April 2021

Pollen-Vegetation Relationships in Upper Tampa Bay

Jaime E. Zolik
University of South Florida

Scholar Commons Citation

Zolik, Jaime E., "Pollen-Vegetation Relationships in Upper Tampa Bay" (2021). *USF Tampa Graduate Theses and Dissertations.*
https://digitalcommons.usf.edu/etd/8897

Pollen-Vegetation Relationships in Upper Tampa Bay

by

Jaime E. Zolik

A thesis submitted in partial fulfillment
Of the requirements for the degree of
Master of Arts
Department of Anthropology
College of Arts and Sciences
University of South Florida

Major Professor: Charles Stanish, Ph.D.
Christopher Kiahtipes, Ph.D.
Diane Wallman, Ph.D.

Date of Approval:
April 22, 2021

Keywords: Archaeology, paleoecology, palynology, estuaries

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

ABSTRACT

Archaeological and environmental studies reveal prehistoric human-environmental interactions and resolve baseline conditions for estuaries. Paleoecological proxies, such as pollen, aid archeologists in investigating past vegetation dynamics and human impacts. An issue with collecting this information today is that most present-day estuaries in Tampa Bay have been succeeded by mangrove communities and do not represent baseline vegetation dynamics. This is believed to be the consequences of widespread mosquito ditching. As a result of this, the once complex mangrove, salt marsh, juncus marsh, salt prairie, and coastal upland mosaics were converted to monodominant mangrove forests. Upper Tampa Bay (UTB) park contains some of the last intact complexes of estuary wetlands vegetation types. This area also contains archeological site complexes, making UTB a unique opportunity to investigate vegetation response to past land use. This project creates a baseline vegetation-pollen dataset by collecting surface pollen samples and record vegetation across UTB Park. The analysisof this data reveals the difficulty with equifinality and relates to the issue of regional vs local pollen signals. Open sites are especially vulnerable to an abundance regional pollen, reducing thesignal of the proportionally less frequent local pollen signal. This can have implications for the interpretations of pollen assemblages of open archaeological sites. This implies a need for a greater focus on locally distributed taxa and for a greater pollen count for samples in this region.

INTRODUCTION

Archaeological and environmental studies reveal prehistoric human-environmental interactions and resolve baseline conditions for estuaries relevant to future restoration efforts (Rick and Lockwood 2013; Crumley 2004; Erickson 2008). Palaeoecological proxies, such as pollen, aid archeologists and resource management plans by improving the detection of past vegetation dynamics and human impacts. Surface pollen datasets and vegetation baselines give us better tools to reconstruct past vegetation, but it is difficult to collect this data for vegetation communities that no longer occupy their historic distributions. Most present-day estuaries in Tampa Bay are dominated by mangroves as a result of historic-era mosquito-ditching and the remainder is threatened by local and global anthropogenic impacts (Raabe et al. 2012; Austin et al. 2014). Upper Tampa Bay (UTB) park is one of the last intact areas of intertidal wetland and an ideal candidate for creating vegetation-pollen datasets for calibrating UTB sedimentary records. UTB also contains shell mounds, making it possible to test questions about anthropogenic impacts. The primary goal of this project is to conduct vegetation surveys and analyze surface sample pollen assemblages to create a vegetation-pollen dataset for the various estuary vegetation communities within in UTB.

BACKGROUND

Tampa Bay

Tampa Bay, located on the west-central coast of Florida, is an embayment where freshwater runoff meets the Gulf of Mexico. It is a large open-water subtropical estuary fed by a freshwater watershed of about 5,700 km^2 and it supports a diversity of salt and freshwater ecosystems (Yates and Greening 2011). Along the coast, mangrove forests, salt prairies, and salt marshes form essential habitats for the diverse flora and fauna of Tampa Bay. In addition to supporting high biodiversity, the physical characteristics of these estuaries also play an important role mitigating against shoreline erosion (Gerold et al. 2009).

Estuaries in Tampa Bay provide critical ecological services and form an important part of the region's economy, but their future is seriously threatened by the effects of climate change. This environment is sensitive to salinity, temperature, and water level, all of which are expected to change as a result of climate change. The rate of sea level rise (SLR), around 3 mm/yr today, continues to increase and push back Tampa's shorelines (Gerold et al. 2009). The distribution of coastal wetlands is related to their adaptations to inundation frequency (Friess et al. 2012) and accelerating SLR threatens to surpass the ability of estuary vegetation communities to cope with these changes (Friess et al. 2012). Coupled with the lack of available upland area due to urbanization, SLR will continue to result in the loss of these estuaries (Gerold et al. 2009).

Anthropogenic effects and climate change are major threats to future of Tampa Bay's estuaries and its archeological sites. Mosquito ditching, dredging networks created to reduce mosquito breeding, is believed to be responsible for the recent domination of mangrove forest resulting in the loss of most salt marsh communities (Raabe et al. 2012; Gerold et al. 2009). Sea level rise (SLR), a consequence of climate change, has led both ecologists and archeologists to worry about the loss of coastal heritage and habitat (Friess et al. 2012). Coastal wetlands are naturally faced with the difficulty of maintaining their position of proper elevation and inundation frequency that they are best adapted towards. SLR adds more difficulty to this challenge and threatens the ability for the vegetation to cope with their environment and will lead to a loss in coastal wetlands. While ecologists and land management are searching for additional data to better understand the historical dynamics of Tampa Bay's estuaries (Sherwood and Greening 2012; Yates and Greening 2011; Friess et al. 2012), the archeological record, a major source of ecological data, is also at risk of being lost as a result of SLR (Reeder-Myers 2015).

The archeological record holds important data (i.e. soil, micro and macrofossils, isotope analysis, and settlement patterns, etc.) for understanding historical human-environmental dynamics (Sandweiss and Kelley 2012). Using proxies, such as pollen, paleoecology and archeology can reconstruct past environments and apply a more balanced focus on the human-environment relationship which provide a realistic picture of the complex web of connections for future management plans. These approaches investigate how humans interacted with their environment, how the environment affected their behavior, and the ecological roles of past human societies. Robust pollen-vegetation datasets improve our ability to interpret pollen records, but no such dataset exists for Tampa Bay. UTB park is one of the last intact areas of intertidal wetland in Tampa Bay, and is an ideal candidate for establishing a vegetation-pollen baseline relevant to archaeological research and resource management plans.

Theory

Material culture and environmental proxies, such as micro and macrofossils analysis, have allowed archaeologists to better look at the complex interactions between human behavior and regional climate (Lupo et al. 2015; Iglesias et al. 2018; Willard and Cronin 2007). Using the lens of human behavioral ecology (HBE), archeologists pose hypotheses and gather data about how the environment acts as source of selection, shaping human behaviors such as modifying one's environment to maximize survival and reproductive success (Codding and Bird 2015). Integrating palaeoecological datasets allows for a better understanding of how past environments have shaped past human behavior and, in turn, how humans manipulate their environments through fire, soil turnover, and seed dispersal. The investigation into Traditional Ecological Knowledge is critical towards not only understanding the practices of past societies, but also the ecological functions humans play within their environment (Bliege Bird and Nimmo 2018). Although human-environment interactions are not innately positive, understanding and re-introducing these historical ecological functions can be critical in effective maintenance and restoration of ecosystems. My project aims to document pollen signature for estuary vegetation communities in Tampa Bay. This dataset will improve interpretations of the regional pollen record and anthropological investigations of past vegetation during the Weeden Island and Safety Harbor occupations of UTB.

Tampa Bay Archaeology

Florida's archaeological record extends back to the Late Pleistocene (Miller 2016; Anderson et al. 2015). Recent data suggests that beginning in the Middle Archaic (about 6000-

3000 BC), many coastal populations in Florida relied primarily on resources provided by the estuaries (Saunders and Russo 2011). Evidence also suggests that estuary subsistence was sufficient to support dense populations and allow for monumental architecture (Austin et al. 2014). As archeologists continue work towards understanding the cultural dynamics of prehistoric Tampa Bay, they express the need for a better understanding of the role of climatic factor. Paleoecological proxies, such as pollen, help with this by providing tool to reconstruct past vegetations.

This research can apply to investigating the human-environmental relationships from the Weeden Island and Safety Harbor cultural complexes in Tampa Bay. The Weeden Island culture occupied the Tampa Bay area approximately 600 BC-1400 AD (Bullen 1955; Gluckman et al. 1978). Some use of agriculture is evident during this time, but their economic focus was primarilyon hunting and gathering coastal and aquatic foods (Bullen 1955; Austin et al. 2014). The Safety Harbor period occurred approximately 1400-1700 AD, they shared common factors of Mississippian cultures and had a diet primarily consisting of seafood (Bullen 1955). In order to study the relationships between these changes in subsistence strategies, population densities, and past human impacts on the landscape in Upper Tampa Bay environments, we need to better integrate archeological and paleoecological datasets. In particular, this dataset can be useful in the investigation on how the historic use of estuary resources were able to support population growth within this region (Saunders and Russo 2011).

Paleoecology

Plants produce and disperse pollen to reproduce. Pollen is made from sporopollenin, a durable organic compound that is well preserved in inundated settings and pollen grains are morphologically distinct between plant families, genera, and, less frequently, species. Pollen data can be difficult to interpret due to taphonomic bias, sedimentological factors, pollen dispersal and production, and other environmental factors (Gaillard et al. 2008; Bunting et al. 2004; Sugita 1993).

Projects that investigate previous vegetation dynamics through the pollen record, that are found in cores in areas similar to Upper Tampa Bay Park, rely on the interpretation of pollen percentages (van Soelen et al. 2010). Scholars have tried to deal with equifinality in vegetation reconstructions through the use of Modern Analog Technique (MAT) and the Multiple Scenario Approach (MSA) (Sobol and Finkelstein 2018; Williams and Shuman 2008; Bunting and Middleton 2009). The MAT compares fossil pollen records to modern pollen assemblages sampled from a range of climatic conditions to infer past conditions (Birks 2019; Williams and Shuman 2008; Williams et al. 2004). This method reconstructs vegetation by evaluating the degree of dissimilarity between fossil pollen assemblages and modern assemblages, assuming that modern communities are a good analog for past vegetation (Birks 2019). MSA compares multiple hypothetical vegetation distributions and compares modeled pollen signatures with sedimentary records (Bunting and Middleton 2009; Bunting et al. 2018). Both of these methods rely on fine-grained regional sampling strategies and this dataset does not currently exist for UTB estuaries. The purpose of this project is to generate a robust modern analogue of the local vegetation and corresponding surface pollen assemblage that could help improve the interpretation of the Upper Tampa Bay pollen record.

Estuary Vegetation Communities

The gradient of the freshwater watershed with the saltwater from the Gulf supports highly biodiverse flora and fauna found within its seagrass beds, oyster bars, and emergent tidal wetlands (Gerold et al. 2009). The distribution of the vegetation cover in the area is determined through tidal energy, salinity, elevation, soil conditions, and competition (Gerold et al. 2009). These ecosystems provide essential ecological services such as protection from storm flooding, fisheries habitat and production, and blue carbon storage (Dontis et al. 2020; Kelleway et al. 2017; Myers 1990). Over time, salt marshes are succeeded by mangroves by trapping mangrove seeds in their vegetation mangrove seeds (Myers 1990). Once the density of mangroves reaches a certain threshold, salt marsh taxa are no longer able to recruit under the shade of mangrove forests (Myers 1990).

Uplands

UTB uplands consist of pine flatwoods that are characterized by a relatively open pine (*Pinus* spp.) overstory with various woodland species in the shrub and herb understory (*Sabal etonia, Lyonia lucida*, etc.). Pine flatwoods occur at low elevation and flat terrain, which results in poor drainage, are characterized by their sandy, acidic, and nutrient poor soil (Myers 1990). Pine flatwood herb/shrub vegetation include saw palmetto (*Serenoa repens*), scrub palmetto (*Sabal etonia*), gallberry (*Ilex glabra*), fetterbush (*Lyonia lucida*), and staggerbush (*Lyonia ferruginea*) (Myers 1990). The Brazilian pepper tree (*Schinus terebinthifolia*) is an invasive species observed throughout the estuary, especially in the Pine flatwoods. These vegetation regions are stable and tolerate regular fire disturbances, but these stable dynamics are disrupted by human-caused alterations in fire frequencies (Myers 1990).

Salt Marsh

Salt marshes are characterized by their diverse non-woody and salt-tolerating plant communities (Myers 1990; Gerold et al. 2009). They are also characterized by abrupt changes of vegetation communities correlating with the slight changes in elevation (Myers 1990; Gerold et al. 2009). Salt marshes need occasional flooding and are restricted to locations where wave energy is low enough that they will not be damaged by their force (Myers 1990; Gerold et al. 2009). Generally, salt marshes can be characterized by their “low” and “high” elevation zones. These zones may only have an inch difference between elevation but can result in salinity differences which effect the kind of vegetation that will grow there (Whitney et al. 2004).

Low marsh refers to the portion of the marsh closest to the open water and at the lowest elevation. Low marshes experience higher wave energy and are therefore usually dominated by a single grass species such as smooth cordgrass (*Spartina alterniflora*) (Myers 1990; Whitney et al. 2004). The observance of abrupt changes between monospecific areas of smooth cordgrass (*Spartina alterniflora*) to black needlerush (*Juncus roemerianus*) is also a main characteristic of salt marshes (Myers 1990). Although these abrupt changes in vegetation are not completely understood, it is hypothesized to be a result of slight changes in elevation and soil conditions such as salinity (Myers 1990).

High marshes experience less frequent inundation and more evaporation resulting in higher salinity levels (Whitney et al. 2004). In these conditions, high marsh will contain a combination of plants adapted to high salinity levels, such as succulents (Whitney et al. 2004). Plant species found in high marsh include sea purslane (*Sesuvium portulacastrum),* glasswort (*Salicornia* spp.), and saltwort (*Batis meritima),* sea oxeye (*Borrichia* spp.), leather fern (*Acrostichum aureum*), and cordgrass (*Spartina* spp.) (Myers 1990; Gerold et al. 2009).

Salt Pan

A salt pan zone may also form at the landward edge of a salt marsh when there is gradual elevation change and consists of an area with such high salinity that no vascular plants can survive. Salt pans are characterized by their lack of vegetation, openness, and may persist forseveral years (Myers 1990).

Mangrove Forests

Mangrove forests in UTB are co-dominated by red mangrove (*Rhizophora mangle*), white mangrove (*Langncularia racemosa*), black mangrove (*Avicennia germinans*), and buttonwood (*Conocarpus erecta*). These trees share morphological specializations and salt exclusion mechanisms which allow them to thrive in saline conditions with high levels of water fluctuations and anaerobic soils where salt marshes cannot survive (Myers 1990). Red mangroves are most successful in the more inundated areas found in subtidal, lower, and middle intertidal zones (Myers 1990; Gerold et al. 2009). White and black mangroves are found at higher elevations in less-frequent inundated areas (Myers 1990; Gerold et al. 2009). Buttonwood is found at the highest elevations among this group of mangrove taxa. The distribution of mangrove species is influenced by an interplay of light competition, physical conditions (i.e. wave energy), and edaphic factors (Myers 1990).

METHODS

Field Methods

In July- October 2020, I conducted vegetation surveys and soil surface sampling in a 2 km^2 project area located within UTB park (Figure 1) that included mangrove, salt marsh, salt prairie, juncus marsh, and coastal upland vegetation communities. Sampling locations were distributed every 200 m in a grid covering all of the vegetation types of interest. Samples were also collected at 50 m increments along two transects. Transect 1 was placed at a marsh-mangrove boundary and Transect 2 was placed in the path of an exposed shell midden (Figure 1). A total of 30 samples from these sites were analyzed for this study. For every surface sample, a 1x1 test unit was marked off and photographed. Observed vegetation and their relative coverage within the test unit was recorded. Surface soil samples (< 5 cm in depth) were taken from several spots in the unit and combined into a single sample bag for that unit. Fieldwork was conducted by myself, the University of South Florida (USF) postdoctoral fellow Dr. Chris Kiahtipes, and Kendal Jackson, a Ph.D. candidate at USF's department of anthropology studying Tampa Bay archaeology and paleoecology.

Laboratory Methods

In the lab, subsamples were taken from each sample and processed for palynological analysis (Campbell et al. 2016; Lentfer and Boyd 2000). The target volume of the subsample was assigned based of the composition of the sample (1 mL= soil/peat, 2 mL=organic rich loam, and 4 mL =sand) to maximize the probability that an appropriate amount of pollen would be collected. Subsamples were placed into 50 mL sterile falcon tubes, and their mass was recorded. The volume of the subsample was recorded using a 10 mL glass pipette and Deionized (DI) water to measure the sample's liquid displacement. Two *Lycopodium* tablets were added into each sample as identifiable marker that is used to calculate the concentration of collected pollen within each subsample. The *Lycopodium* tablets were produced by the University of Lund, Sweden (batch 1031) and contained 20848 ±1546 spores per tablet.

10% of HCl was added into each sample to dissolve the *Lycopodium* tablets, releasing the spores, and to remove carbonates. Samples were rinsed with DI water and centrifugated until pH neutral. Sand and heavy minerals were removed by gravity separation, then macrobotanical material was removed by passing the sample through a sterile 250 µm sieve using DI water.

HF was carefully added into each sample to remove any remaining silica material. The samples sat overnight in the HF solution and were carefully neutralized the following day. To breakdown an remove the humus in the samples, 10% KOH solution was added into each sample. The samples were place in an 80˚C water bath for 10 minutes for the reaction to fully take place. After that time, samples were quickly removed from the bath and a small amount (~ 1 ml) concentrated HCl (37%) was added to help remove complex organic molecules before undergoing the neutralization process using DI water.

Samples were treated using the acetolysis reaction to break down and remove cellulose and lignin. A 9:1 solution of acetic anhydride and sulfuric acid was added to each sample after removal of water using glacial acetic acid. After the acetolysis solution was added, samples were place into a 90˚C water bath for 6 minutes. Once the reaction was completed, a small amount glacial acetic acid was added to help stop the reaction and samples were centrifugated, decanted, washed with glacial acetic acid again before neutralization with DI water.

Density separation was used to extract pollen spored from the remaining mineral and heavy organics in the sample. All samples were centrifugated, decanted, and invert onto a piece of paper towel in the fume hood. After completely drying for 15 minutes, 2 mL of 2.23g/ml $ZnBr_2$ solution was added to the sample and vortexed. Carefully, 2 mL of ethanol was added to the sample and set aside for 5 minutes. After this time, the samples were centrifuged for 5 minutes at 500 RPMs and then for 2 minutes at 2500 RPMs. The suspended layer of pollen/charcoal layer, at the interface of the $ZnBr_2$ and EtOH layers, was extracted from the solution using a sterile pipette. All samples were centrifugated, decanted, the remaining EtOH was removed, and drops of glycerol were added to the sample for preservation.

Pollen Identification and Counting

Samples were placed on glass slides and sealed under a cover slip. Pollen taxa were identified at 400x and 1000x magnification with a binocular light microscope. Pollen taxa were identified using pollen atlases (Willard et al. 2004; Kapp et al. 1969), and the pollen database The Global Pollen Project (Martin and Harvey 2017). A goal of above 200 pollen grains were recorded for each sample, along with the number of *Lycopodium* spores observed during the counting process.

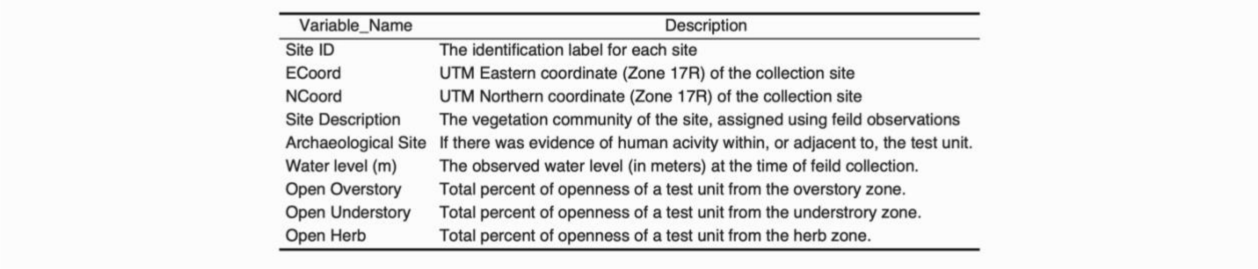
Data Collection and Quantitative Methods

The first objective was completed by creating a dataset of observed vegetation with their respective pollen assemblage using field and laboratory methods. The dataset was then analyzed, using the statistical computing environment R (R Core Team 2021) implemented through the RStudio (RStudio Team 2020) software package, to investigate the potential for pollen assemblages to predict their corresponding vegetation communities.

Site Conditions

Site conditions were recorded at every field sampling location, including: observed water level, vegetation community, description of surroundings, anthropogenic effects, and amount of open vegetation were recorded. We recorded vegetation coverage as a percent of the canopy (above 2 m), understory shrub layer (0.5-1m), and the herbaceous ground cover at the surface. The following table includes a description of the site condition variables listed in the dataset.

Table 1: Variable names and descriptions of site conditions.



Variable_Name	Description
Site ID	The identification label for each site
ECoord	UTM Eastern coordinate (Zone 17R) of the collection site
NCoord	UTM Northern coordinate (Zone 17R) of the collection site
Site Description	The vegetation community of the site, assigned using feild observations
Archaeological Site	If there was evidence of human acivity within, or adjacent to, the test unit.
Water level (m)	The observed water level (in meters) at the time of feild collection.
Open Overstory	Total percent of openness of a test unit from the overstory zone.
Open Understory	Total percent of openness of a test unit from the understrory zone.
Open Herb	Total percent of openness of a test unit from the herb zone.

Observed vegetation was recorded for each sample within a 1x1 meter test unit. Vegetation species were identified and their total vegetation coverage between the overstory, understory, and herb vegetation zones were recorded as a percentage. The following table includes all of thevegetation coverage variables within the dataset, their scientific name, common name, and family.

Table 2: Observed vegetation, their common name, family, and vegetation communities they were observed in.

Scientific Name	Common Name	Family	Juncus	Mangrove	Marsh	Marsh/Mangrove	Salt Prairie	Uplands
Acrostichum aureum	Leather fern	PTERIDACEAE			x		x	
Andropogon glomeratus	Bushy brook grass	POACEAE						x
Aster species	Aster	ASTERACEAE						x
Avicennia germinans	Black mangrove	AVICENNIACEAE		x		x		
Batis maritima	Saltwort	BATACEAE		x	x	x		
Bacopa species	Water-hyssops	SCROPHULARIACEAE			x			x
Borrichia species	Sea oxeye	ASTERACEAE			x	x		x
Conocarpus erectus	Buttonwood mangrove	COMBRETACEAE		x				x
Cyperus species	Sawgrass, spikerush, etc.	CYPERACEAE						x
Distichlis spicata	Salt grass	POACEAE			x	x		
Heliotropium curassavicum	Seaside heliotrope	BORAGINACEAE						x
Ilex species	Gallberry	AQUIFOLIACEAE						x
Juncus roemerianus	Black needlerush	JUNCACEAE	x	x		x		x
Laguncularia racemosa	White mangrove	COMBRETACEAE		x	x	x		
Limonium carolinianum	Sea lavender	PLUMBAGINACEAE				x	x	
Lycium carolinianum	Christmas berry	SOLANACEAE		x				
Panicum species	Panic grasses	POACEAE		x		x		x
Paspalum species	Paspalum	POACEAE			x			x
Pinus species	Pine	PINACEAE			x			x
Psidium cattleyanum	Strawberry guava	MYRTACEAE						x
Quercus species	Oak	FAGACEAE						x
Rhizophora mangle	Red mangrove	RHIZOPHORACEAE		x				x
Sabal palmetto	Cabbage palm	ARECACEAE						x
Salicornia bigelovii	Annual glasswort	AMARANTHACEAE		x		x		
Schinus terebinthifolia	Brazillian pepper tree	ANACARDIACEAE		x				x
Serenoa repens	Saw palmetto	ARECACEAE						x
Smilax species	Catbrier, sarsaparilla	SMILACACEAE						x
Spartina species	Coordgrass	POACEAE			x	x		x
Tephrosia species	Hoary pea	FABACEAE						x
Unknown species	Unknown	Unknown						x

Pollen

Pollen types were identified and counted for each sample. The table below (Table 3) includes a list of the pollen types identified during pollen analysis, their listed variable name within the dataset, and the taxa type they are associated with. The dataset includes the number of observedpollen grains for each pollen type within the sample.

Table 3: Pollen variable names and assigned pollen type.

Variable Name	Pollen Type
ASTERACEAE_high_P	Aster spp. Highspine
ASTERACEA_low_P	Aster spp. Lowspine
AMARANTHACEAE_P	AMARANTHACEAE
Avicennia_germinans_P	Avicennia germinans
Batis_maritima_P	Batis maritima
COMBRETACEAE_P	COMBRETACEAE
CYPERACEAE_P	CYPERACEAE
Euphorbaceae_P	EUPHORBACEAE
FABACEAE_P	FABACEAE
Ilex spp_P	Ilex species
Laguncularia_racemosa_P	Laguncularia racemosa
LYRTHRACEAE_P	LYRTHRACEAE
Morella_spp_P	Morella species
MYRTACEAE_P	MYRTACEAE
Pinus spp_P	Pinus species
POACEAE _P	POACEAE
Quercus_spp_P	Quercus species
Rhizophora_mangle_P	Rhizophora mangle
Rubiaceae_P	RUBIACEAE
Sagiteria_spp_P	Sagitaria species
Salviniaceae_P	SALVINIACEAE
Schinus_terebinthifolia_P	Schinus terebinthifolia
Smilax_spp_P	Smilax species
TCT_P	Taxodiaceae-Cupressaceae-Taxaceae (TCT)
Typha_spp_P	Typha species
VITACEAE_P	VITACEAE
JUGLANDACEAE_P	JUGLANDACEAE
Myrcia_spp_P	Myrcia species
ASTERACEAE_high_P	Aster spp. Highspine
ASTERACEA_low_P	Aster spp. Lowspine

The total amount of *Lycopodium* spores observed during counting and total amount of pollen counted for each sample was recorded in the dataset. Pollen frequency was calculated by dividing each pollen-type count by the total amount of pollen counted within each sample. Total pollen concentration was also calculated for each sample using the following equation:

$$\text{pollen concentration}\ \left(\frac{1000\ \text{grains}}{\text{ml}}\right) = \frac{\text{amount of Lycopodium grins added}}{\text{ml of Sample}}\ x\ \frac{\text{total pollen counted}}{\text{total Lycopodium counted}}\ x\ \frac{1}{1000}$$

RESULTS

Sites Sampled

Site conditions and observed vegetation coverage was recorded from a total of 49 sample locations within Upper Tampa Bay Park (Table 4). Among the samples, 4 were from juncus marshes, 19 from mangrove communities, 3 from salt marshes, 4 from salt marsh-transitioning-to-mangrove communities, 5 from salt prairies, and 14 from the uplands (Figure 1). The samples T2A, T2A.1, and T2B were located on the archeological site known as Rattle Snake Midden (8Hi981) (Whitehurst 1988). Rattle Snake Midden is a shell midden located right next to the Double Branch Bay and extends 75 m north-south, and 30 m east-west. The site contained tempered plain sherds that indicated human occupation post-1000 BC.

Table 4: Site conditions for collected samples

SiteID	ECoord	NCoord	UTM Zone	Latitude	Longitude	Archeological_Site	Pollen Analyzed	Waterlevel (m)
N01E02	340202	3100138	17 R	28.016888	-82.625374		X	0.01
N01E06	340602	3100097	17 R	28.0165661	-82.621301		X	0.03
N01E92	339199	3100101	17 R	28.0164331	-82.635567			0
N01E94	339400	3100099	17 R	28.0164394	-82.633523		X	0
N01E96	339597	3100105	17 R	28.0165173	-82.631521			0
N03E04	340400	3100300	17 R	28.0183736	-82.623383		X	0
N03E06	340601	3100300	17 R	28.0183977	-82.621339			0
N03E92	339202	3100298	17 R	28.0182111	-82.635564		X	0
N05E00	339999	3100502	17 R	28.0201482	-82.627487			0.03
N05E02	340200	3100500	17 R	28.0201543	-82.625443			0
N05E92	339201	3100498	17 R	28.0200157	-82.635601		X	0
N05E98	339800	3100502	17 R	28.0201242	-82.629511		X	0.03
N87E00	340000	3098700	17 R	28.0038877	-82.627233		X	0.01
N87E92	339200	3098700	17 R	28.0037912	-82.635366			0
N87E94	339400	3098700	17 R	28.0038153	-82.633333			0
N87E96	339600	3098700	17 R	28.0038395	-82.631299			0.01
N87E98	339800	3098700	17 R	28.0038636	-82.629266			0.02
N89E92	339200	3098900	17 R	28.0055959	-82.635393			0.01
N89E94	339400	3098898	17 R	28.005602	-82.63336		X	0.04
N89E96	339600	3098900	17 R	28.0056442	-82.631327			0.03
N91E92	339198	3099100	17 R	28.0074004	-82.635441		X	0.03
N91E94	339396	3099104	17 R	28.0074604	-82.633429			0
N91E96	339600	3099101	17 R	28.007458	-82.631354		X	0.02
N93E94	339400	3099300	17 R	28.0092295	-82.633415		X	0
N93E98	339799	3099300	17 R	28.0092777	-82.629358			0.5
N95E04	340394	3099505	17 R	28.0111991	-82.623336		X	0.8
N95E06	340652	3099511	17 R	28.0112842	-82.620713		X	0.5
N95E98	339809	3099500	17 R	28.0110836	-82.629283		X	0.6
N96E03	339599	3100281	17 R	28.0181057	-82.631525			0.4
N97E00	339982	3099709	17 R	28.0129904	-82.627553		X	0.2
N97E02	340200	3099697	17 R	27.471468	-82.617316			0.2
N97E04	340401	3099700	17 R	28.0129596	-82.623291			0.1
N97E06	340557	3099681	17 R	28.0128068	-82.621702		X	0.5
N97E94	339391	3099701	17 R	28.0128469	-82.633561			0
N99E02	340200	3099900	17 R	28.0147401	-82.625362			0.04
N99E92	339199	3099901	17 R	28.0146284	-82.63554			0
N99E94	339404	3099902	17 R	28.0146622	-82.633456		X	0
T1A	340400	3099900	17 R	28.0147642	-82.623328		X	0.06
T1B	340400	3099950	17 R	28.0152153	-82.623335		X	0.06
T1C	340400	3100001	17 R	28.0156756	-82.623342		X	0.07
T1D	340400	3100049	17 R	28.0161087	-82.623349		X	0.7
T1E	340402	3100098	17 R	28.0165511	-82.623335		X	0.01
T1F	340400	3100150	17 R	28.0170201	-82.623362		X	0.01
T2A	339700	3098900	17 R	28.0056563	-82.63031	X	X	0
T2A.1	339607	3098896	17 R	28.005609	-82.631255	X		0
T2B	339665	3098935	17 R	28.0059679	-82.630671	X	X	0
T2C	339630	3098970	17 R	28.0062795	-82.631031		X	0

Figure 1: Map of sample location collected from Upper Tampa Bay Park .

**Earth Explorer image of Upper Tampa Bay Park courtesy of the U.S. Geological Survey (https://earthexplorer.usgs.gov/)*

Vegetation

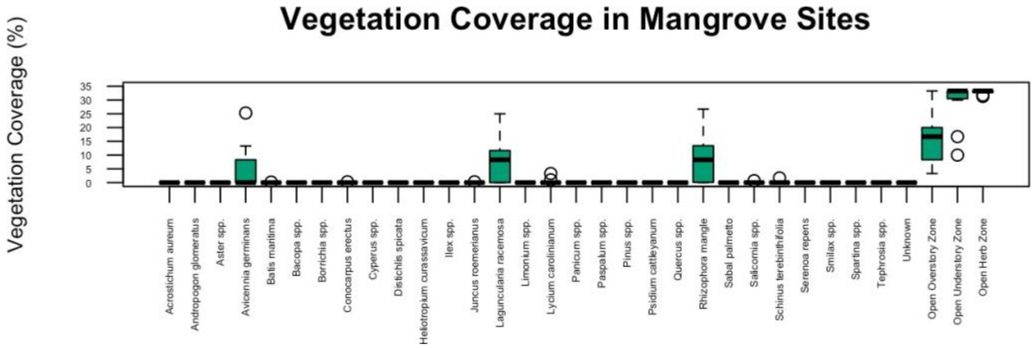


Figure 2: Boxplots of the vegetation coverage data from the mangrove sites.

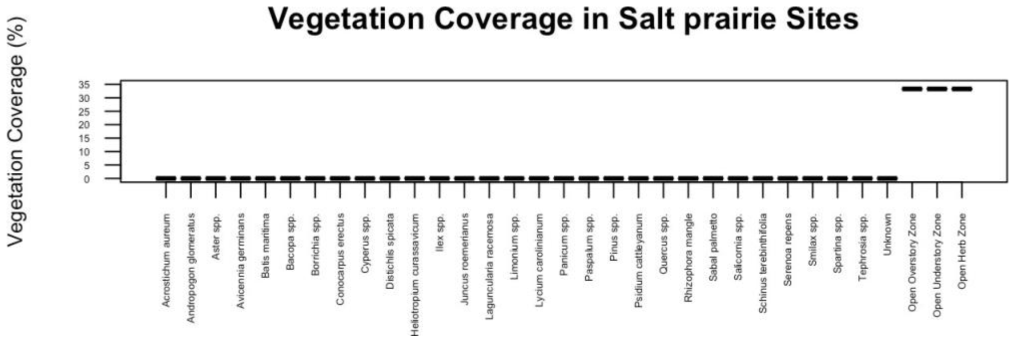


Figure 3: Boxplots of the vegetation coverage from the salt prairie sites.

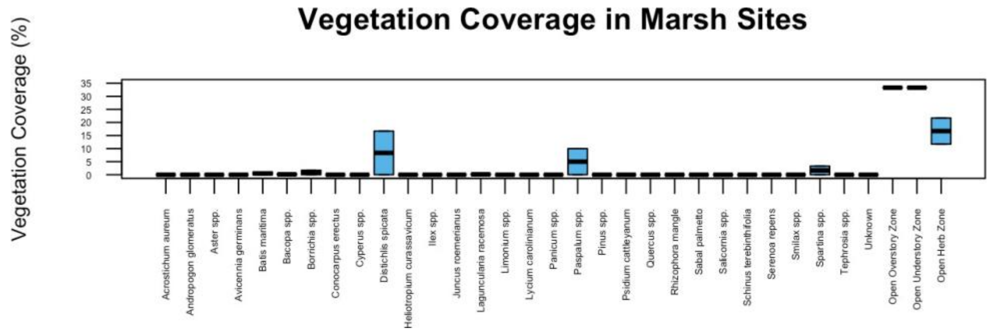


Figure 4: Boxplots of the vegetation coverage from the marsh sites.

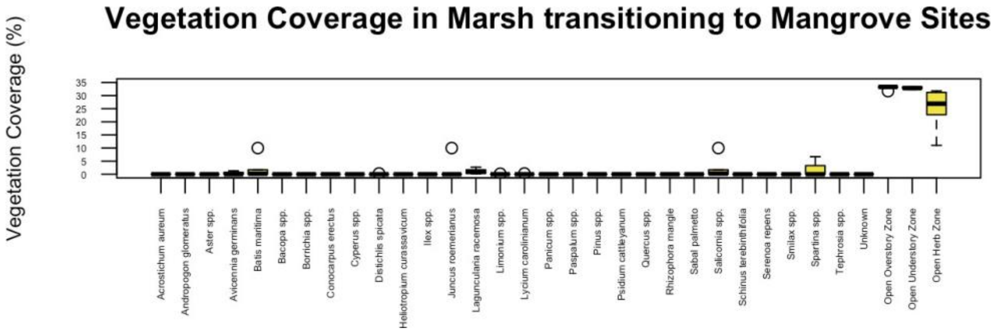


Figure 5: Boxplots of the vegetation coverage from the marsh transitioning into mangrove sites.

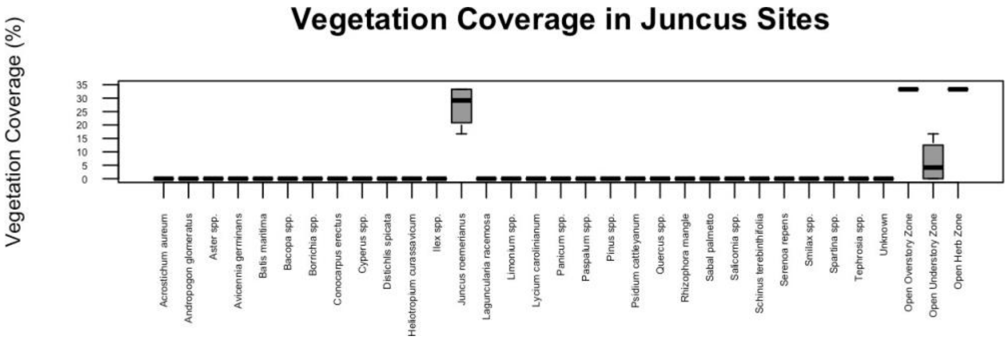


Figure 6: Boxplots of the vegetation coverage from the juncus marsh sites.

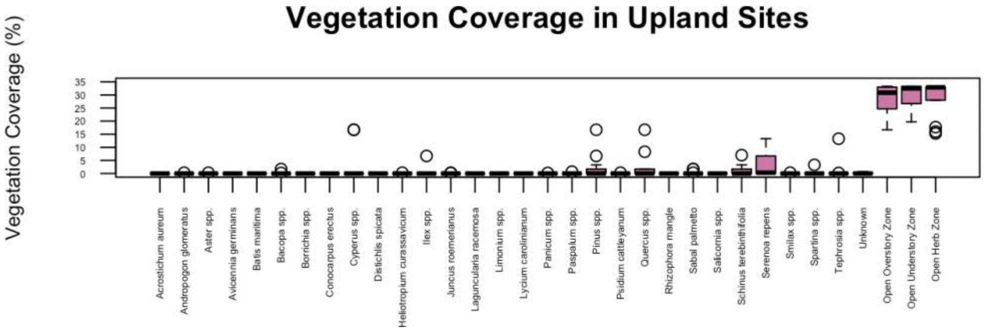


Figure 7: Boxplots of the vegetation coverage from the upland sites.

Mangrove Communities

Mangrove communities were observed to contain dense areas of the *Rhizophora mangle*, *Langncularia racemose*, and *Avicennia germinans* mangrove species with little understory present (Figure 2). Vegetation surrounding mangrove communities varied greatly and included salt marshes, juncus marshes, and salt prairies, and uplands. While the presence of black mangroves (*Avicennia germinans*) varied between many of the sites, with a mean coverage of

4.5%, white (*Langncularia racemose*) and red (*Rhizophora mangle*) mangroves had similar distributions, with x̄ of 7.7% and 7.8% respectively. A few of the sites contained traces of the invasive Brazilian Pepper Tree (*Schinus terebinthifolia*) and some marsh-related species such as *Batis maritima*, *Juncus roemerianus*, *Lycium carolinianum*, and *Salicornia*.

Salt Prairies

Salt prairie sites lacked the general presence of vegetation and were completely open (Figure 3). This community was always located between a mangrove/marsh community and the upland boundary.

Salt Marshes

Salt marshes contained little to no vertical structures and were mostly open (Figure 4). These sites were usually surrounded by mangroves or located between a mangrove community and an upland boundary. Salt marshes were shown to contain *Acrostichum aureum* (x̄ = 5.6%) *Distichlis spicata* (x̄ = 5.6*%), Paspalum* spp. (x̄ = 3.3%), and *Spartina* spp. (x̄ =1.1%). Some sites also had low coverages (x̄ <0.5%) of *Batis maritima, Borrichia* spp., *Bacopa* spp.*, and Laguncularia racemosa.* Most of the vegetation present was located in the herb vegetation zone with no vegetation in the overstory zone.

Salt Marshes Transitioning into Mangrove

These sites were categorized by the presence of salt marsh vegetation with high abundance of juvenile mangroves (Figure 5). Similar to salt marsh communities, these sites lacked overstory coverage. These sites were always adjacent to a mangrove community. The majority of juvenile mangroves present at sites were *Laguncularia racemose* (x̄ =1.3%) Many of these sites contained Spartina spp. (x̄ =2.5%) with low abundances (x̄ >1%) of *Avicennia germinans, Batis maritima, Limonium* spp., *Lycium carolinianum, and Salicornia* spp.

Juncus Marsh

These sites contained dense monodominant areas of *Juncus roemerianus* (x̄ =27.1%) with no overstory coverage (Figure 6). These areas were usually surrounded, on all sides, by mangrove vegetation and inundated by freshwater runoff.

Uplands

Upland vegetation coverage varied between the herb, understory, and overstory zones (Figure 7).Some areas had light levels of overstory coverage, such as *Pinus* spp., while other areas were open fields of *Sabal palmettos.* Most of these samples were surrounded by additional upland communities. The main vegetation observed within these sites were *Serenoa repens* (x̄ =3.0%), *Cyperus* spp. (x̄ =2.3%), *Pinus* spp. (x̄ =2.1%), and *Schinus terebinthifolia* (x̄ =1.0%). Other vegetation that occurred in lower abundance (x̄ >1%) were *Andropogon glomeratus, Aster* spp., *Bacopa* spp., *Heliotropium curassavicum, Juncus roemerianus, Panicum* spp., *Psidium cattleyanum, Sabal palmetto, Smilax* spp., *Spartina* spp., and *Tephrosia* spp.

Vegetation PCA

I conducted a scaled principal components analysis (PCA) to investigate how well samples can be grouped together by their vegetation coverage. The PCA was scaled using the RStudio ‘vegan’ Package (Oksanen et al. 2020). Looking at the plotted scaled PCA, we see that the vegetation communities begin to group together through their vegetation coverage data (Figure 8). When plotting a scree plot of the first four principal components, we see that all together they explain less than 40% of the variance (Figure 9). The following vegetation coverage variables had the highest relative eigenvalue values: *Andropogon glomeratus* (PC1 eigenvalue= 0.33, PC2 eigenvalue =-0.33), *Cyperus* spp. (PC1 eigenvalue= 0.36, PC2 eigenvalue= -0.30), and *Heliotropium curassavicum* (PC1 eigenvalue=0.33, PC2 eigenvalue= -0.33).

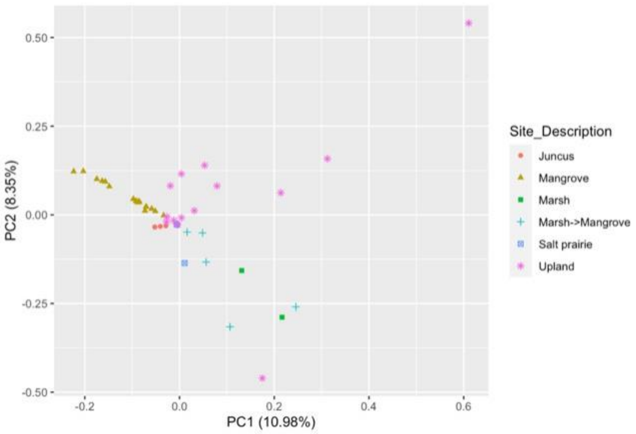


Figure 8: Scaled PCA of vegetation coverage

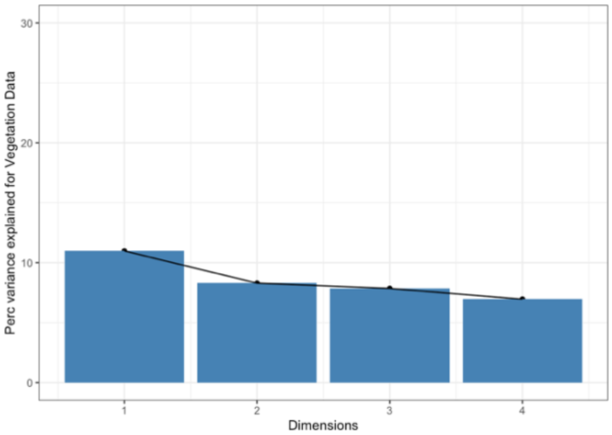


Figure 9: Scree plot of the scaled PCA of vegetation coverage showing first four components.

Pollen

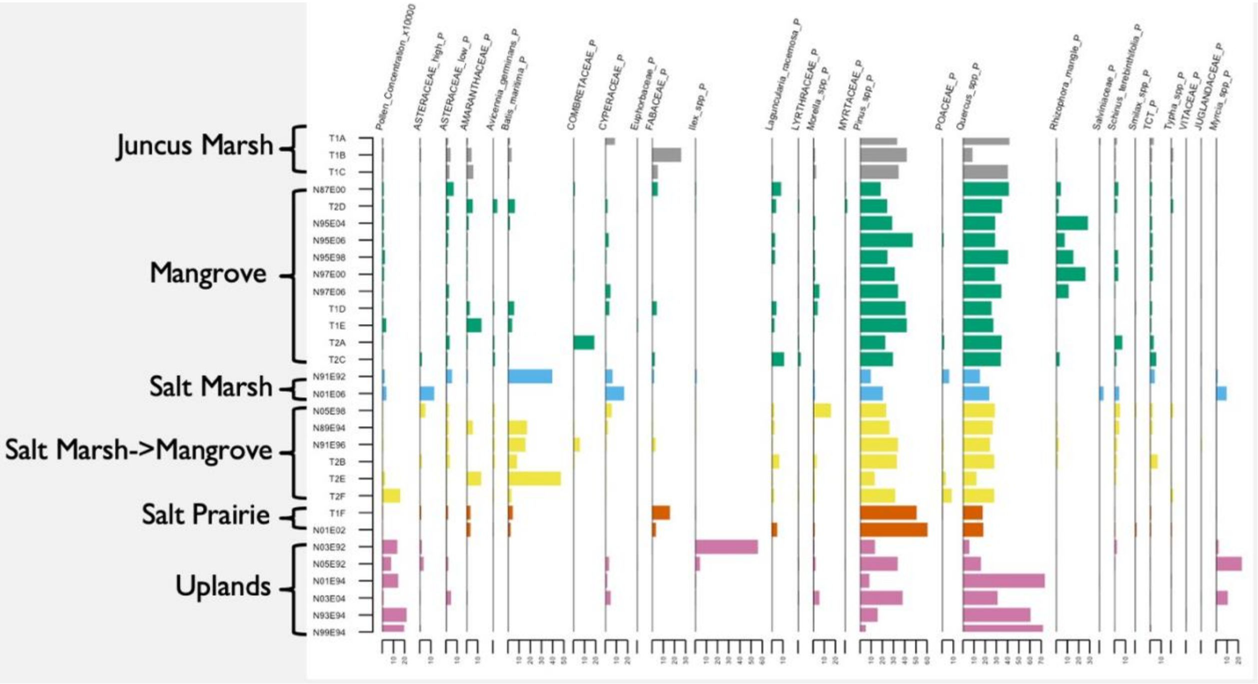
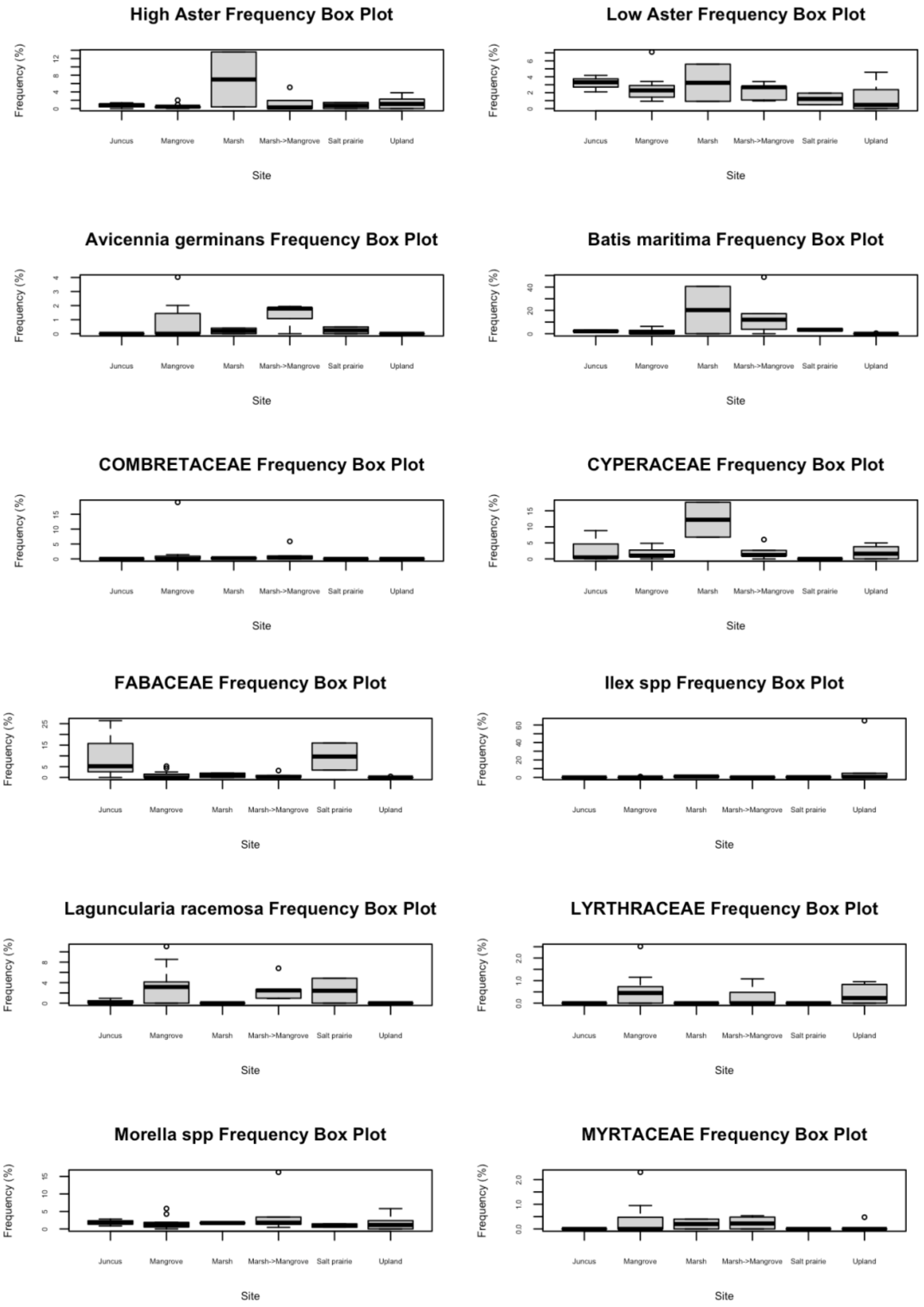


Figure 10: Pollen frequencies across all of the different vegetation communities.



High Aster Frequency Box Plot

Low Aster Frequency Box Plot

Avicennia germinans Frequency Box Plot

Batis maritima Frequency Box Plot

COMBRETACEAE Frequency Box Plot

CYPERACEAE Frequency Box Plot

FABACEAE Frequency Box Plot

Ilex spp Frequency Box Plot

Laguncularia racemosa Frequency Box Plot

LYRTHRACEAE Frequency Box Plot

Morella spp Frequency Box Plot

MYRTACEAE Frequency Box Plot

Figure 11: Boxplots of pollen frequencies by vegetation community (Part 1)

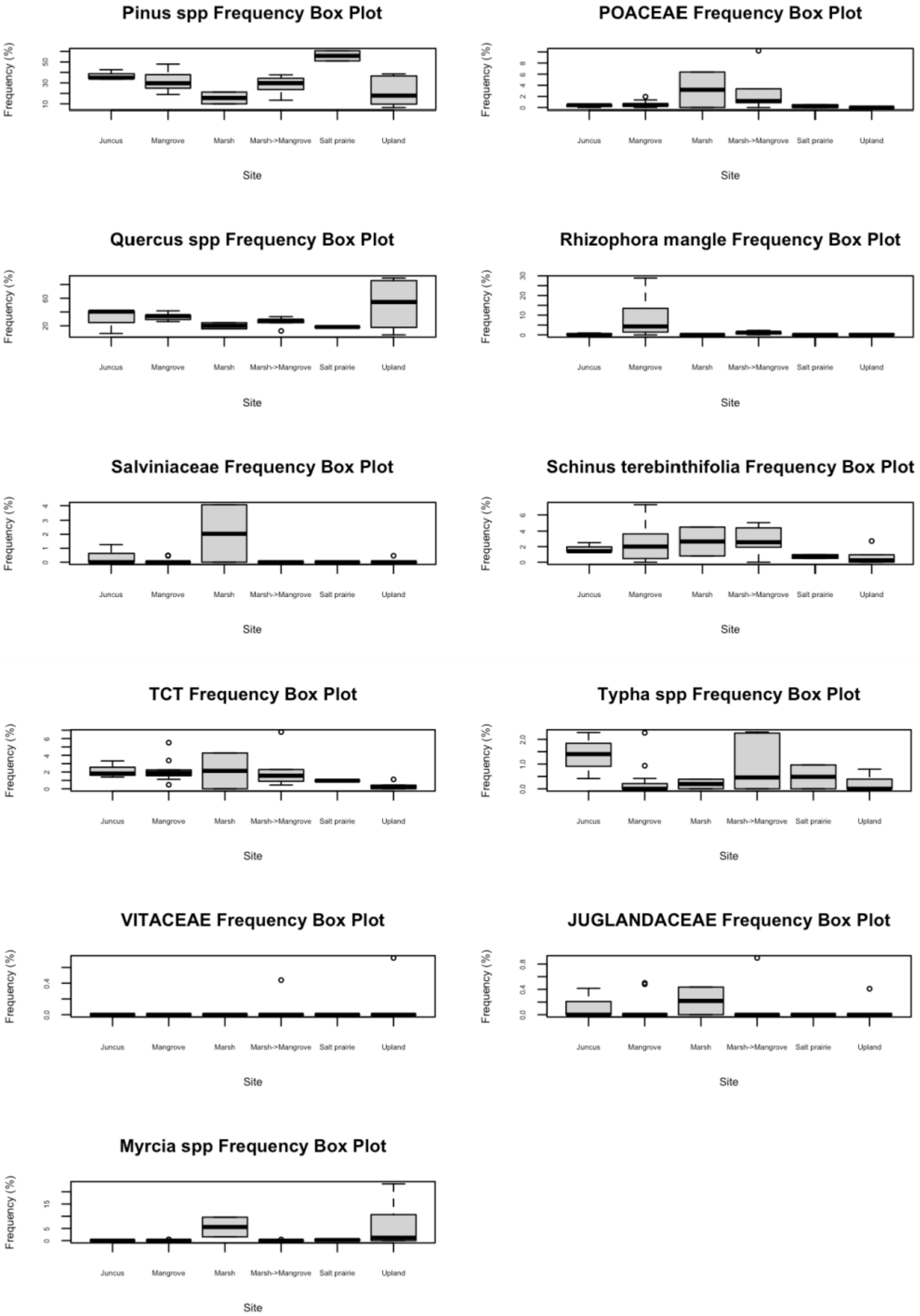


Figure 12: Boxplots of pollen frequencies by vegetation community (Part 2)

Juncus Marsh

The pollen assemblages from this vegetation community (Figures 10,11,12) presented the second highest frequency of pine pollen (x̄ =39.7%, sd=0.05%). The juncus samples also had relatively high abundances of low spine Asteraceae (x̄ =3.2%, sd=0.01%), *Typha* spp. (x̄ =1.4%, sd=0.01%), and Fabaceae (x̄ =10.4%, sd=0.14%). These sites notably lacked the presence of *Avicennia germinans*, and only a slight presence of *Laguncularia racemose* (x̄ =0.3%) and *Rhizophora mangle* (x̄ =0.3%).

Mangrove Communities

The mangrove communities (Figures 10,11,12) had a fairly high abundance of pine pollen (x̄ =31.27%, sd=8.93%) and *Quercus* spp. (x̄ =32.65%, sd=5.2%). Compared to the following community types, samples from mangrove communities had high variation in *Laguncularia racemose* (x̄ =3.3%, sd=0.04%), *Avicennia germinans* (x̄ =0.8%, sd=0.01%), and *Rhizophora mangle* (x̄ =9.0%, sd=0.1%), pollen frequencies. While the frequency of *Avicennia germinans* was highest in marsh-to-mangrove transitioning sites, and *Laguncularia racemose* frequency matched those found in salt prairie and marsh-to-mangrove transitioning sites, the *Rhizophora mangle* pollen frequency is noticeable greater in these mangrove communities. The mean and spread of the *Rhizophora mangle* signal in other vegetation communities is small (x <1%). The sites had a fairly low abundance marsh relative vegetation such as Amaranthaceae (x =2.67), *Batis maritima* (x̄ =1.81).

Salt Marshes

Samples from salt marsh communities (Figures 10,11,12) had the highest abundance and spread of Astraceae pollen types. High-type Astraceae frequency had a mean of 7.0% and an interquartile range of 3.3%, and low-type Astraceae had a mean of 3.2% and an interquartile range of 2.3%. These samples also presented the highest frequency of *Batis maritima* (x =20.0%), Cyperaceae-type pollen ($\bar{x}$ =12.1%) Salviniaceae-type pollen ($\bar{x}$ =2.0%) Juglandaceae-type pollen ($\bar{x}$ =0.2%) and *Schinus terebinthifolia* ($\bar{x}$ =2.7%). There was also an absence of *Laguncularia racemose* and *Rhizophora mangle* pollen within these samples, and only a slight presence of *Avicennia germinans* ($\bar{x}$ =2%).

Salt Marshes Transitioning into Mangrove

Samples from this vegetation community (Figures 10,11,12) presented the highest frequency of *Avicennia germinans* ($\bar{x}$ =1.4%) and had relatively high frequency and low spread of *Laguncularia racemose* pollen ($\bar{x}$ =2.6%). Interestingly, there was a low *Rhizophora mangle* pollen signal ($\bar{x}$ =1.1%) within this vegetation community. Samples from these locations also presented a generally high *Schinus terebinthifolia* ($\bar{x}$ =2.7%) and had a notably high spread in *Typha* spp. frequency ($\bar{x}$ =0.95).

Salt Prairies

These samples (Figures 10,11,12) had the highest frequency of Pinus spp. ($\bar{x}$ =55.8%) among all of the vegetation communities. These samples also had the lowest frequency of

Quercus spp. (x̄ =18.2%) and a relatively low *Schinus terebinthifolia* signal (x̄ =0.7%). The salt prairies notably had similar mean and spread of *Laguncularia racemose* (x̄ =2.4%) to samples from mangrove communities. These samples also had relatively high abundance of Fabaceae pollen-types (x̄ =9.7%).

Uplands

The uplands (Figures 10,11,12) had the lowest abundance of pine pollen but with a large spread(x̄ =19.1%) These sites did present high frequencies of oak (x̄ =43.2%) and *Myrcia* spp pollen (x

=6.0%). Samples from the uplands lack the presence of *Avicennia germinans, Laguncularia racemos* and *Rhizophora mangle.* Notably, many of these samples presented the slight presence of the *Ilex* spp. (x̄ =10.3%) with one particular site, N03E92, containing a hyper abundance of *Ilex* spp. (62.4%).

Transects

Transect 1's sampling starting in a Juncus marsh (T1A, T1B, T1C) and continued north though a mangrove community (T1D, T1E), ending in a salt prairie (T1F) that was close to the upland border. The pollen data from these transects (Figure 13) demonstrates that pollen assemblages can greatly differ within short distances of their location. For example, between the three samples taken within the same juncus community, there is a huge difference in the oak pollen frequency with the highest frequency around 40.0% (T1A and T1C) and the lowest at 8.6% (T1B). Similarly, there are large differences in the Fabaceae frequency, with the highest frequency at 26.0% (T1B) and the lowest at 0.0% (T1A). Differences are also found between the mangrove communities relative to their Amaranthaceae pollen type, with site T1E having 13.9%

and site T1D 2.8%. This data also illustrates the similarity between vegetation communities, such as the case for T1B and T1F. The samples from a juncus community is similar to that of the salt marsh with their Fabaceae, *Batis maritima*, Amaranthaceae, and Asteraceae (high and low spine). The most notable difference is the slight presence (>3% abundance) of *Rhizophora mangle*, *Schinus terebinthifolia*, and *Typha* spp. type pollen in T1B and not T1F.

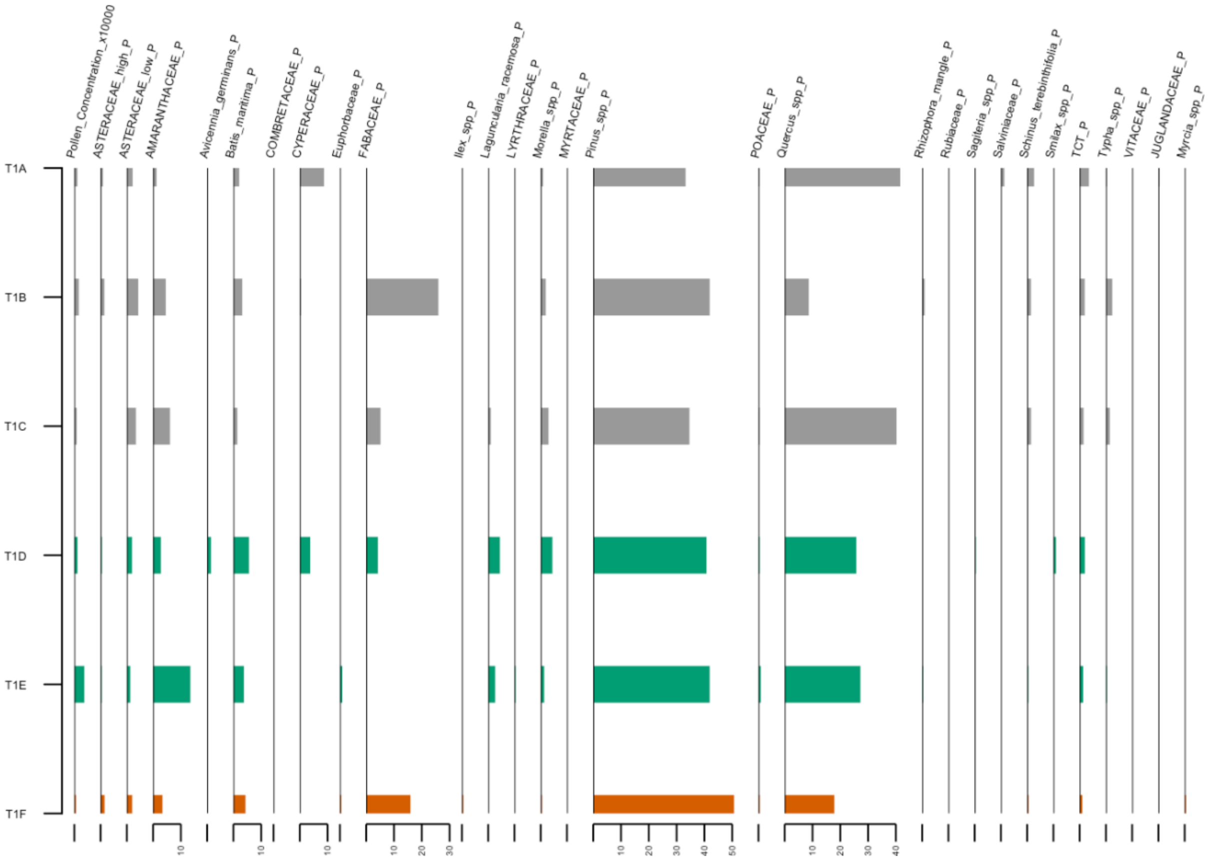


Figure 13: Pollen frequencies as percent of pollen sum across Transect 1.

Transect 2 began in a mangrove community (T2A) sampling every 50 m North-West traveling through a marsh-transitioning-into-mangrove site (T2B), two mangrove sites (T2C and T2D), and finally sampling through 2 more marsh-transitioning-into-mangrove sites (T2E and T2F). Much like what was observed in Transect 1, Transect 2 shows that there is difference in the pollen assemblage within vegetation communities (Figure 14). For example, the mangrove samples vary in the presence of Combretaceae (absent in T2C and T2D) and *Rhizophora mangle* (absent in T2A). The marsh-transitioning-into-mangrove sites also present various pollen type abundances, most notably in the level of *Batis maritima*. T2B and T2F have a frequency of 8.2% and 3.2%, while T2E has a frequency of 47.3%. It is also worth noting that T2F had 8x the level of pollen concentration (16.2 x10^5 per ml) between all these Transect 2 samples and was the closest to the uplands.

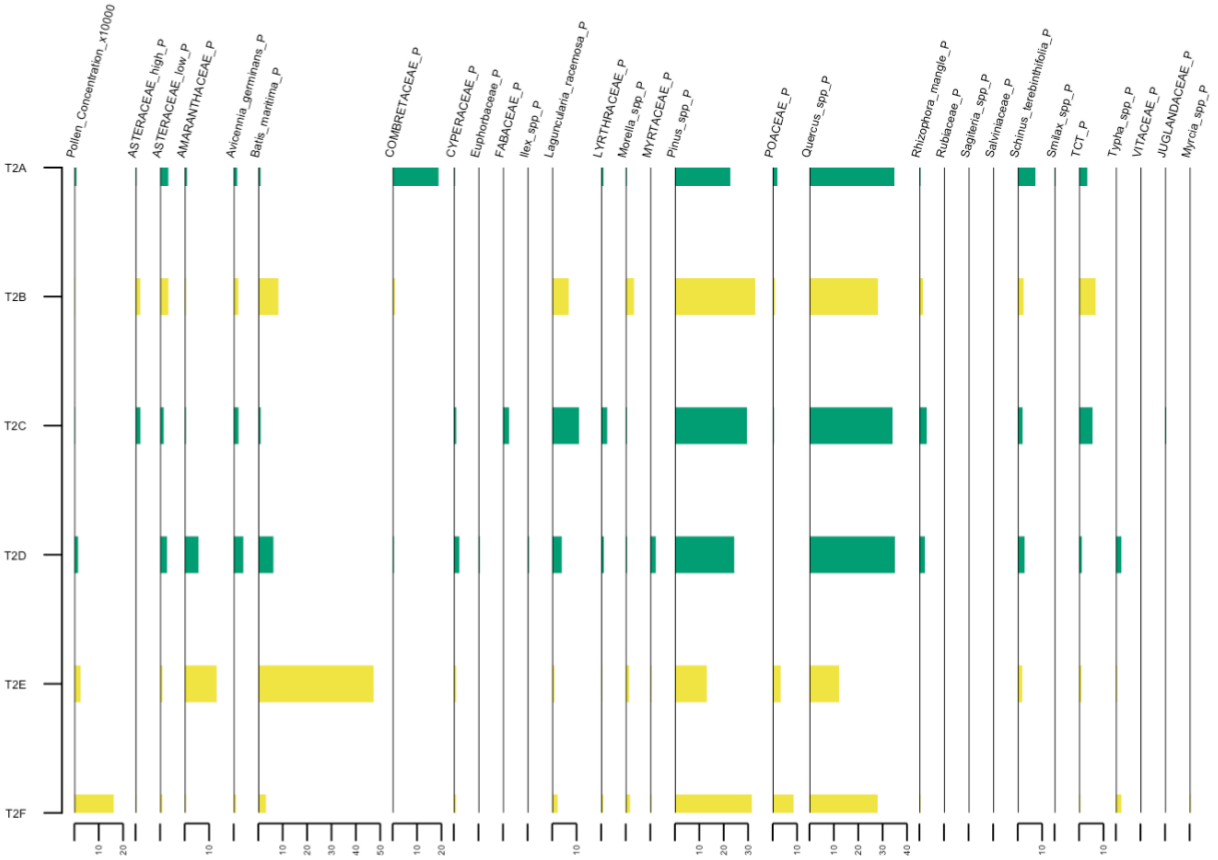


Figure 14: Pollen frequencies as percent of pollen sum across Transect 2.

Pollen Data PCA

I used a scaled PCA analysis (Oksanen et al. 2020) to investigate how well samples can be grouped together by their pollen assemblages. Looking at the plotted scaled PCA, we see that vegetation communities do not group well through their raw pollen assemblage data (Figure 15). This suggest that that there is a good degree of equifinality between pollen samples from different vegetation communities. When plotting a scree plot of the first four principal components, we see that all together they explain less than 60% of the variance (Figure 16). The following pollen frequency variables had the highest relative eigenvalue values: *Aster* spp. high-spine (PC1 eigenvalue= -0.27, PC2 eigenvalue= -0.37), Cyperaceae (PC1 eigenvalue= -0.26, PC2 eigenvalue=-0.39), and Salviniaceae (PC1 eigenvalue= -0.32, PC2 eigenvalue=-0.31)

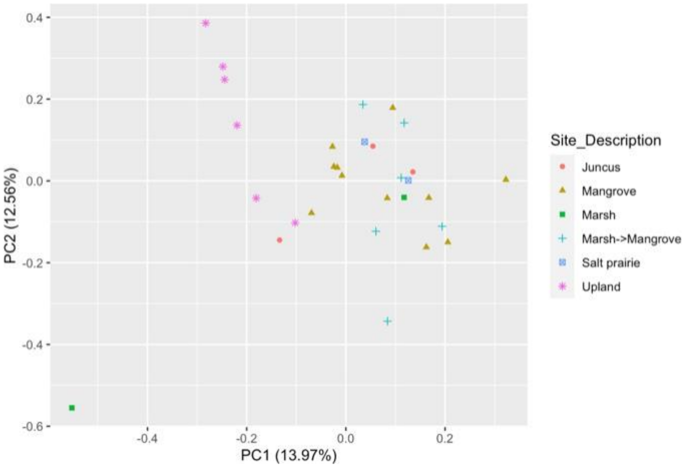


Figure 15: Scaled PCA of pollen frequencies

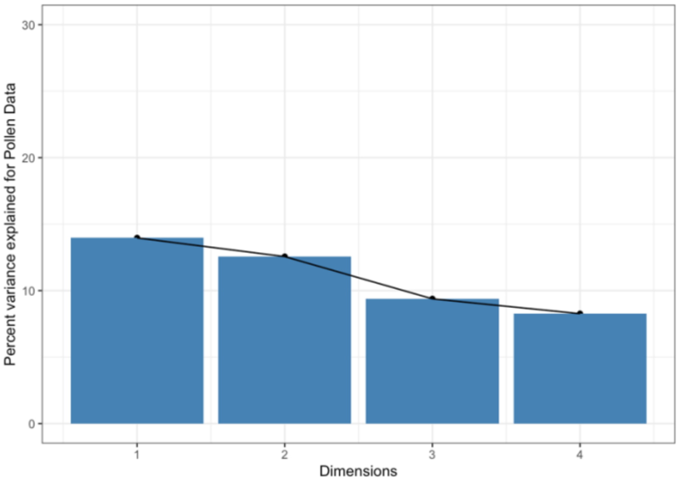


Figure 16: Scree plot of the scaled PCA of pollen frequencies showing first four components.

Pollen-Vegetation Data PCA

To investigate the relationship between pollen and their respective vegetation coverage, we isolated the pollen variables whose vegetation was observed in the field and vice versa. This sub data set included vegetation coverage from the following species: *Andropogon glomeratus, Avicennia germinans, Batis maritima, Conocarpus erectus, Cyperus* spp.*, Distichlis spicata, Ilex* spp.*, Laguncularia racemosa, Pinus* spp.*, Quercus* spp.*, Rhizophora mangle, Salicornia* spp.*, Schinus terebinthifolia,* and *Spartina* spp. In addition to this subset of vegetation species, we also selected the pollen types: Amaranthaceae, *Avicennia germinans, Batis maritima,* Combretaceae, Cyperaceae, Euphorbaceae, Fabaceae, *Ilex* spp.*, Laguncularia racemosa, Pinus* spp., Poaceae, *Quercus* spp.*, Rhizophora mangle,* and *Schinus terebinthifolia*.

I used a scaled PCA analysis to investigate how well samples can be grouped together by their vegetation and pollen assemblages using the RStudio "vegan" Package (Oksanen et al. 2020). Looking at the plotted scaled PCA, we see that vegetation communities do not group well through their raw pollen assemblage data (Figure 17). The following pollen and vegetation variables had the highest relative eigenvalue values: *Andropogon glomeratus* (PC1 eigenvalue= 0.25, PC2 eigenvalue= -0.34), *Batis maritima* PC1 eigenvalue= -0.41, PC2 eigenvalue= -0.14), *Batis maritima*-pollen (PC1 eigenvalue= -0.44, PC2 eigenvalue= -0.09), *Cyperus* spp. (PC1 eigenvalue= 0.25, PC2 eigenvalue=-0.37), Amaranthaceae-pollen (PC1 eigenvalue=-0.32, PC2 eigenvalue=-0.33), and *Rhizophora mangle*-pollen (PC1 eigenvalue= 0.27, PC2 eigenvalue=-0.20)

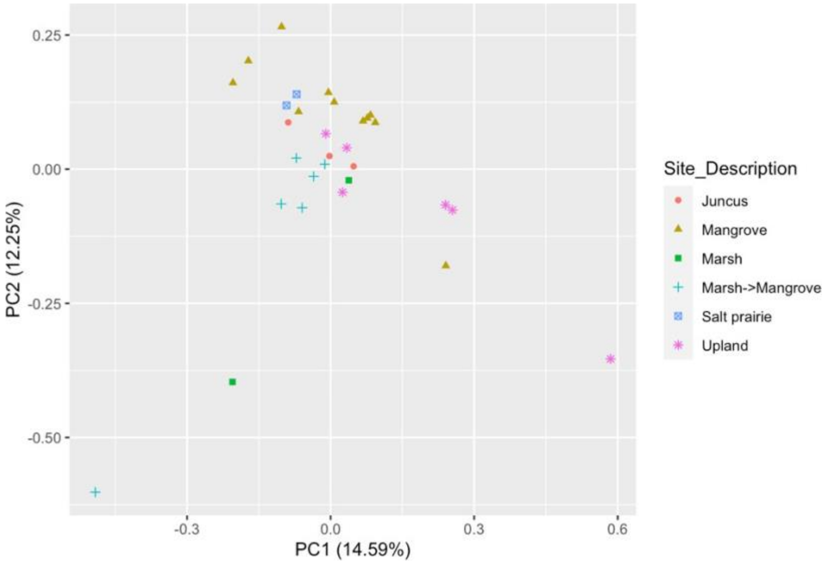


Figure 17: Scaled PCA of vegetation coverage and pollen frequencies

DISCUSSION

The analysis of this data reveals the difficulty with equifinality and the need to account for abundant pollinators signals such as *Quercus* spp. and *Pinus* spp. within this study area. The data shows that the estuary vegetation types are often swamped by abundant pollinators, demonstrating that equifinality is a major challenge in identifying some important estuary vegetation types. For example, although pine found primarily within the uplands, its pollen can reach all of the surrounding communities in very high frequencies (between 5.0%-60.4%). The pine pollen frequencies were lower in the upland samples and were at their highest in the salt prairies (Figures 10 and 12). This pattern might be the result of most salt prairies being located at the upper boundary of marshes, right where they meet the uplands. In combination with the proximity to the uplands, salt prairies have little to no local vegetation thus resulting in a pollen assemblage primarily consisting of the regional pollen signal. This is also most likely true for the pollen assemblage seen within the juncus community, whose pollen is often not preserved during the pollen extraction process (Marsh and Cohen 2008). This analysis shows that the frequency of pollen taxa can differ between communities that are in close proximity to one another. This is observed in the overlapping clustering of vegetation communities in the pollen PCA analysis (Figure 15). This further supports the need for robust modern vegetation-pollen analogues in order to better interpret the palaeoecological record. The analysis also showed no noticeable pattern in the pollen assemblage from the archaeological sites.

At the start of the project, general pollen dispersal methods were taken into account and it was expected that wind pollenated plants would produce some kind of pollen signal in all vegetation types. It was interesting to see that the majority of pollen species reached vast communities at such high frequencies. For example, *Aster* spp. low-spine pollen types are seen throughout every vegetation community, especially in the juncus communities. These issues have resulted in a largely mixed signal of pollen produced by the vegetation locally and from surrounding areas from almost all pollen of the types.

Although pollen assemblages have signals from vegetation that is not actively present at that location, their frequencies may help reveal how close or abundant that vegetation is. For example, very low frequencies of *Ilex* spp. were generally found across all of the vegetation communities. Only one upland sample, N03E92, contained a high frequency of *Ilex* spp. (62.4%). This was also the only sample to have an *Ilex* spp. plant growing within the test unit. This suggests that although low frequencies of *Ilex* spp. pollen may show up in pollen assemblage of communities where the vegetation is not present, the presence of it in high frequencies may be a more reliable indicator that its corresponding vegetation existed at that location.

CONCLUSION

This project compiled a dataset of vegetation observation and pollen assemblages of multiple vegetation types across a range of environments therefore creating a robust vegetation-pollen modern analogue dataset for the vegetation communities in Upper Tampa Bay Park. This study demonstrates some of the empirical challenges with identifying estuary vegetation in the sedimentary record. For example, the dataset showed that there was a hyper abundance of regional pollen types that dampen local pollen signals. At the beginning of the project, it was predicted that samples would naturally have some trace of the hyper-abundant wind pollenated types (*Quercus* spp. and *Pinus* spp.) due to its far-reaching pollinating method. It was also expected that, despite having a hyperabundance of a few regional pollen-types, that there would still be some locally distributed pollen types that could serve as indicators of regional vegetation. This latter assumption was not supported by the data.

One possible solution to this hyperabundance problem would be to exclude these hyper abundant pollen types in the counting process of these estuary systems, thus increasing the local pollen signal. Future work could be put towards investigating the specific pollen dispersal methods of the observed pollen within Upper Tampa Bay Park and using that information to better interpret its local pollen signals. Another tool that used to better interpret the pollen record from the estuaries of Upper Tampa Bay Park would be to apply the Multiple Scenario Approach (MSA). Again, this approach is useful in predicting multiple vegetation scenarios that could have produced a certain pollen assemblage (Bunting and Middleton 2009; Bunting et al. 2018). This is useful because it takes equifinality into account and allows a researcher to investigate the most probable scenarios.

This study highlights that it is important to take regional pollen signals into consideration when interpreting the pollen record. Regional pollen signals are heightened in open areas therefore reducing the local pollen signal, this is especially important when working with archeological sites that are open. This project also highlights that regional pollen signals can affect how well we can interpret heterogenous plant communities, such as estuaries. Without a clear understanding of the relationships between pollen deposition and vegetation, our use of the pollen record to reconstruct past estuary vegetation will be will not be as reliable as it could be. In this site area, that means that we are underestimating the coverage of estuary vegetation as well as underestimating past human influence in the region. These findings indicate that to improve studies that use pollen to investigate past relationships between humans and their environment, that we need to continue collecting robust pollen and vegetation datasets for the Tampa estuary systems.

REFERENCES

Anderson, David G., Ashley M. Smallwood, and D. Shane Miller
2015 Pleistocene Human Settlement in the Southeastern United States: Current Evidence and Future Directions. *PaleoAmerica* 1(1):7–51. DOI:10.1179/2055556314Z.00000000012.

Austin, Robert J., Jeffrey M. Mitchem, and Brent R. Weisman
2014 Radiocarbon dates and the late prehistory of Tampa bay. *New Histories of Pre-Columbian Florida*:94–120. DOI:10.5744/florida/9780813049366.003.0006.

Barak, Rebecca S., Andrew L. Hipp, Jeannine Cavender-Bares, William D. Pearse, Sara C. Hotchkiss, Elizabeth A. Lynch, John C. Callaway, Randy Calcote, and Daniel J. Larkin
2016 Taking the long view: Integrating recorded, archeological, paleoecological, and evolutionary data into ecological restoration. *International Journal of Plant Sciences* 177(1):90–102. DOI:10.1086/683394.

Birks, H. John B.
2019 Contributions of Quaternary botany to modern ecology and biogeography. *Plant Ecology and Diversity* 12(3–4):189–385. DOI:10.1080/17550874.2019.1646831.

Bliege Bird, Rebecca, and Dale Nimmo
2018 Restore the lost ecological functions of people. *Nature Ecology and Evolution* 2(7):1050–1052. DOI:10.1038/s41559-018-0576-5.

Bullen, Ritley P.
1955 Archeology of the Tampa Bay Area. *The Florida Historical Quarterly* 34(1):51–63.

Bunting, M. J., M. J. Gaillard, S. Sugita, R. Middleton, and A. Broström
2004 Vegetation structure and pollen source area. *Holocene* 14(5):651–660. DOI:10.1191/0959683604hl744rp.

Bunting, M. J., and R. Middleton
2009 Equifinality and uncertainty in the interpretation of pollen data: The multiple scenario approach to reconstruction of past vegetation mosaics. *Holocene* 19(5):799–803. DOI:10.1177/0959683609105304.

Bunting, M. Jane, Michelle Farrell, Alex Bayliss, Peter Marshall, and Alasdair Whittle
2018 Maps From Mud-Using the multiple scenario approach to reconstruct land cover dynamics from pollen records: A case study of two Neolithic Landscapes. *Frontiers in Ecology and Evolution* 6(APR):1–20. DOI:10.3389/fevo.2018.00036.

Campbell, J. F.E., W. J. Fletcher, P. D. Hughes, and E. L. Shuttleworth
2016 A comparison of pollen extraction methods confirms dense-media separation as a reliable method of pollen preparation. *Journal of Quaternary Science* 31(6):631–640. DOI:10.1002/jqs.2886.

Codding, Brian F., and Douglas W. Bird
2015 Behavioral ecology and the future of archaeological science. *Journal of Archaeological Science* 56:9–20. DOI:10.1016/j.jas.2015.02.027.

Crumley, Carole L
2004 Historical Ecology: 59-70. *History* 4(1974):314–320.

Dontis, Emma E., Kara R. Radabaugh, Amanda R. Chappel, Christine E. Russo, and Ryan P. Moyer
2020 Carbon Storage Increases with Site Age as Created Salt Marshes Transition to Mangrove Forests in Tampa Bay, Florida (USA). *Estuaries and Coasts*. DOI:10.1007/s12237-020-00733-0.

Erickson, Clark L.
2008 Amazonia: The Historical Ecology of a Domesticated Landscape. *The Handbook of South American Archaeology*:157–183. DOI:10.1007/978-0-387-74907-5_11.

Friess, Daniel A., Ken W. Krauss, Erik M. Horstman, Thorsten Balke, Tjeerd J. Bouma, Demis Galli, and Edward L. Webb
2012 Are all intertidal wetlands naturally created equal? Bottlenecks, thresholds and knowledge gaps to mangrove and saltmarsh ecosystems. *Biological Reviews* 87(2):346–366. DOI:10.1111/j.1469-185X.2011.00198.x.

Gaillard, Marie José, Shinya Sugita, M. Jane Bunting, Richard Middleton, Anna Broström, Christopher Caseldine, Giesecke, Thomas, Sophie E.V. Hellman, Sheila Hicks, Kari Hjelle, Catherine Langdon, Anne Birgitte Nielsen, Anneli Poska, Henrik Von Stedingk, and Sim Veski
2008 The use of modelling and simulation approach in reconstructing past landscapes from fossil pollen data: A review and results from the POLLANDCAL network. *Vegetation History and Archaeobotany* 17(5):419–443. DOI:10.1007/s00334-008-0169-3.

Gerold, By, Morrison Amec, Doug Robison Pbs, Kimberly K Yates, U S Geological Survey, and St Petersburg
2009 Chapter 8. Habitat Protection and Restoration(1995):239–280.

Gluckman, J Stephen, S. Gayle Russell, and Barry R Wharton
1978 *A Preliminary Survey of the Upper Tampa Bay Park Site*.

Iglesias, Virginia, Simon G. Haberle, Andrés Holz, and Cathy Whitlock
2018 Holocene dynamics of temperate rainforests in west-central Patagonia. *Frontiers in Ecology and Evolution* 5(JAN):1–12. DOI:10.3389/fevo.2017.00177.

Oksanen, Jari, F. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan McGlinn, Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos, M. Henry H. Stevens, Eduard Szoecs and Helene Wagner
2020 vegan: Community Ecology Package. R package version 2.5-7. https://CRAN.R-project.org/package=vegan

Kapp, Ronald O., Owen K. Davis, and James E. King
1969 *Pollen and Spores*. Second Edi. American Association of Stratigraphic Palynologists, Dallas, Texas.

Kelleway, Jeffrey J., Kyle Cavanaugh, Kerrylee Rogers, Ilka C. Feller, Emilie Ens, Cheryl Doughty, and Neil Saintilan
2017 Review of the ecosystem service implications of mangrove encroachment into salt marshes. *Global Change Biology* 23(10):3967–3983. DOI:10.1111/gcb.13727.

Krauss, Ken W., Karen L. Mckee, Catherine E. Lovelock, Donald R. Cahoon, Neil Saintilan, Ruth Reef, and Luzhen Chen
2014 How mangrove forests adjust to rising sea level. *New Phytologist* 202(1):19–34. DOI:10.1111/nph.12605.

Laland, Kevin N., and Gillian R. Brown
2006 Niche construction, human behavior, and the adaptive-lag hypothesis. *Evolutionary Anthropology* 15(3):95–104. DOI:10.1002/evan.20093.

Lentfer, C. J., and W. E. Boyd
2000 Simultaneous extraction of phytoliths, pollen and spores from sediments. *Journal of Archaeological Science* 27(5):363–372. DOI:10.1006/jasc.1998.0374.

Lupo, Karen D., Dave N. Schmitt, Christopher A. Kiahtipes, Jean Paul Ndanga, D. Craig Young, and Bernard Simiti
2015 On intensive late Holocene iron mining and production in the northern Congo Basin and the environmental consequences associated with metallurgy in central Africa. *PLoS ONE* 10(7):1–23. DOI:10.1371/journal.pone.0132632.

Marsh, Pamela E., and Arthur D. Cohen
2008 Identifying high-level salt marshes using a palynomorphic fingerprint with potential implications for tracking sea level change. *Review of Palaeobotany and Palynology* 148(1):60–69. DOI:10.1016/j.revpalbo.2007.09.001.

Martin, A. C. and Harvey, W. J.
2017 The Global Pollen Project: a new tool for pollen identification and the dissemination of physical reference collections. Methods Ecol Evol, 8: 892–897. doi:10.1111/2041-210X.12752.

McCarthy, Matthew J., Kara R. Radabaugh, Ryan P. Moyer, and Frank E. Muller-Karger
2018 Enabling efficient, large-scale high-spatial resolution wetland mapping using satellites. *Remote Sensing of Environment* 208(April 2017):189–201. DOI:10.1016/j.rse.2018.02.021.

Miller, D. Shane
2016 Modeling Clovis Landscape Use and Recovery Bias in the Southeastern United States Using the Paleoindian Database of the Americas (PIDBA). *American Antiquity* 81(4):697–716. DOI:10.7183/0002-7316.81.4.697.

Myers, Ronald L.
1990 *Ecosystems of Florida*. Edited by Ronald L. Myers and John J. Ewel. University of Central Florida Press, Orlando.

Phelps, Leanne N., Manuel Chevalier, Timothy M. Shanahan, Julie C. Aleman, Colin Courtney-Mustaphi, Christopher Albert Kiahtipes, Oliver Broennimann, Rob Marchant, John Shekeine, Lynne J. Quick, Basil A.S. Davis, Antoine Guisan, and Katie Manning
2020 Asymmetric response of forest and grassy biomes to climate variability across the African Humid Period: influenced by anthropogenic disturbance? *Ecography* 43(8):1118–1142. DOI:10.1111/ecog.04990.

R Core Team
2021 R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Raabe, Ellen A., Laura C. Roy, and Carole C. McIvor
2012 Tampa Bay Coastal Wetlands: Nineteenth to Twentieth Century Tidal Marsh-to-Mangrove Conversion. *Estuaries and Coasts* 35(5):1145–1162. DOI:10.1007/s12237-012-9503-1.

Reeder-Myers, Leslie A.
2015 Cultural Heritage at Risk in the Twenty-First Century: A Vulnerability Assessment of Coastal Archaeological Sites in the United States. *Journal of Island and Coastal Archaeology* 10(3):436–445. DOI:10.1080/15564894.2015.1008074.

Rick, Torben C., and Rowan Lockwood
2013 Integrating Paleobiology, Archeology, and History to Inform Biological Conservation. *Conservation Biology* 27(1):45–54. DOI:10.1111/j.1523-1739.2012.01920.x.

RStudio Team
2020 RStudio: Integrated Development for R. RStudio, PBC, Boston, MA URL http://www.rstudio.com/.

Sandweiss, Daniel H., and Alice R. Kelley
2012 Archaeological Contributions to Climate Change Research: The Archaeological Record as a Paleoclimatic and Paleoenvironmental Archive. *Annual Review of Anthropology* 41(1):371–391. DOI:10.1146/annurev-anthro-092611-145941.

Saunders, Rebecca, and Michael Russo
2011 Coastal shell middens in Florida: A view from the Archaic period. *Quatertnary International* 239(1–2):38–50. DOI:10.1016/j.quaint.2010.08.008.

Sherwood, Ed, and Holly Greening
2012 Critical Coastal Habitat Vulnerability Assessment for the Tampa Bay Estuary : Projected Changes to Habitats due to Sea Level Rise and Climate Change 33701(727):96.

Sobol, Magdalena K., and Sarah A. Finkelstein
2018 Predictive pollen-based biome modeling using machine learning. *PLoS ONE* 13(8):1–29. DOI:10.1371/journal.pone.0202214.

van Soelen, E. E., E. I. Lammertsma, H. Cremer, T. H. Donders, F. Sangiorgi, G. R. Brooks, R. A. Larson, J. S. Sinninghe Damsté, F. Wagner-Cremer, and G. J. Reichart
2010 Late Holocene sea-level rise in Tampa Bay: Integrated reconstruction using biomarkers, pollen, organic-walled dinoflagellate cysts, and diatoms. *Estuarine, Coastal and Shelf Science* 86(2):216–224. DOI:10.1016/j.ecss.2009.11.010.

Sugita, Shinya
1993 A model of pollen source area for an entire lake surface. *Quaternary Research* 39:239–244.

Trofimova, S. S., N. E. Zaretskaya, E. G. Lapteva, E. L. Lychagina, and A. V. Chernov
2019 Methods of Paleoecological Investigations: A Case Study of the Holocene Environmental Reconstruction. *Russian Journal of Ecology* 50(6):543–550. DOI:10.1134/S1067413619060122.

Whitehurst, John
1988 Archaeological Investigations at Rattlesnake Midden (8-Hi-981), Hillsborough County, Florida. Unpublished Master's Thesis, Department of Anthropology, University of South Florida.

Whitney, Ellie, D. Bruce Means, and Anne Rudloe
2004 *Priceless Florida: Natural Ecosystems and Native Species*. Pineapple Press Inc.

Willard, Debra A., Christopher E. Bernhardt, Lisa Weimer, Sherri R. Cooper, Desiré Gamez, and Jennifer Jensen
2004 Atlas of pollen and spores of the Florida Everglades. *Palynology* 28(1):175–227. DOI:10.1080/01916122.2004.9989597.

Willard, Debra A., and Thomas M. Cronin
2007 Paleoecology and ecosystem restoration: Case studies from Chesapeake Bay and the Florida Everglades. *Frontiers in Ecology and the Environment* 5(9):491–498. DOI:10.1890/070015.

Williams, J. W., and B. Shuman
2008 Obtaining accurate and precise environmental reconstructions from the modern analog technique and North American surface pollen dataset. *Quaternary Science Reviews* 27(7–8):669–687. DOI:10.1016/j.quascirev.2008.01.004.

Williams, John W., Bryan N. Shuman, Thompson Webb, Patrick J. Bartlein, and Phillip L. Leduc
2004 Late-Quaternary vegetation dynamics in north America: Scaling from taxa to biomes. *Ecological Monographs* 74(2):309–334. DOI:10.1890/02-4045.

Yates, Kimberly K., and Holly Greening
2011 Chapter 1 . An Introduction to Tampa Bay. *Integrating Science and Resource Management in Tampa Bay, Florida*:1–16.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES