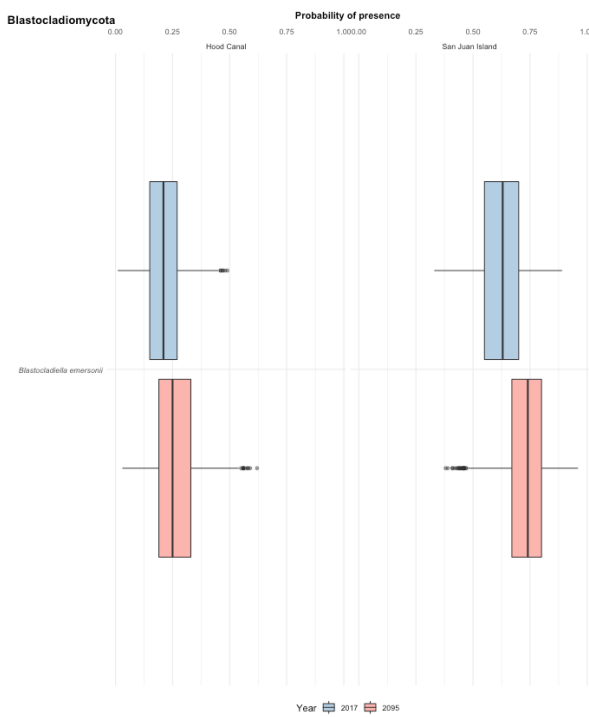
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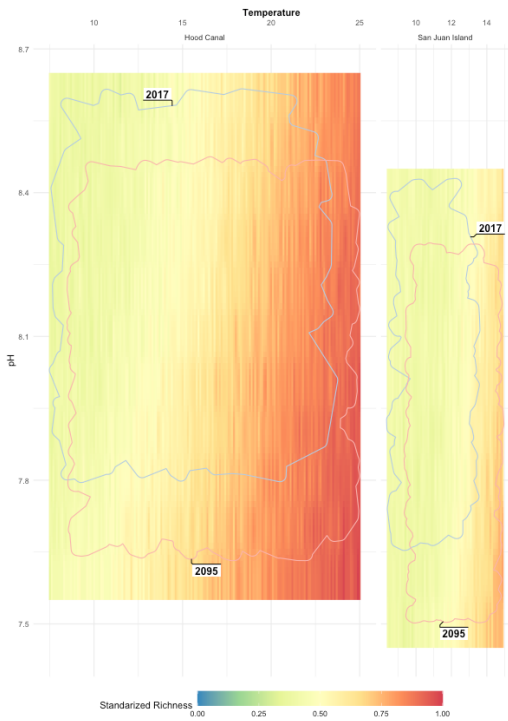
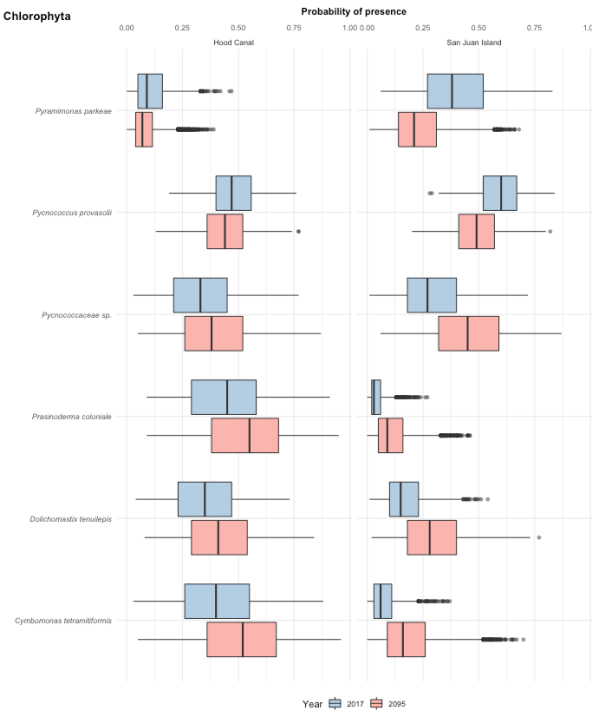
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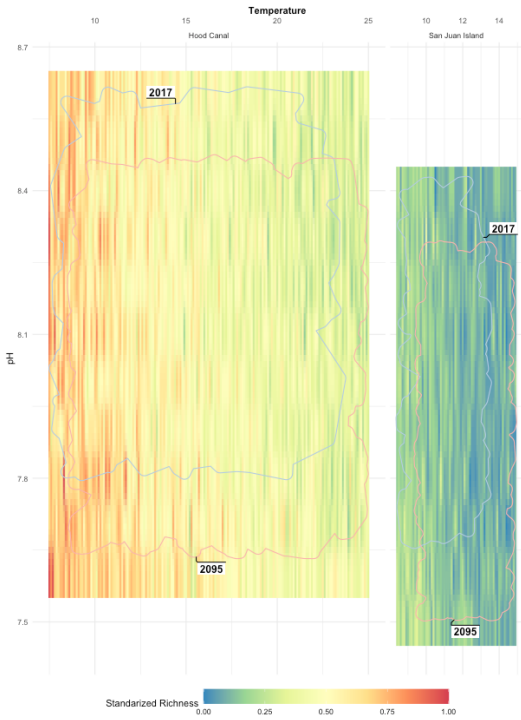
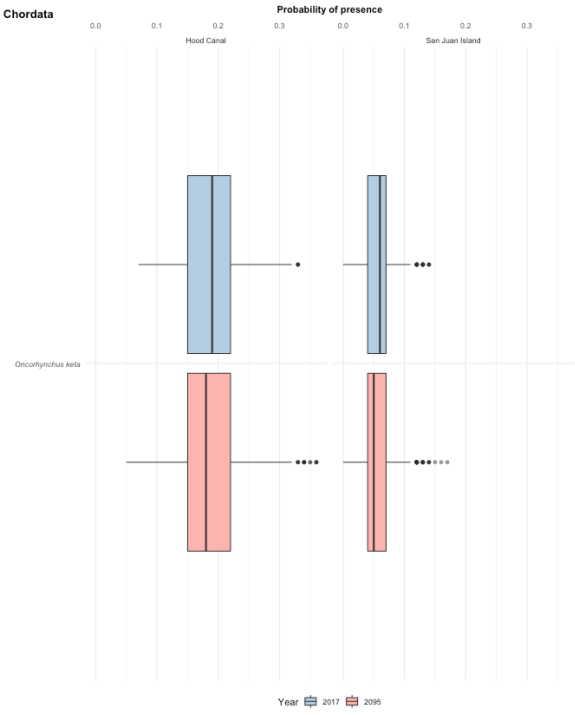
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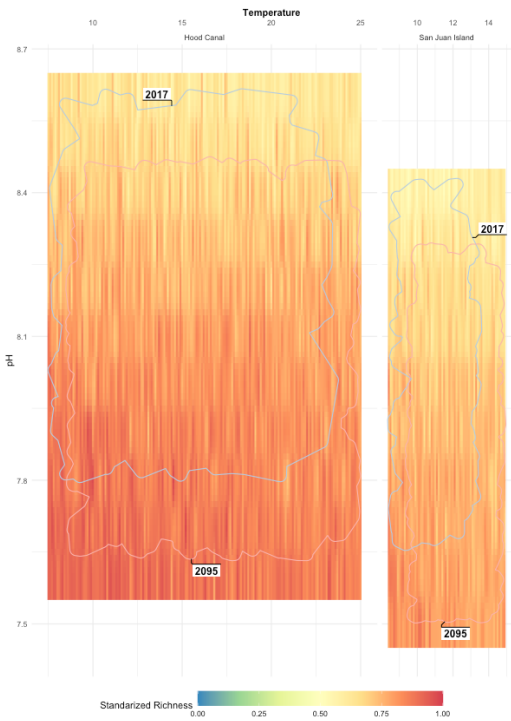
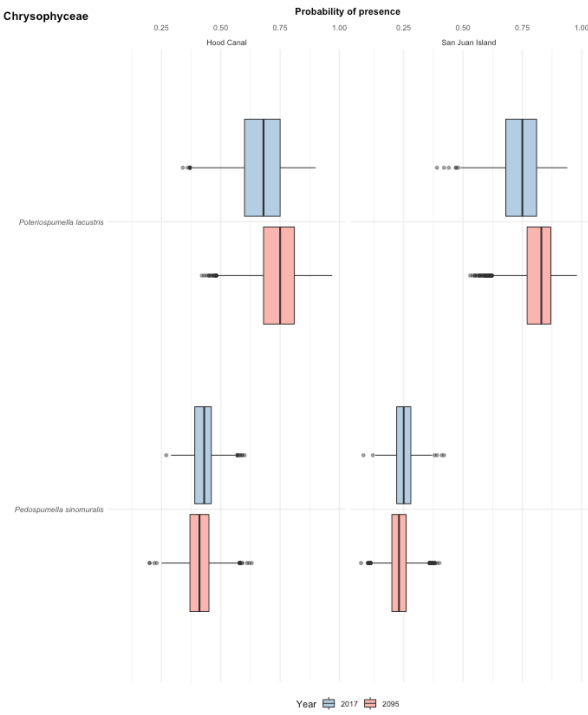
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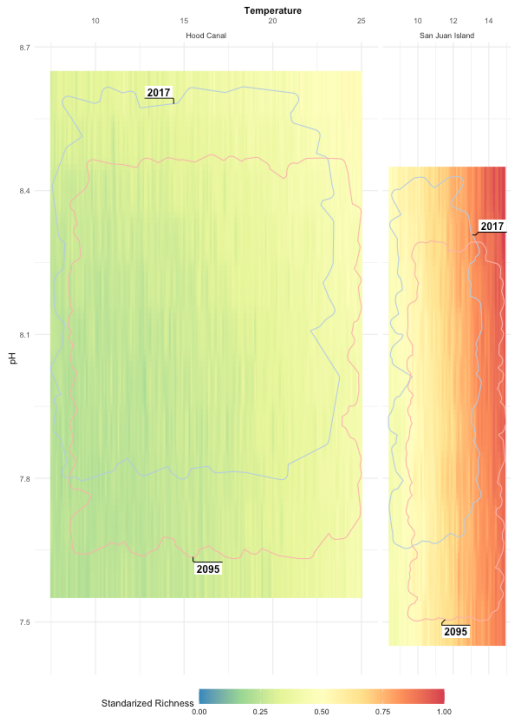
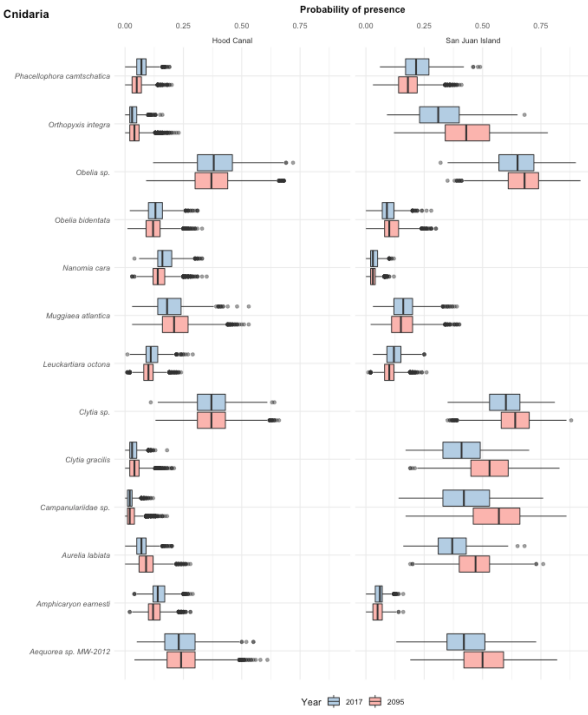
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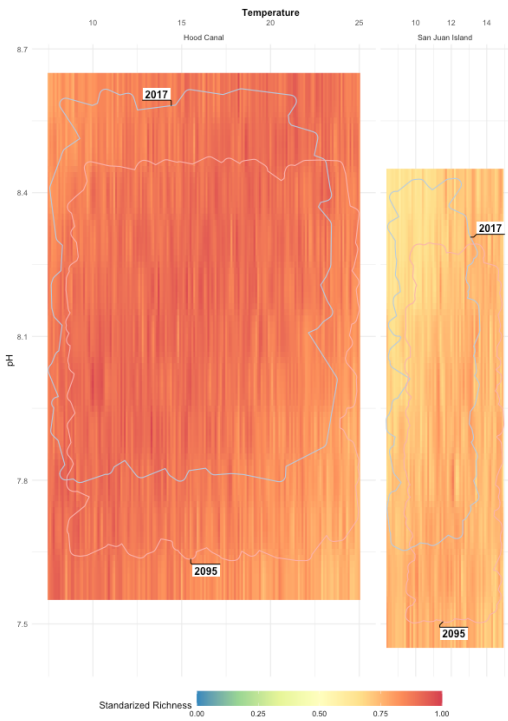
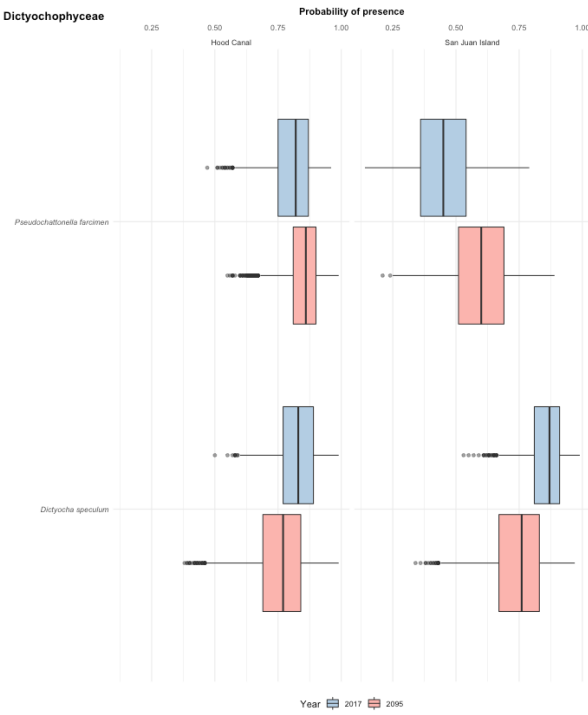
Chrysophyceae



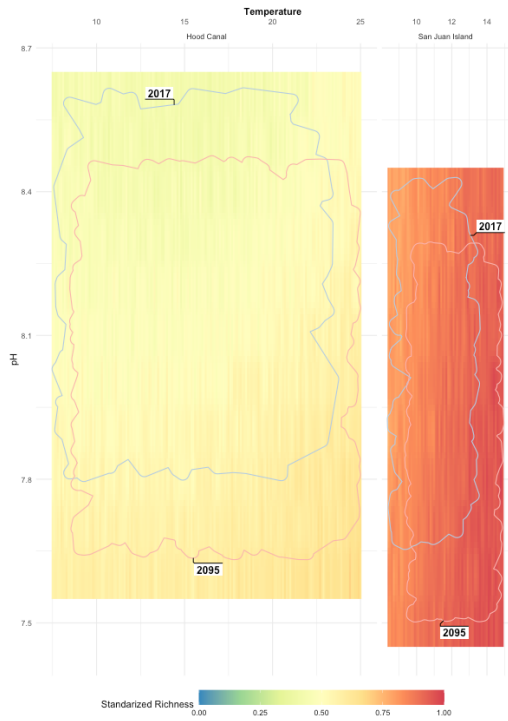
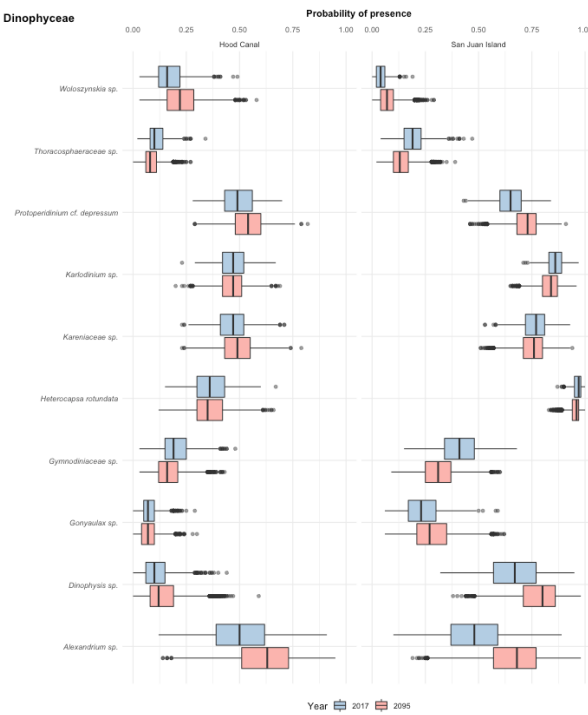
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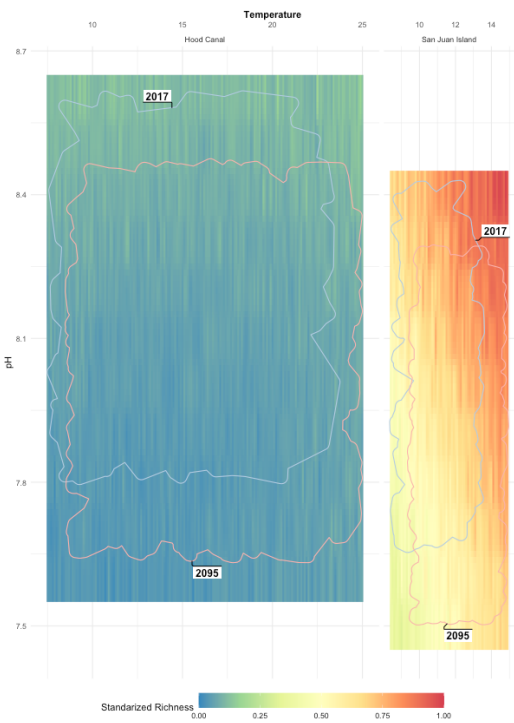
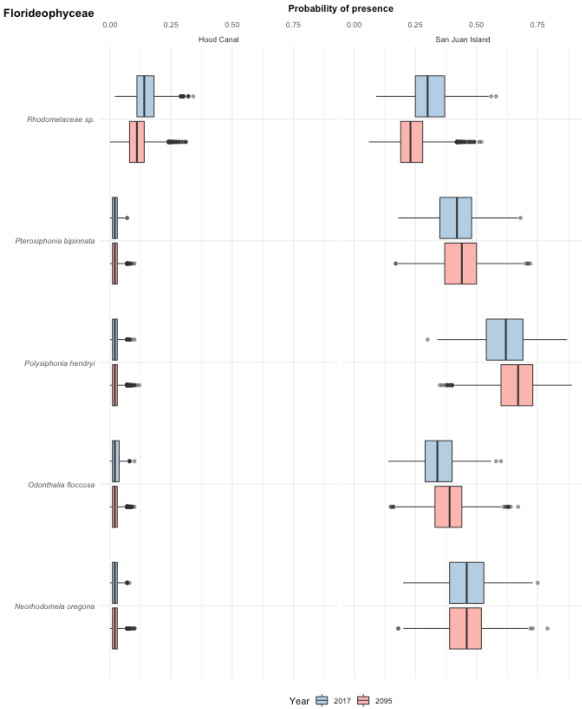
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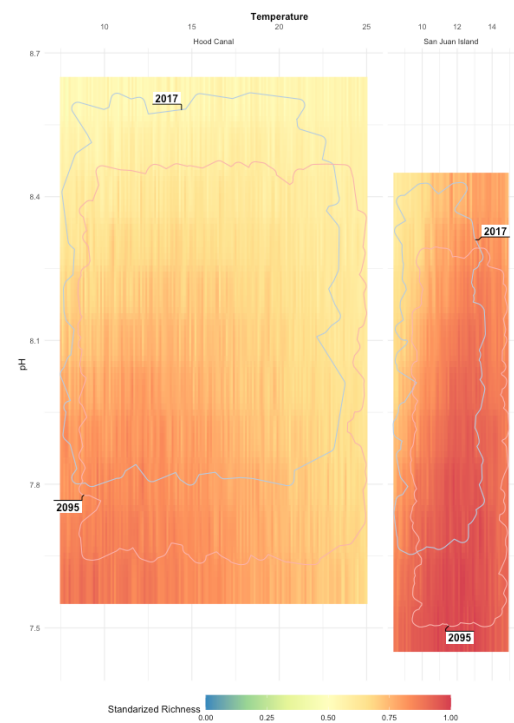
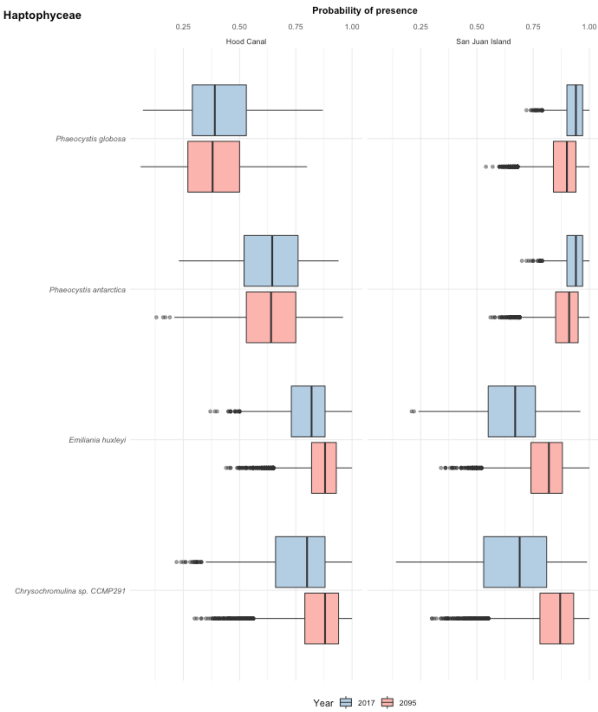
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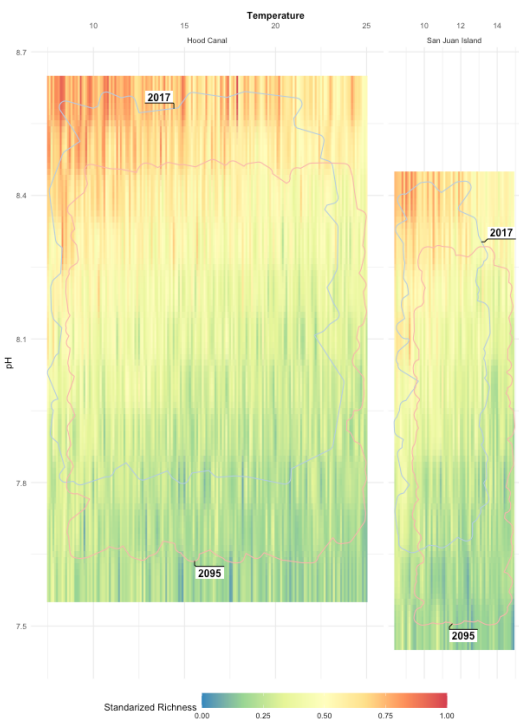
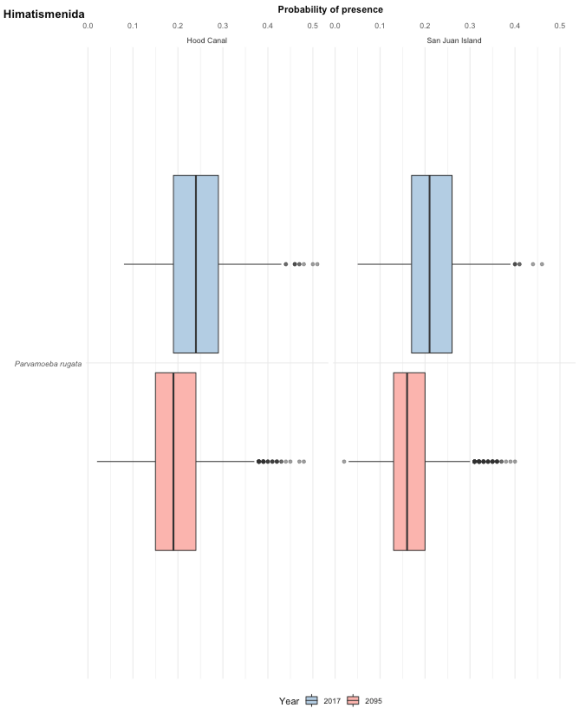
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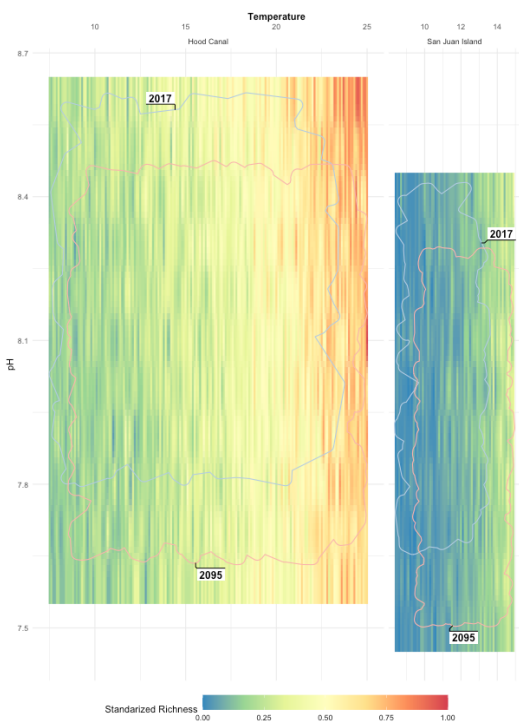
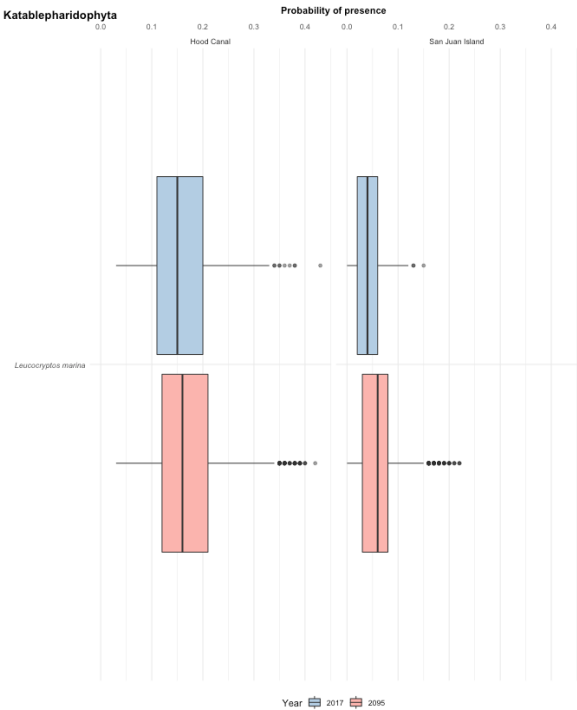
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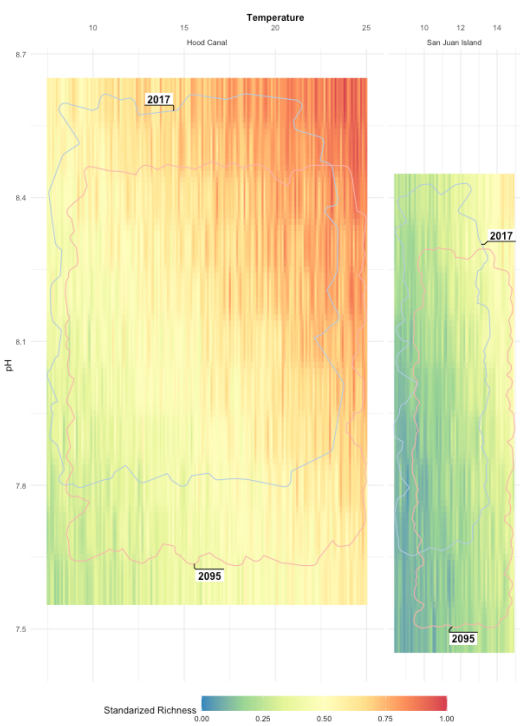
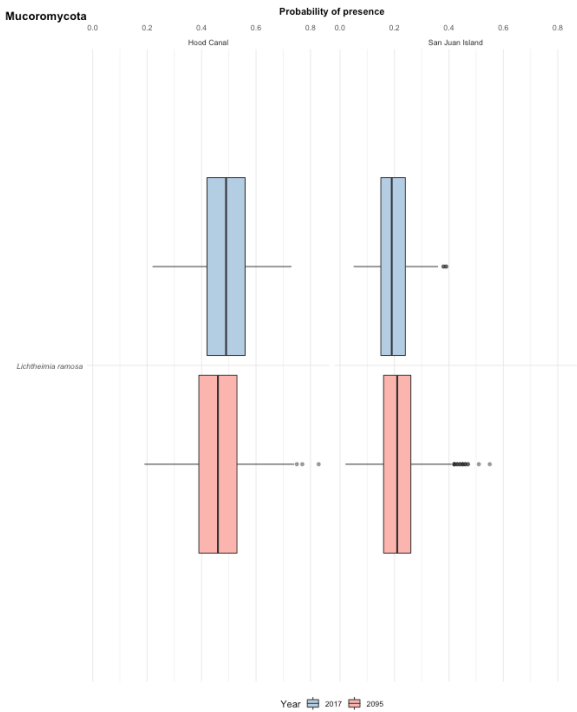
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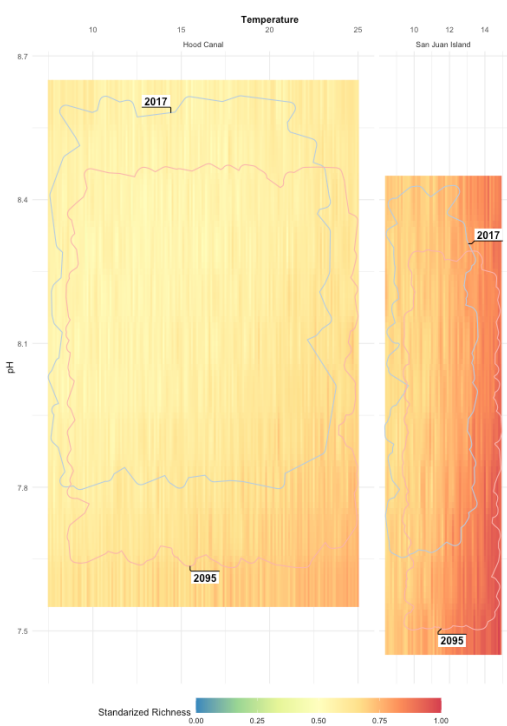
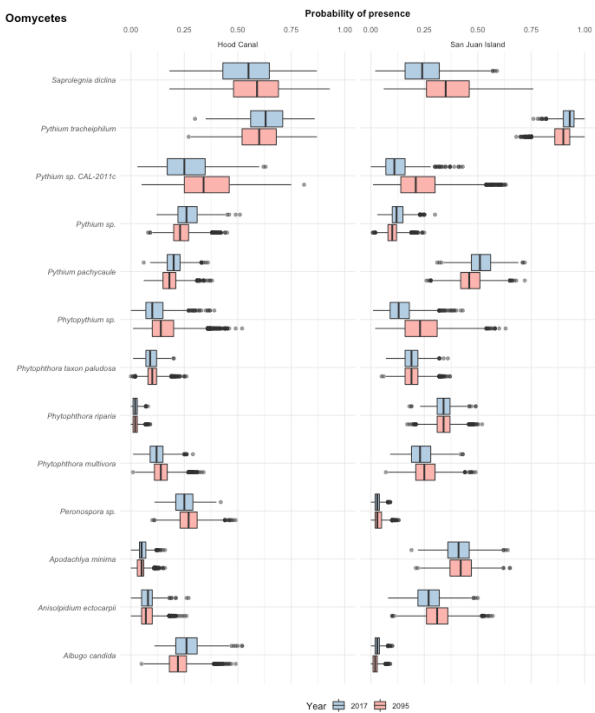
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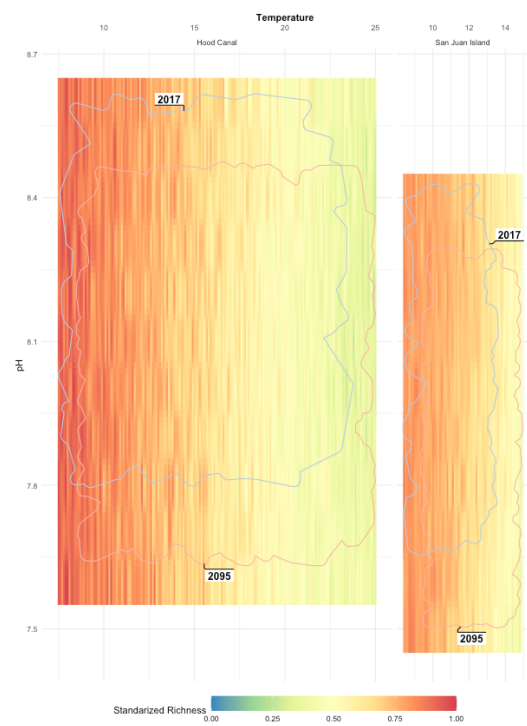
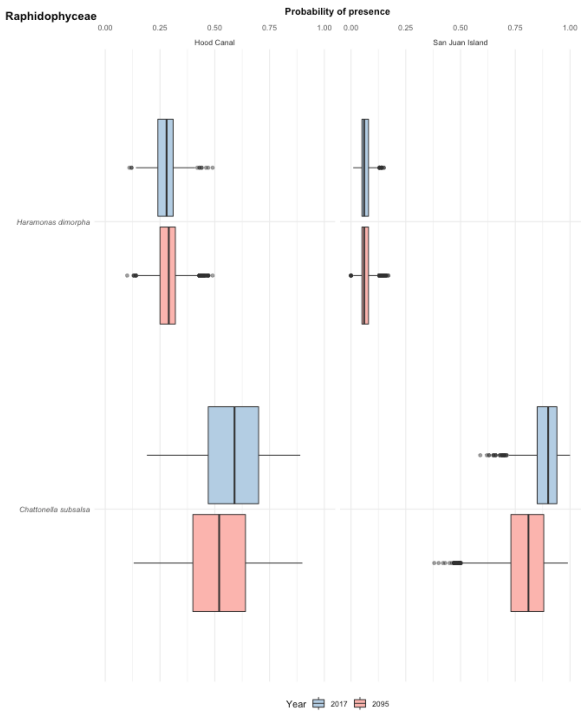
Mucoromycota



Oomycetes



Raphidophyceae



Synurophyceae

