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# Through time and space: mapping *Schoenoplectus americanus* population change in the salt marshes of the Chesapeake Bay

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## INTRODUCTION

One of the greatest challenges of coastal habitats is adapting to climate change. It is imperative to understand how marsh organisms like *Schoenoplectus americanus*, a common C3 sedge distributed along both the US and international coastlines, are responding to changes such as sea level rise, salinity level changes, ocean acidification, and more. *S. americanus* seed banks make up a substantial part of most salt marshes and its seeds can be resurrected after a hundred years, allowing for a unique study of the plant's population through both time and space.

## HYPOTHESES

*S. americanus* live seed abundances were used as a proxy for population. The three null hypotheses being tested are that the seed abundances of *S. americanus* do not differ:

- a) within a single core
- b) between a pair of cores (adjacent cores from a single site)
- c) between different sampling sites

## METHODS

Twelve sediment cores (collected in pairs) were obtained from three sites in the Chesapeake Bay in Maryland during the spring of 2016 (Figure 1): Corn Island, Hog Island, and Sellmann. Cores were cut in layers that were two centimeters thick and sieved for seeds. Live, dead, and total seed abundances were recorded for each respective layer and graphed to show population abundance through time.

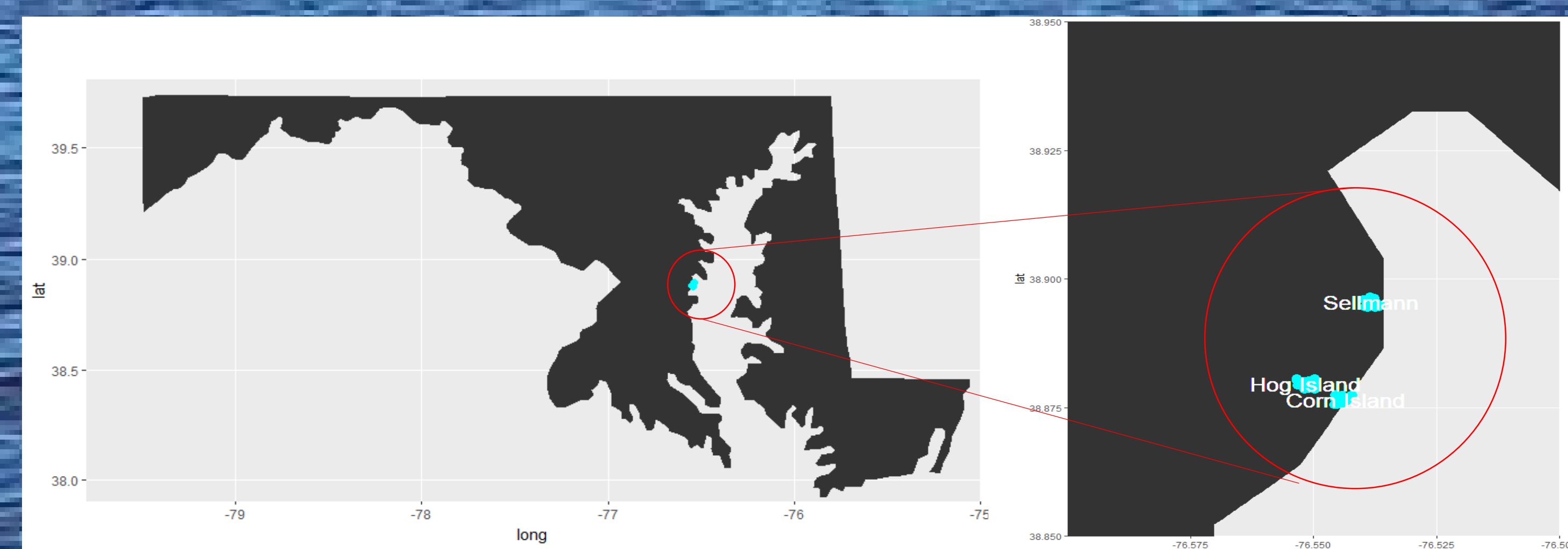


FIGURE 1. Map of Maryland – study site

A total of twelve sediment cores were collected from three primary locations known as Corn Island, Hog Island, and Sellmann. Sellman has 3 pairs of cores, Hog Island has 2 pairs, and Corn Island has 1 pair. These sites have been indicated on a map of Maryland by the blue points.

## RESULTS

Three null hypotheses regarding the variation of live seed abundance were tested: a) within a single core  
b) between a pair of cores (adjacent cores from a single site)  
c) between different sampling sites

For hypothesis (a), there was a wide array of variation through time as seen in Figure 3. For hypothesis (b), a one-way ANOVA confirmed that pairs of cores taken from a single site were always similar to each other. This same ANOVA revealed that hypothesis (c) was wrong however – there were significant differences between seed abundances between sites ( $F(11, 175) = 13.1, p < 0.001$ ). A post hoc Tukey's HSD test demonstrated that all sites were similar except for Corn Island - any across-site comparisons involving one core from Corn Island and one core from either Hog Island or Sellmann differed (p value less than 0.001).

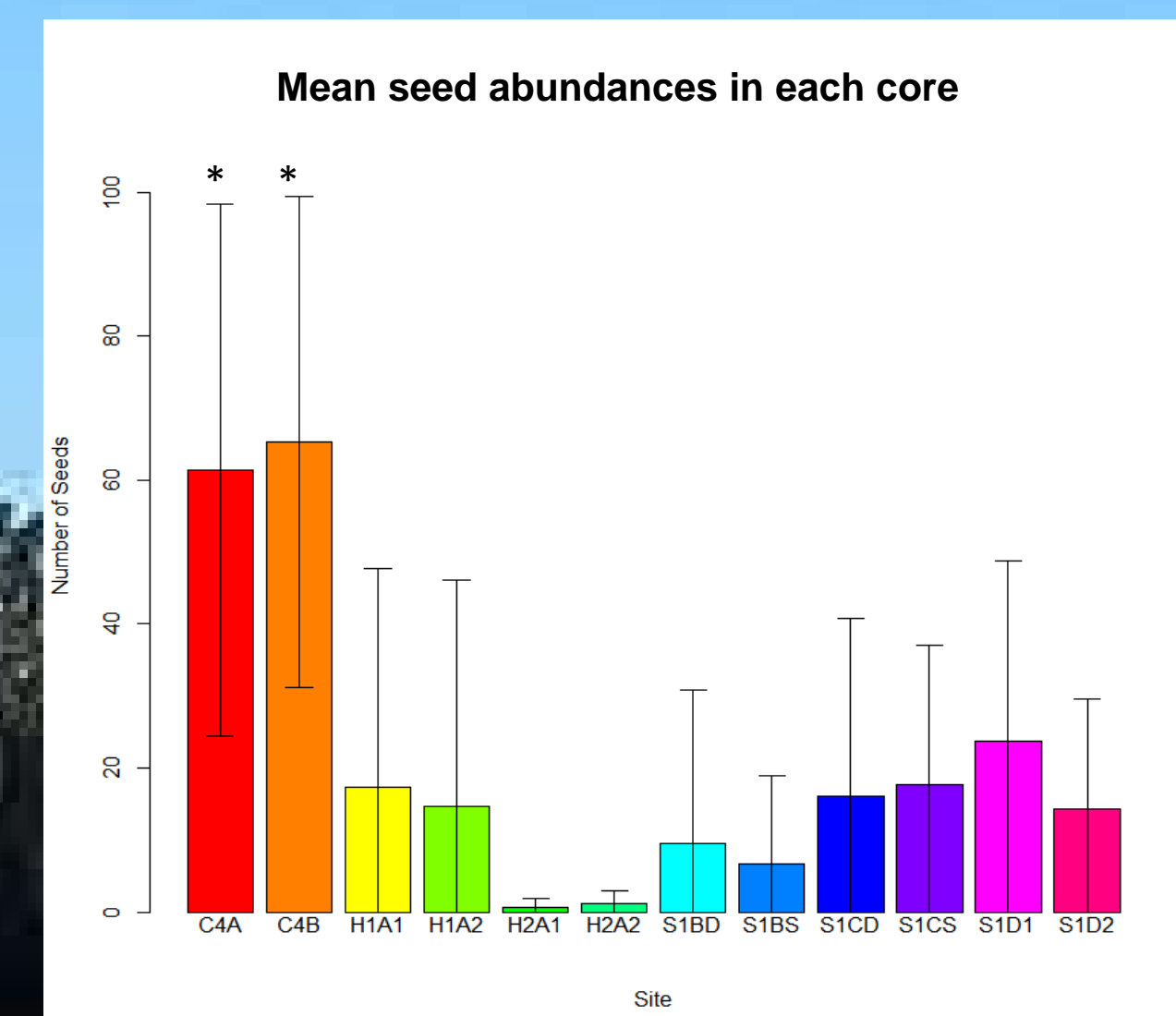


FIGURE 2. Average live seed abundance

Average seed abundances and error for each of the twelve cores collected are shown here. Cores from Corn Island tested significantly higher than all other sites (p value < 0.001).

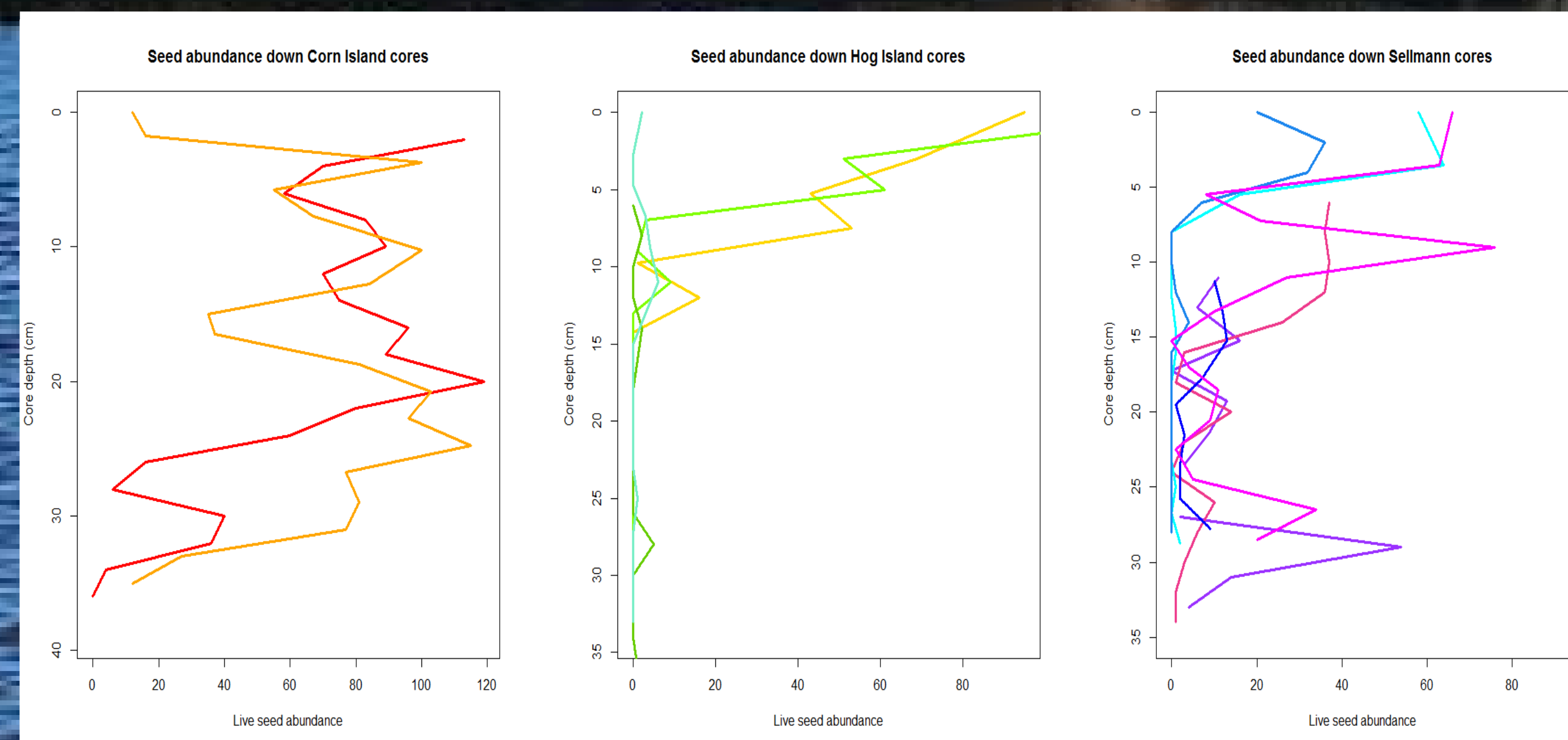


FIGURE 3. Population changes by site

Live seed abundances were tracked through the course of approximately one hundred years per core, per site. The top of the graph represents the most modern layer of *S. americanus* and the bottom of the graph represents the deepest and oldest seeds.

## DISCUSSION

Contrary to the expected findings, two of the three null hypotheses were rejected: within a single core, seed abundances and thus, *S. americanus* populations were variable; across sites, pairs of cores differed significantly in their seed abundance. There was no difference between paired cores from any one site.

Even with this variation, *S. americanus* populations have changed dramatically within a single core. Between site comparisons indicate that Corn Island, despite its proximity to Hog Island was not at all similar, instead yielding significantly higher live and total seed abundances than any other location (Figure 2). These results indicate that other environmental factors such as salinity, distance inland, nutrient levels, etc., may play a critical role in determining how abundant a population is and how well-preserved its seeds are.

Future studies will compare germination rates across layers within a single core and across the three testing sites to assess for possible spatial-temporal trends.

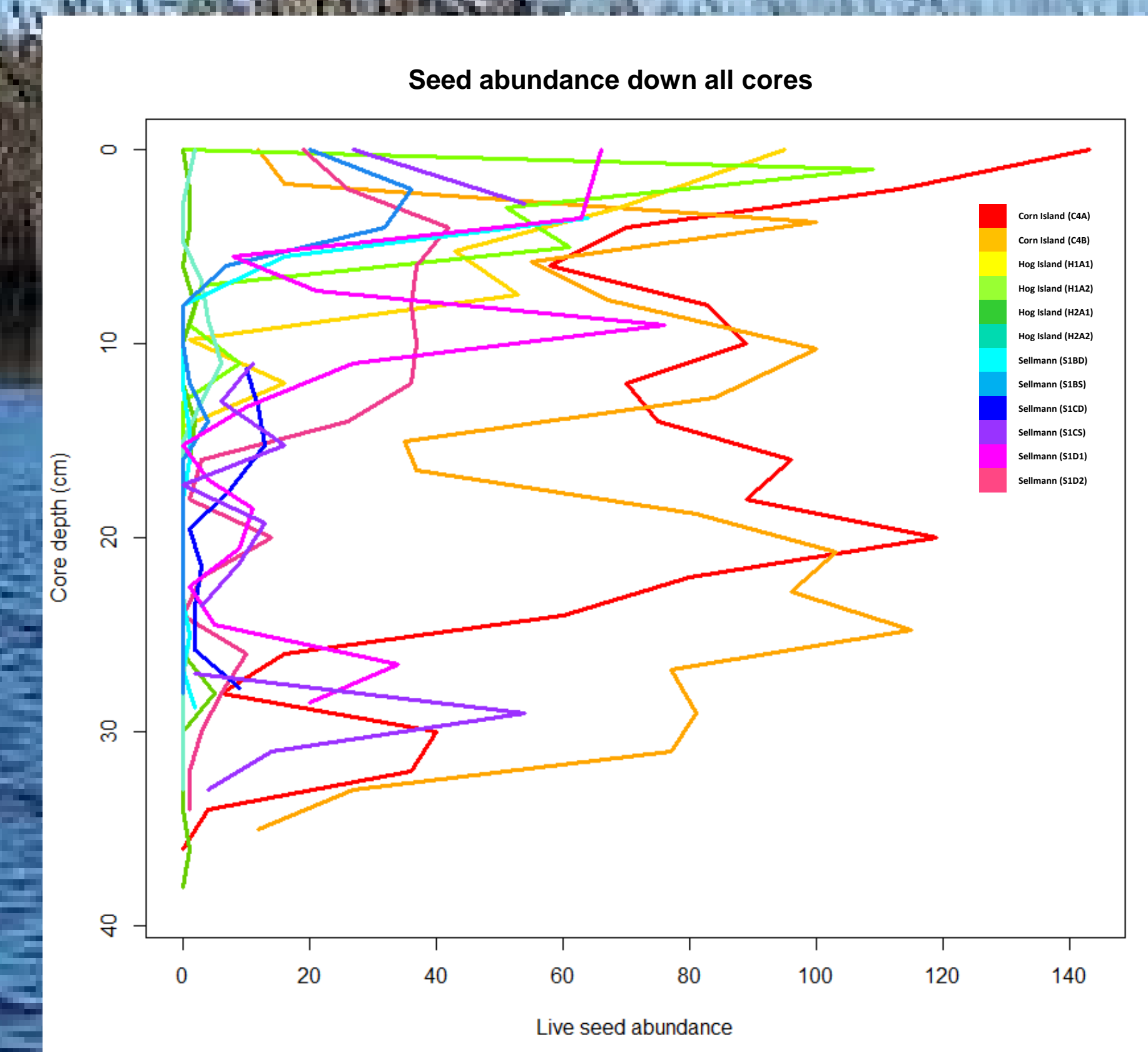


FIGURE 4. Population changes across all sites

Live seed abundances across all sites. No distinct trend to be found across all twelve cores but Corn Island appears consistently higher in count.

## ACKNOWLEDGMENTS

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