



Kalaupapa National Historical Park Marine Fish Trend Report for 2006–2015

Pacific Island Network

Natural Resource Report NPS/KALA/NRR—2022/2363



ON THE COVER

Bluespine unicornfish (*Naso unicornis*) and other herbivores at Kalaupapa National Historical Park, Moloka'i, Hawai'i.
NPS

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Eric Brown¹, Senifa Annandale^{1,2}, Kazuki Kageyama^{1,3}, Sylvester J. Lee^{1,2}, and Kimberley Tice^{1,2}

¹National Park Service

Kalaupapa National Historical Park

P.O. Box 2222

Kalaupapa, Moloka‘i, Hawai‘i 96742

²Pacific Island Network

Inventory and Monitoring Program

National Park Service

Hawai‘i Volcanoes National Park

P.O. Box 52, 1 Crater Rim Drive

Hawai‘i National Park, Hawai‘i 96718

³Research Corporation of the University of Hawai‘i

2800 Woodlawn Drive, Suite 200

Honolulu, Hawai‘i 96822

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Executive Summary

Kalaupapa National Historical Park (NHP) is located on the north shore of the island of Moloka‘i and encompasses a wide variety of habitats from submerged marine resources to lowland coastal, mesic, and rainforest habitats as well as three offshore islands. The marine boundary of the park extends a quarter mile offshore around the park shoreline and covers approximately 2,000 acres. Kalaupapa NHP is one of four parks within the Inventory and Monitoring (I&M) Program of the Pacific Island Network (PACN) where marine Vital Signs (i.e., an indicator of physical, chemical, biological elements, or ecosystem processes selected to represent the overall health or condition of natural resources within parks) for the fish and benthic communities are monitored by peer-reviewed standardized protocols.

The objective of the I&M PACN Marine Fish Monitoring Protocol at Kalaupapa NHP is to annually determine the density and size of reef fishes at sites randomly selected on hard substrata between the 10 and 20 m depths (Brown et al. 2011a). From 2006–2015, a total of 165 transects (the sampling unit), each 25 m in length, were sampled. A split panel sampling design was used with 30 transects sampled annually on hard-bottom substrate. Fifteen transects were randomly established in 2006 as permanent transects and subsequently surveyed on an annual basis. The remaining 15 temporary transects were randomly selected each year and surveyed only in that year. Data collection consisted of a visual count and size estimation of all fishes within 25 x 5 m underwater belt transects. Scientific divers were used to conduct these surveys and focused on all diurnal or day-active fish species.

This report includes the status and trends of the fish populations observed at Kalaupapa NHP from 2006–2015 as determined by implementation of the I&M PACN Marine Fish Monitoring Protocol (Brown et al. 2011a).

Spatial patterns for the fish data pooled across all transects indicated that:

- Fish species richness ranged from 11–45 per transect (125 m²) with a total of 151 species documented from 2006–2015. Overall mean richness was 27.2 ± 6.7 (Standard Deviation; SD) species per transect from 2006–2015. Transects with the highest species richness values were found near the northern tip and northeast side of the peninsula while the transect with the lowest species richness was found along the northwestern portion of the peninsula. Low species richness was also found along the southeastern portion of the peninsula to the easternmost boundary of the park.
- Fish species numerical density ranged from 0.3–7.4 fish m⁻². Overall mean was 1.6 ± 1.1 SD fish m⁻² from 2006–2015. Fish density was higher around the northern tip and northeast side of the peninsula, while the lowest fish densities were located along the eastern and western boundaries of the park at the base of the cliffs.
- Fish biomass estimates ranged from 4.1 to 2,733.4 grams (g) m⁻². Overall mean was 215.6 ± 186.7 SD g m⁻² from 2006–2015. Fish biomass was generally higher around the northern tip of the peninsula due to large predators such as bluefin trevally (*Caranx melampygus*), whitetip reef shark (*Triaenodon obesus*), and spotted eagle ray (*Aetobatus narinari*). One fixed transect

on the northwestern coast of the peninsula consistently had the lowest biomass over the last 10 years corresponding to low reef complexity.

- Fish diversity (H') ranged from 0.73 to 3.18 at all transects from 2006–2015. Overall mean was 2.24 ± 0.53 SD H' . Diversity was relatively uniform around the park, but slightly lower on the northern tip of the peninsula.

Vanderbilt's chromis (*Chromis vanderbilti*), a small planktivorous damselfish, was by far the most abundant species found at Kalaupapa from 2006–2015. It was eight times more abundant than the next most common species in the park, the rudderfish (*Kyphosus* spp), a primary consumer. Four of the top ten most abundant species by numerical density were primary consumers, and six were secondary consumers. Ten fish species made up 60.0% of the total fish biomass with *Kyphosus* spp. accounting for 21.2% of the total. Of the top ten species in terms of biomass, two were top predators, five were primary consumers, and three were secondary consumers.

Trends for the fish data indicated that:

- Mean fish species richness had similar levels at the start of the monitoring program in 2006 (27.0 ± 6.7 SD species) and at the end of the study period in 2015 (27.3 ± 6.7 SD) but the overall trend increased significantly due to increases observed since 2009. Temporary transects had on average 3.3 more species than fixed transects.
- Mean fish numerical density varied considerably from 2006 to 2015 and the overall trend for this time period was not statistically significant. Mean fish numerical density in 2006 was 1.8 ± 1.3 SD fish m^{-2} , was higher in 2013 at 2.3 ± 1.6 SD fish m^{-2} and then was lower at 1.2 ± 0.8 SD fish m^{-2} in 2015.
- Mean fish biomass increased significantly from 2006 to 2015 with temporary transects on average recording nearly 90 g m^{-2} more than the fixed transects. Average annual biomass among all transects ranged from 186.4 ± 167.5 SD g m^{-2} in 2009 to 253.4 ± 203.5 SD g m^{-2} in 2015.
- Mean fish diversity (H') ranged between 1.92 ± 0.64 SD in 2008 to 2.56 ± 0.38 SD in 2014. Diversity did show a significant increase from 2006 to 2015.
- Forty-six endemic fish species (30% of the total number of fish species) comprised 14.4% of the average fish numerical density and 6.4% of the total fish biomass. For the three most abundant species, numerical density of the saddle wrasse (*Thalassoma duperrey*) and the Hawaiian chromis (*Chromis ovalis*) decreased from 2006 to 2015 whereas the goldring surgeonfish (*Ctenochaetus strigosus*) increased. Biomass remained relatively stable for four of the top five endemic species except for *T. duperrey*, which increased. Other endemic species were excluded from the statistical analyses because of low numbers, which produced spurious results.
- Four invasive fish species (<3% of the total number of fish species), three introduced by humans and one recent colonizer, comprised 1.6% of the total fish numerical density and 6.2% of the total fish biomass. The two primary introduced species (bluestripe snapper [*Lutjanus kasmira*] and peacock grouper [*Cephalopholis argus*]) accounted for nearly 95% of the

invasive fish biomass. The patterns for the top two most frequently observed invasive species did not change from 2006–2015, but one introduced species, the blacktail snapper (*L. fulvus*), did show a significant increase in biomass since 2006. Historically, there was an early spread of invasive species from O‘ahu and Hawai‘i Island, but numerical density and biomass of these species appears to have stabilized and not increased in recent years at Kalaupapa NHP.

Factors influencing the fish assemblage.

- Direction of wave exposure at Kalaupapa was a significant predictor for species richness with 5.5 more species per transect on the northern tip of the peninsula compared to sites on the northwestern side. Fish numerical density and biomass were also higher at the northernmost sites than at sites on the western side of the peninsula, but not statistically different from other locations.
- Rugosity of the substrate appeared to be the strongest predictor for most of the fish assemblage metrics with higher topographic complexity associated with higher values for species richness and biomass.
- Percent coral cover also featured prominently in the fish assemblage with higher coral cover observed with higher fish species richness compared to lower coral cover with higher fish diversity.
- Positive relationships with the fish assemblage were documented for crustose coralline algae cover, site water pH, and minimum annual water temperature.
- Benthic species richness had a negative relationship with diversity.

Other factors discussed to explain the entire fish assemblage included physical disturbances (e.g., hurricanes, tsunamis, and wave climate), currents, and factors influenced by anthropogenic activities such as water quality and fishing pressure.

At present, the fish assemblage at Kalaupapa NHP appears to be improving and relatively healthy in terms of numerical density and biomass compared to other sites around the main Hawaiian Islands (MHI). Impacts from fishing pressure, however, are still evident in this remote section of Hawai‘i compared to areas around the Pacific that have not been overfished. Consequently, continued monitoring of the assemblage must be viewed in the context of a baseline that has shifted to an overfished state. This is a critical perspective given the impending changes in the climate and potential negative impacts on the coral reef ecosystem at Kalaupapa NHP from ocean warming and acidification. To continue improving the fish assemblage to a healthier state it is recommended that management actions include establishment of more marine protected or marine managed areas, banning certain gear types such as gill nets, and incorporating traditional knowledge and associated practices focused on spawning seasons and areas.

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List of Terms and Acronyms

KALA: Kalaupapa National Historical Park

km: kilometers

I&M: Inventory and Monitoring Program

m: meters

MHI: main Hawaiian Islands

NWHI: northwestern Hawaiian Islands

PACN: Pacific Island Network

SD: Standard Deviation

SE: Standard Error

Trophic groups: groups of fish classified by nutritional habits and requirements

Introduction

The marine fish assemblages in the Pacific Island Network (PACN) of U.S. National Parks are ecologically diverse with numerous trophic groups intertwined within extensive coral reef ecosystems. In most tropical marine parks, coral reefs form the geomorphologic framework of the ecosystem. These ecosystems have been compared to tropical rainforests because of their high species diversity and complex interactions (Connell 1978, Birkeland 1997). Because of their importance ecologically, culturally, and economically, it is critical that parks have scientifically rigorous data on the current health and long-term trends of the marine fish assemblages within their boundaries. Within coral reefs, marine fishes are one of the most visible and certainly the most exploited resource.

Coral reef fish assemblages are essential to the traditional lifestyles and cultures of Hawaiian, Samoan, Chamorro, Carolinian and other peoples in the islands throughout the Pacific (Kittinger 2013). Furthermore, coral reef fishes provide critical elements of commerce from local and charter-sport fishing, as well as other visitor recreational activities (e.g., snorkeling, scuba diving, and boating), which are major economic drivers throughout the Pacific islands (Cesar et al. 2002, Waddell 2005). Because of the ecological, cultural, and economic importance of these assemblages, it is critical that the Pacific Island parks with marine areas continue to collect scientifically rigorous data on the current health and long-term trends of these crucial fish communities as well as their associated habitats.

The Pacific Island Network (PACN) is one of 32 National Park Service (NPS) Inventory and Monitoring (I&M) Networks across the country facilitating collaboration, information sharing, and economies of scale in natural resources monitoring. The NPS I&M program was funded by Congress in 1998 to implement peer-reviewed standardized protocols to collect data on numerous Vital Signs for natural resources. A Vital Sign is an indicator of physical, chemical, biological elements, or ecosystem processes selected to represent the overall health or condition of natural resources within parks. The PACN marine fish Vital Sign is closely linked with the benthic marine Vital Sign, and monitoring efforts are co-located and sampled at the same time to maximize data value (Brown et al. 2011a). This Vital Sign monitoring protocol is implemented in four parks: Kaloko-Honokōhau National Historical Park, Kalaupapa National Historical Park, National Park of American Samoa, and War in the Pacific National Historical Park.

Kalaupapa National Historical Park is located in Hawai‘i on the north shore of the island of Moloka‘i, and encompasses not only submerged marine resources, but also lowland coastal, mesic, and rainforest habitats (Figure 1). This park is one of the few in the NPS system that includes entire watersheds and their adjacent nearshore marine habitats within its boundaries. The park preserves and interprets the history and story of the Kalaupapa settlement and Hansen’s disease patients, but public visitation is restricted by state permit to 100 people per day. Encompassing approximately 2,000 ac (809 hectares), the marine boundary of the park extends from the shoreline to a quarter mile (0.4 km) offshore, where waters are about 33 m deep. Significant marine resources include threatened (green sea turtle [*Chelonia mydas*]) and endangered (monk seal [*Monachus*

schauinslandi], humpback whale [*Megaptera novaeangliae*]) species, high wave energy coral reef communities, and relatively intact marine intertidal and fish resources. The hard-bottom substrate consists of basalt pavement and boulders colonized by coral communities with <25% coral cover (Fung Associates, Inc. and SWCA Environment Consultants 2010). Sandy bottoms extend out from the rivers draining the three principal watersheds within the park. Several offshore islands within the park boundaries also contain relatively intact marine assemblages typical of vertical, exposed coastlines (Coles et al. 2008). The primary physical disturbance to the marine community consists of large (8 to 10 m) northwest Pacific swells in the winter months (October–April) (Fung Associates, Inc. and SWCA Environment Consultants 2010).

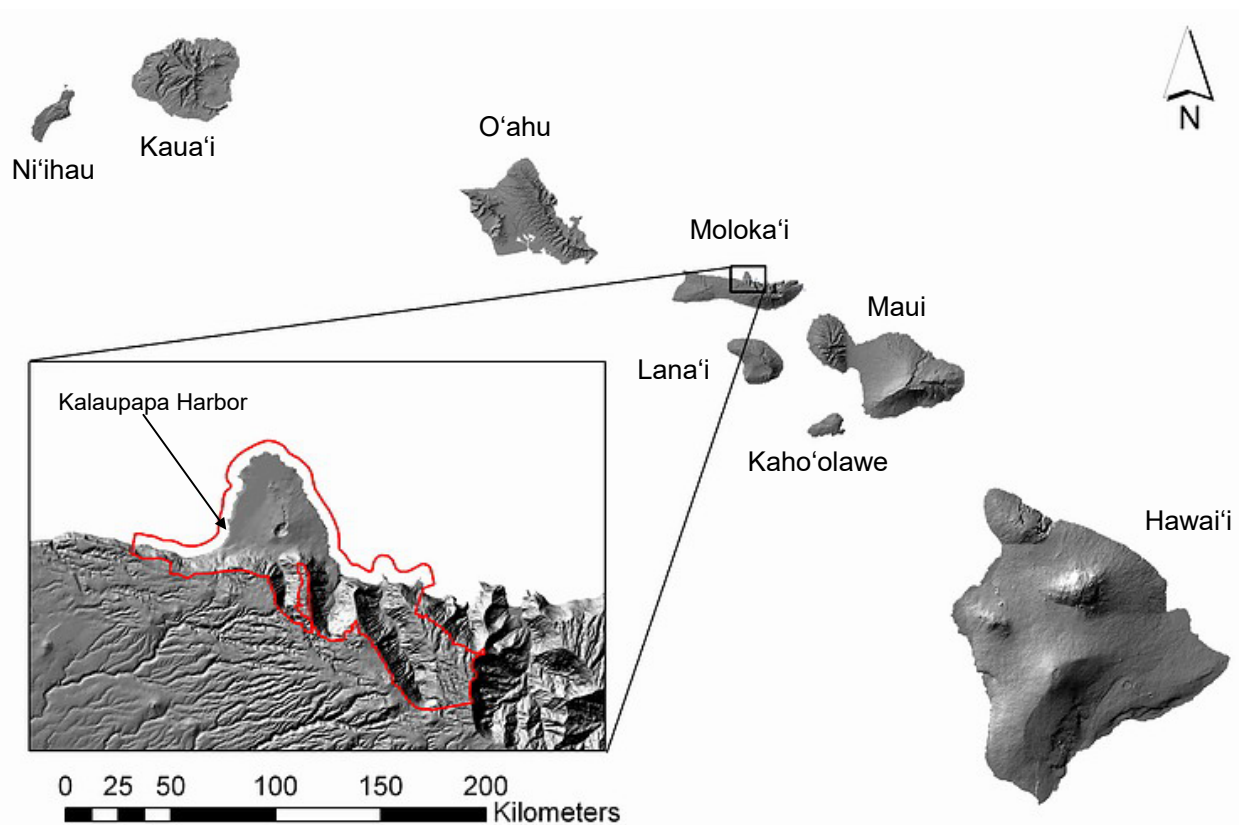


Figure 1. Map of the main Hawaiian Islands (MHI) showing Kalaupapa National Historical Park with the park boundary delineated as a red line in the inset.

The initial source of information on fish assemblages at Kalaupapa NHP is from Beets et al. (2010) who surveyed the reefs from 2004 to 2005. Their data on species richness, numerical density, biomass, and diversity was the first known study to document fish habitat utilization patterns within the park boundaries. Beets et al. (2010) reported that Kalaupapa NHP had the fish species most commonly found in Hawai'i with high fish density and biomass compared to other areas around the state. More recently, Coles et al. (2008) surveyed the offshore islands in and around the park for unique fish species, numerical density levels, biomass, and diversity. Reef Environmental Education Foundation (REEF; www.reef.org) also has two sites on the north coast of Moloka'i that provide

species checklist information in similar habitats to the park. The most comprehensive study to date by Friedlander et al. (2018) uses the data included in this report as part of a larger study comparing fish assemblages across the main Hawaiian Islands. The two areas with the highest fish biomass in the state are the north shore of Molokaʻi within the park boundaries, and around the island of Kahoʻolawe (Friedlander et al. 2018).

The methodology to monitor coral reef fishes has been developed over the past 25 years, resulting in several commonly used survey techniques (e.g., Bohnsack and Bannerot 1986, Rogers et al. 1994, English et al. 1997, Samoilys 1997, Sweatman et al. 1998, Atlantic and Gulf Rapid Reef Assessment 2000, Hill and Wilkinson 2004). The technique adopted to collect scientifically rigorous data on the status and long-term trends of the fish communities for PACN consisted of a visual count and size estimation of fish by scientific divers along underwater 25 m x 5 m belt transects (Brown et al. 2011a). This non-destructive technique initiated in 2006 addressed one primary monitoring question; what are the long-term trends in the numerical density, biomass, and size of reef fishes in a park? The objective of the monitoring protocol is to annually determine the density, biomass, and size of one major component of the coral reef fish community—the diurnal or day-active fish species that are highly visible due to their mobile behavior and generally larger size. These species are the most heavily targeted by local fishers. While the small, cryptic or nocturnal species contribute to biodiversity and may be of ecological or management importance, the additional effort and time required to sample these fishes is not feasible with available resources in a park. The sampling frame for this protocol is hard substrata between the 10 and 20 meter depths (selected for both ecological and safety reasons).

The visual estimate of fish size is an important component of these surveys for several reasons. First, lengths allow a conversion from fish numbers to biomass by using established length-weight relationships (e.g., Friedlander et al. 2007). Second, lengths are often a useful indicator of fishing pressure or population dynamics, e.g., a trend of decreasing sizes may indicate overfishing, or recruitment year classes (Bejarano et al. 2013). Third, there is a strong positive correlation between fish size and fecundity (reproductive potential) which, along with recruitment success, is important in assessing ecological services provided by park fish assemblages (Saenz-Aquedelo et al. 2015).

Fishing is allowed in Kalaupapa NHP, but State of Hawaiʻi laws and County of Kalawao community rules regulate resource use within the park’s marine waters (National Park Service, 2015). NPS law enforcement rangers, who are also deputized in the County of Kalawao, enforce these laws and community rules. The rules and regulations listed below vary depending on whether the fisher is a Hansen’s disease patient, employee resident, or visitor/guest. Overall, fishing pressure at Kalaupapa NHP is considered lighter than at other locations around the MHI (Tom 2011, Friedlander et al. 2018).

Hansen’s disease patients are exempt from state laws regarding gear type, seasonal closure, bag limits and size limits. Community sentiment, however, does oppose the sale of any fisheries catch, especially outside of the settlement.

State and federal employees at Kalaupapa must follow state laws for seasonal closures, bag limits, gear types, and size limits. Employee residents are allowed to subsistence fish and take fish out for their families but are discouraged from selling their catch. Community rules specifically prohibit employees from scuba diving except on behalf of the NPS marine research program.

Visitors on boats may legally fish and even travel within the park boundaries, but this is discouraged unless they are sponsored by patients or employee residents of Kalaupapa. Regardless of sponsorship, they must still follow state laws regarding seasonal closures, bag limits, gear types, and size limits. These fishing practices by people outside of the settlement, however, are discouraged by patients and employee residents and viewed as disrespectful of the stewardship ethic that is currently in place. It should be noted that commercial activities within the park boundary, such as charter dive boats and fishing vessels, must adhere to the park's enabling legislation which states that patients have a "first right of refusal to provide revenue-producing visitor services" (State of Hawai'i Public Law 96-565, Section 107). Sponsored visitors on boats who do come ashore have to follow the same rules and regulations as visitors who arrive by plane or on land (See "Onshore visitors" below).

Onshore visitors must have a park-based sponsor and are more tightly regulated than patients, government employees, or boat visitors. They may only pole and line fish from shore. They may not use nets or spears, pick intertidal invertebrates, or scuba dive at any point within the park. The Kalaupapa Patient Advisory Council instituted the rule to limit outside visitors from most fishing activities and picking intertidal invertebrates (Langlas et al. 2008). An additional rule for visitors is that they can fish within the settlement without an escort but going outside of the settlement requires a patient or employee resident escort. Violators of these rules are banned from future visits. Even though it is not a community rule or state law, patients and employee residents prefer that any fishery resources caught within the park be consumed at Kalaupapa.

The purpose of this report was to examine the changes in the marine fish assemblage at Kalaupapa NHP from 2006 to 2015. First, an overview of fish assemblage characteristics from 2006 to 2015 is presented for species richness, density, biomass, and diversity using spatial distribution maps. Second, the trophic composition of the entire assemblage averaged over the study period was examined for both density and biomass. Third, the top ten species from 2006 to 2015 in terms of density and biomass were listed to examine specific components of the assemblage. Fourth, trends in the entire assemblage from 2006–2015 were plotted for species richness, density, biomass, and diversity. Fifth, temporal patterns for endemic and invasive fish species were examined in terms of fish density and biomass. Finally, factors influencing the fish assemblage characteristics were examined. It should be noted that there are no endangered or threatened marine fish species reported from Hawai'i (U. S. Fish Wildlife Service 2015).

Methods

Sampling Locations

A split panel design was used with 30 belt transects (25 m long x 5 m wide) sampled annually between 2006 and 2015 (Brown et al. 2011a). All transects were randomly selected using ArcGIS® within the Kalaupapa NHP sampling frame (Figure 2). The frame includes all fore-reef slope, hard-bottom communities between 10 and 20 m depths within the park's legislated boundaries plus adjacent coastal areas that may impact (or be impacted by) the park. The sampling frame was restricted to the depth contours above for safety, logistical, and cost reasons recognizing that many shallow water reef areas in Hawai'i harbor high biomass levels of targeted reef species (Brown et al. 2011). Fifteen fixed (permanent) transects were randomly selected at the onset of the monitoring program in 2006 and marked with stainless steel pins for relocation purposes. These sites were subsequently sampled each year. The remaining 15 temporary transects were randomly selected each year of monitoring and sampled only once. Transects were located in the field using a GPS unit.

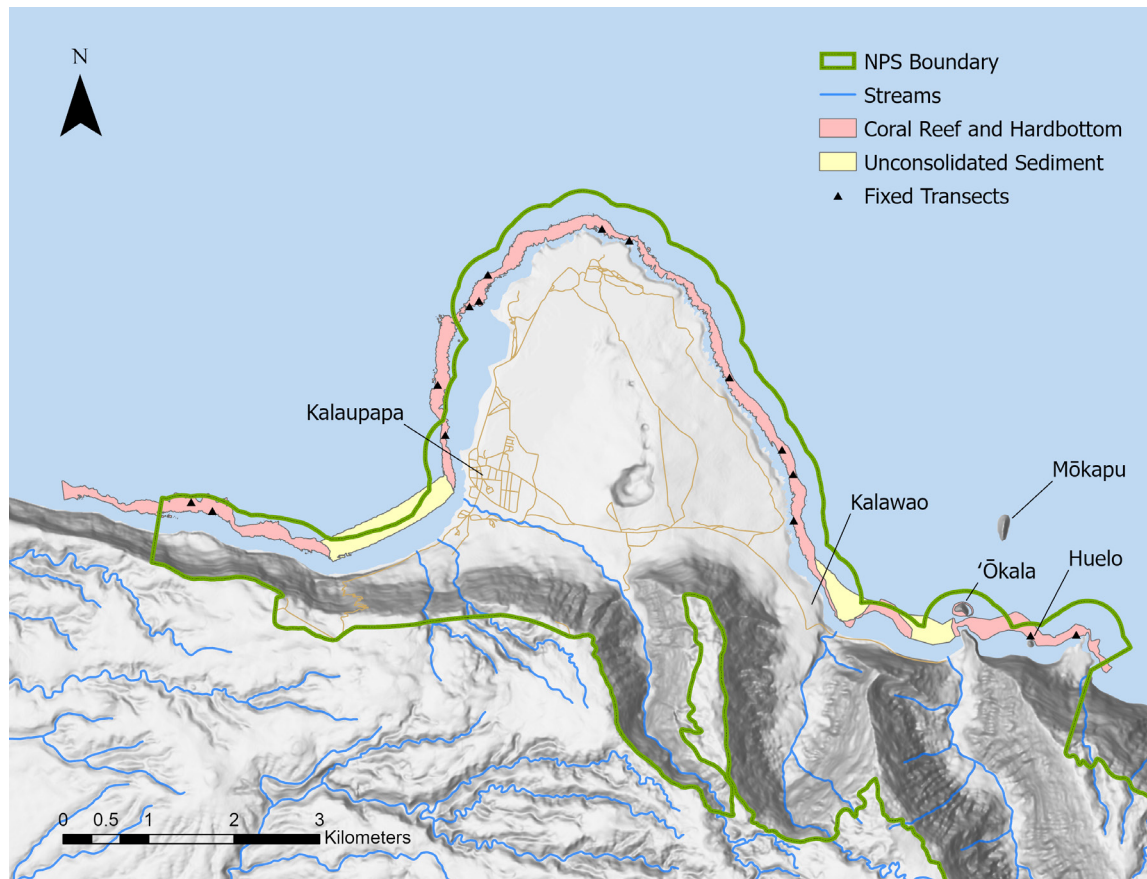


Figure 2. Sampling frame between 10 m and 20 m depth on hard-bottom substrate (light pink polygon) at Kalaupapa National Historical Park. Sand habitat is shown by yellow polygons. Green line indicates park boundary including ¼ mile (0.4 km) into the marine environment.

Survey Methods

Fish surveys occurred during the summer months from July through August in concurrence with the benthic and water quality protocols. At each site, the fish observer, using SCUBA, deployed a transect line along a constant depth contour which was typically parallel to shore. The observer counted and estimated the total length (to the nearest centimeter) of all fishes encountered along the distance of this transect from the bottom to the surface in the 5 m wide belt. Data were recorded on pre-printed waterproof forms attached to a slate. The location, bearing, survey date, and depth of transects, which constituted the sampling unit, were recorded after each dive. Total area sampled on each transect was 125 m² for a total area of 3750 m² across all 30 transects each year. Only one fish observer (Eric Brown) recorded data from 2006–2015.

Data Analysis

Fish species richness for each transect was calculated by summing the number of different species observed per transect area (125 m²).

Fish numerical density at each transect was calculated as the total number of fish observed within each transect area of 125 m². This value was converted to number per square meter (no. m⁻²) to facilitate comparisons with other studies.

Length estimates of fishes were converted to biomass using the following length-mass relationship derived for each species: $\text{Mass} = a * (\text{Fork Length})^b$ where a and b are species-specific constants for the allometric growth equation, fork length (FL) is in centimeters, and mass is in grams (Kulbicki et al. 1993, Friedlander et al. 2003). Total length was converted to FL using conversion factors obtained from FishBase (www.fishbase.org). Length–mass fitting parameters were available for 150 species commonly observed on visual fish transects in Hawai‘i from the Hawai‘i Cooperative Fishery Research Unit (Friedlander et. al., 1997). This was supplemented with information from other published and web-based sources (Appendix A). In the cases where length–mass information did not exist for a given species, the parameters from similar bodied congeners are used. Biomass estimates for each transect were converted to grams per square meter (g m⁻²) to facilitate comparisons with other studies worldwide.

The Shannon-Wiener index (H') was used to calculate species diversity within each transect using the following formula:

$$H' = - \sum_{i=1}^S (p_i \ln p_i)$$

where S is the total number of species and p_i is the frequency of the i th species in that transect (Krebs 1999).

To determine the trophic composition of the fish assemblage, each species was classified as a primary consumer, secondary consumer, or top predator. In a coral reef ecosystem, primary consumers such as surgeonfishes and parrotfishes consume primary producers such as phytoplankton, algae, and sea grasses. Primary consumers were further delineated into functional feeding guilds of browser, farmer, grazer, and scraper/excavator. Secondary consumers include larger

reef fishes such as triggerfishes and wrasses that feed on the primary consumers as well as producers. Planktivores were separated out of this group for the graphical display since planktivores have different spatial patterns over reef communities compared to other secondary consumers and their response to disturbances provides insights into ecosystem function. Tertiary consumers or top predators are the top of the food chain and include sharks, groupers, jacks, and the larger snappers. Information on fish trophic group classifications was obtained from Friedlander et al. (1997), FishBase, and other web-based sources.

A panel linear mixed model in the R statistical software (ver. 4.0.3, *plm* in the *plm* package) was used for trend estimation of fish species richness, density, biomass, and diversity (R Core Team 2020). To meet the assumptions of normality, data were transformed using a square root ($\sqrt{x}$) transformation for density and a $\log(x+1)$ transformation for biomass (Zar 1999). The raw data for species richness and diversity were used in the analysis since the error was normally distributed for these data. The main fish assemblage characteristics (fish species richness, density, biomass, and diversity) were analyzed separately in the panel linear mixed model as the dependent variables. For each fish assemblage characteristic, a fixed and random effects model was run and compared using a Hausman test for panel models (*phptest* in the *plm* package). The null hypothesis is that the preferred model is the random effects model. A p-value less than 0.05 rejects the null hypothesis and chooses the alternative fixed effects model.

To incorporate the split panel design into the panel analysis, a unique identifier for transect number was treated as a random site effect. Fixed transects were labeled 1–15 and repeated every year. Temporary transects were labeled 16–30 in 2010 and then incremented sequentially in subsequent years (e.g., 31–45 in 2011, 46–60 in 2012, etc.). This approach incorporated both fixed and temporary transects to examine temporal patterns for trend estimation with increased spatial distribution for robust status estimation (Starceovich 2013). Transect type (fixed, temporary) was also included in the model as a fixed effect to evaluate any overall differences between panels. The structure of the data, however, did not allow for estimation of any interaction terms to evaluate the relationship between transect type and year. In future years with a larger data set, it may be informative to conduct additional analyses with just fixed or temporary transects or comparisons between the transect types to examine the measurement effects of sampling in the same location compared to new areas. This analysis was not conducted in the present study due to the small data set.

Trends in numerical density and biomass for the top three endemic species (Numerical density: *Thalassoma duperryi*, *Ctenochaetus strigosus*, *Chromis ovalis*, Biomass: *Chlorurus perspicillatus*, *Ctenochaetus strigosus*, *Parupeneus porphyreus*) and top three invasive fish species (*Cephalopholis argus*, *Lutjanus fulvus*, *Lutjanus kasmira*) were examined using the panel linear mixed model approach described above. Each species was analyzed separately with a $\sqrt{x}$ transformation for density and a $\log(x+1)$ transformation for biomass. Other endemic species as well as a fourth invasive fish species (*Abudefduf vaigiensis*) were excluded from the statistical analyses because of low numbers, which produced spurious results.

Temporal autocorrelation was examined post hoc by assessing the homogeneity of random effects groups using paired plots of the site effects for each year. The slopes of the random sites were plotted against random site intercepts by year and included both fixed and temporary transects. The patterns for the fixed transects displayed no obvious relationship, but a linear relationship did exist for the temporary transects. This result for the temporary transects, however, may be due to the lack of replication for a given site, so it is reasonable to assume independence among years and temporary sites (Piepho and Ogutu 2002). Overall, the results indicated that the assumptions were met, and that autocorrelation was not a significant issue.

The importance of various independent variables on fish assemblage characteristics (species richness, density, biomass, and diversity) was investigated using a generalized additive mixed model in R (ver. 4.0.3, *gamm* in the *mgcv* package). The *gamm* is similar to a generalized linear mixed model, but the package uses smoothing functions to explore non-linearity in the relationships with no *a priori* assumptions (Wood 2019). The continuous predictors were entered into the model as spline smoothed terms with $k = 5$ dimensions. The model variables are listed below in Table 1.

Wave exposure for each site was visually determined by the shoreline angle to the prevailing swells and wave climate described by Moberly and Chamberlain (1964). Percent benthic cover data and benthic species richness were acquired from the NPS I&M benthic protocol described in Brown et al. (2011b, 2014). Rugosity is a dimensionless index of spatial relief and the methodology is described by Brown et al. (2014). Hourly benthic temperature data were obtained from two sites (21.1938, -156.9869; 21.1843, -156.9477) at 12 m depth on either side of the Kalaupapa peninsula using Onset data loggers (NPS, unpublished data). Minimum, average, and maximum temperatures were calculated for each year to integrate what the fish assemblages were experiencing on an annual basis. Survey date abiotic parameters (Temperature, pH, salinity, turbidity, dissolved oxygen, chlorophyll) were collected using a YSI 6600 multiparameter sonde following the I&M water quality protocol (Jones et al. 2011). Water quality sampling did not begin until 2008 and no samples were collected in 2012 due to equipment failure. Other socio-economic predictors (e.g., fishing pressure, distance to market, management type, level of economic development) were considered for the model, however, the resolution or spatial scale of the study area was not sufficient to differentiate among sites. Year of sampling (2006–2015) and transect number were entered in the model as random effects. The transect number was given a unique identifier in the same manner as in the panel linear mixed model setup to differentiate between fixed and temporary transects. For the dependent variables, raw species richness and the derived diversity (H') values were used, numerical density was transformed using a square root ($\sqrt{x}$) transformation and a $\log(x+1)$ transformation was applied to biomass to meet the assumptions of a normal error distribution. Statistical significance was evaluated at $\alpha = 0.05$.

Table 1. Generalized additive mixed model design to examine the influence of various predictor variables on fish species richness, density, biomass, and diversity.

Predictor variable	Type	Effect	Transformation
Wave exposure (Levels: NW swell, NE swell, Both)	Categorical	Fixed	None
Coral cover (%)	Continuous	Fixed	Arcsine-square root
CCA cover (%)	Continuous	Fixed	Arcsine-square root
Macroalgae cover (%)	Continuous	Fixed	Arcsine-square root
Turf algae cover (%)	Continuous	Fixed	Arcsine-square root
Depth (m)	Continuous	Fixed	None
Benthic species richness (# of spp transect ⁻¹)	Continuous	Fixed	None
Rugosity (See Brown et al. 2014)	Continuous	Fixed	None
Minimum annual temperature (°C)	Continuous	Fixed	None
Average annual temperature (°C)	Continuous	Fixed	None
Maximum annual temperature (°C)	Continuous	Fixed	None
benthic temperature (°C)	Continuous	Fixed	None
benthic pH (0–14)	Continuous	Fixed	None
benthic salinity (‰)	Continuous	Fixed	None
benthic turbidity (FNU)	Continuous	Fixed	None
benthic dissolved oxygen (% saturation)	Continuous	Fixed	None
benthic chlorophyll ($\mu\text{g l}^{-1}$)	Continuous	Fixed	None
Year (2006–2015)	Continuous	Random	None
Transect (1–15 fixed, 16–165 temporary)	Continuous	Random	None

It is anticipated that in future versions of this report, size-spectra analysis and multivariate approaches (PERMANOVA, PCO, RDA, etc.) will be utilized to help elucidate the drivers of temporal changes in the fish assemblages. At present, however, the focus of this report is on the general patterns and trends to lay the foundation for future analyses.

Spatial distribution figures were generated in ArcGIS Pro v. 2.4.0 using an Inverse Density Weighted (IDW) analysis with a variable search radius and an exponential distance power of two. Twelve of the nearest input sample points were used with an output cell size of 10 and the results were clipped to the extent of the NPSA interpolation area.

Results

A total of 15 fixed (once each year) and 150 temporary transects (total all years) were surveyed at Kalaupapa National Historical Park from 2006–2015. The queries used to retrieve the data for the ArcGIS maps, charts, and statistical analyses are listed in Appendix B.

Status of Fish Assemblage Characteristics

Fish species richness ranged from 11 to 45 species per transect (125 m²) from 2006 to 2015 with a total of 151 species found around the park (Figure 3, Appendix A). The overall average species richness was 27.2 ± 6.7 SD fish species per transect. Transects with the highest species richness values (e.g., temporary transect 8 in 2007) were found at the northern tip and northeast side of the peninsula while the transect with the lowest species richness (i.e., fixed transect 6 in 2006 and 2007) was found along the northwestern portion of the peninsula. Pockets of low species richness were also found along the southeastern portion of the peninsula to the eastern edge of the park.

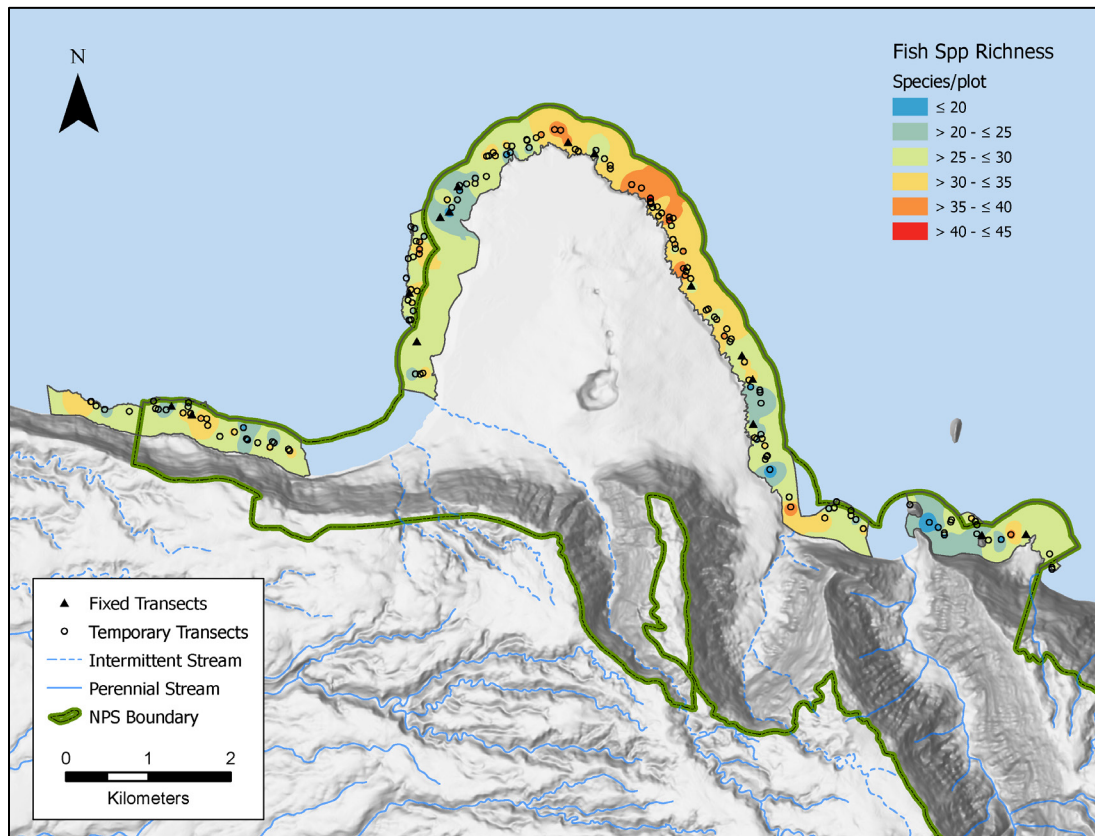


Figure 3. Fish species richness (no. 125 m²) at the 15 fixed sites (averaged over 10 years) and 150 temporary sites surveyed in Kalaupapa National Historical Park from 2006–2015 (N = 300 total transects represented by black dots). Contour plots include the hard-bottom sampling frame and other habitats to visually accentuate the spatial patterns and are not intended as realistic representations of actual distributions. The legend displays the range of species richness values at equally spaced intervals. Shoreline areas excluded are soft bottom habitats outside of the sampling frame.

The numerical density of fishes at all transects from 2006 to 2015 ranged from 0.3–7.4 fish m⁻² (Figure 4) with an overall average of 1.6 ± 1.1 SD fish m⁻². Transects with the highest densities (e.g., fixed transect 5 in 2006) were concentrated near the northeastern portion of the peninsula. The lowest densities (e.g., temporary transect 13 in 2009) were located near the eastern and western boundaries of the park at the base of the cliffs.

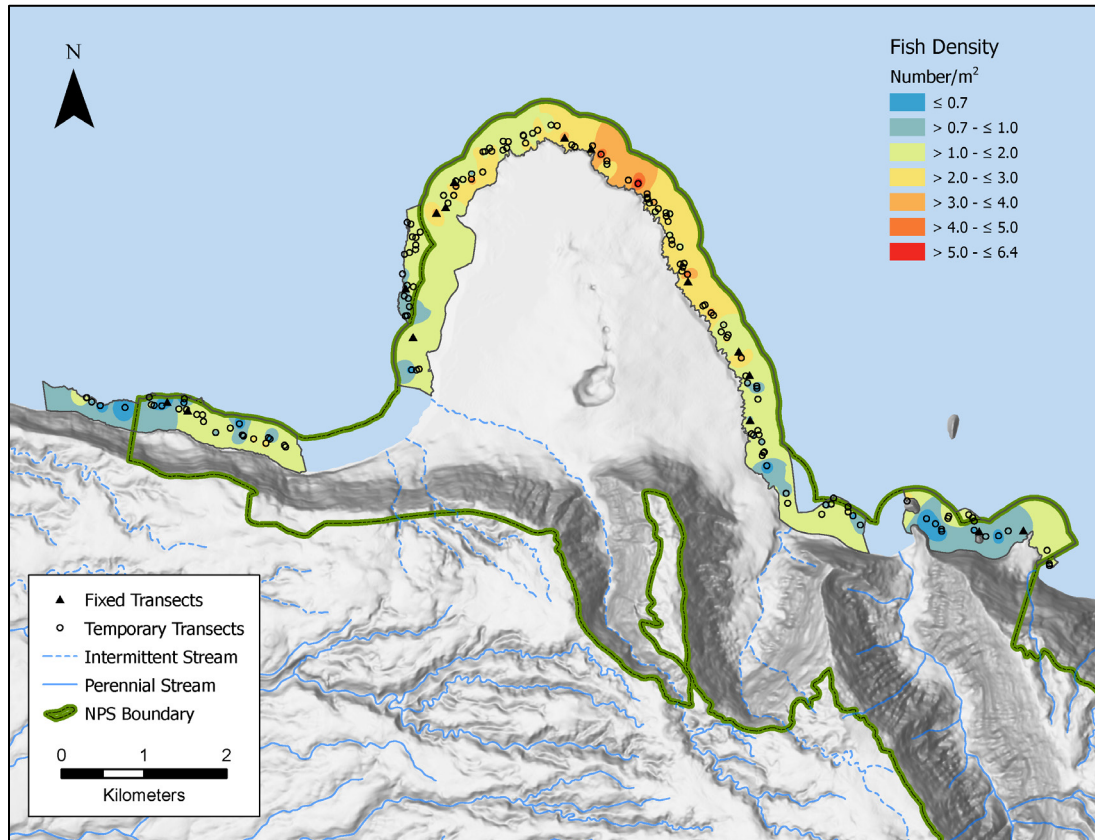


Figure 4. Fish numerical density (no. m⁻²) at the 15 fixed sites (averaged over 10 years) and 150 temporary sites surveyed in Kalaupapa National Historical Park from 2006–2015 (N = 300 total transects represented by black dots). Contour plots include the hard-bottom sampling frame and other habitats to visually accentuate the spatial patterns and are not intended as realistic representations of actual distributions. The legend displays the range of species richness values at equally spaced intervals. Shoreline areas excluded are soft bottom habitats outside of the sampling frame.

Fish biomass ranged between 4.1 and 2,733.4 g m⁻² at all transects from 2006 to 2015 and averaged 215.6 ± 186.7 SD g m⁻² (Figure 5). Fixed transect 6, located along the northwestern coast of the peninsula, had the lowest biomass in 2007 at just 4.1 g m⁻². In comparison, fixed transect 9, located on the northern tip of the peninsula, had the highest biomass at 2,733.4 g m⁻² in 2015. Fixed transect 8 in 2011, also located on the northern tip of the peninsula, had a high biomass level of 2,244.8 g m⁻². In both cases the high biomass was due to a few, large individuals recorded on transect 9 (two *Trienodon obesus*, whitetip reef shark) and transect 8 (one *Aetobatus narinari*, spotted eagle ray).

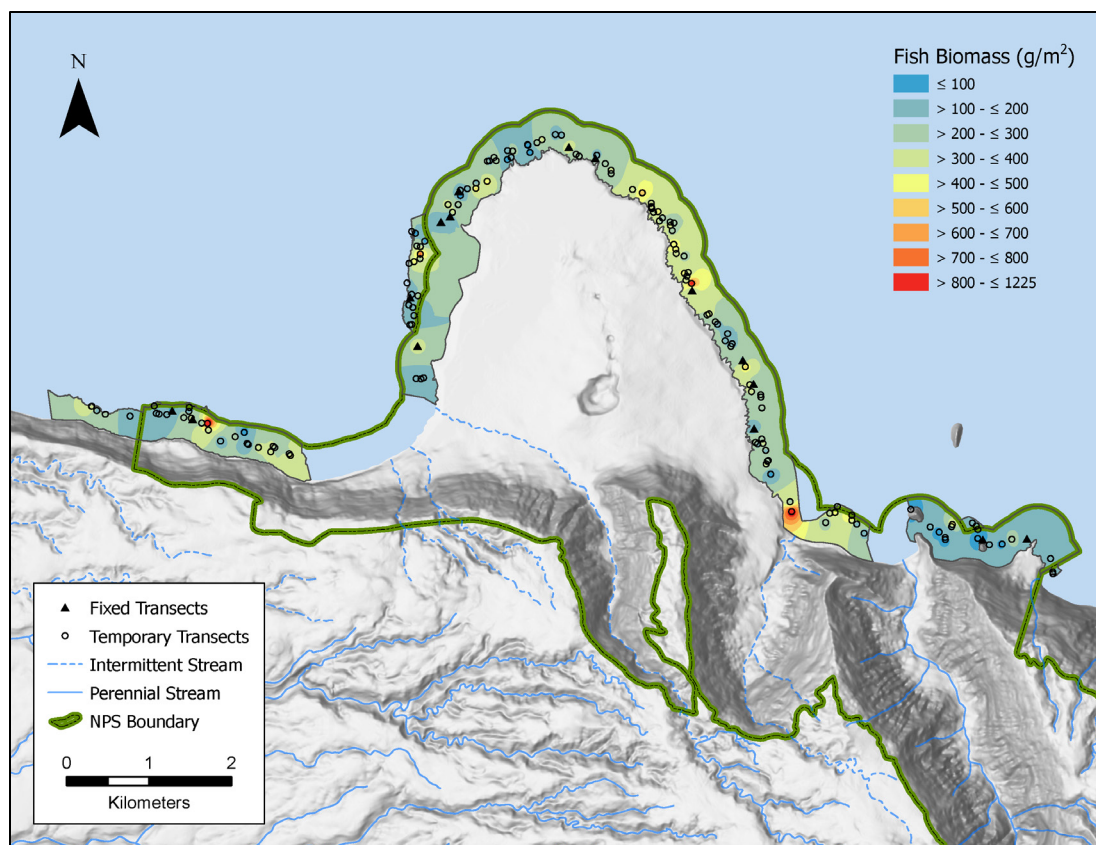


Figure 5. Fish biomass (g m^{-2}) at the 15 fixed sites (averaged over 10 years) and 150 temporary sites surveyed in Kalaupapa National Historical Park from 2006–2015 ($N = 300$ total transects represented by black dots). Contour plots include the hard-bottom sampling frame and other habitats to visually accentuate the spatial patterns and are not intended as realistic representations of actual distributions. The legend displays the range of species richness values at equally spaced intervals. Shoreline areas excluded are soft bottom habitats outside of the sampling frame.

Fish diversity (H') ranged from 0.73 to 3.18 at all transects from 2006 to 2015 (Figure 6). The overall average diversity was $2.24 H' \pm 0.53 \text{ SD}$. Temporary transect 5, which was surveyed in 2008 on the northwestern portion of the peninsula had the lowest species diversity at 0.73 H' . In contrast, fixed transect 15 on the far eastern edge of the park boundary had the highest species diversity at 3.18 in 2013. Diversity was relatively uniform around the park, but slightly lower on the northern tip of the peninsula.

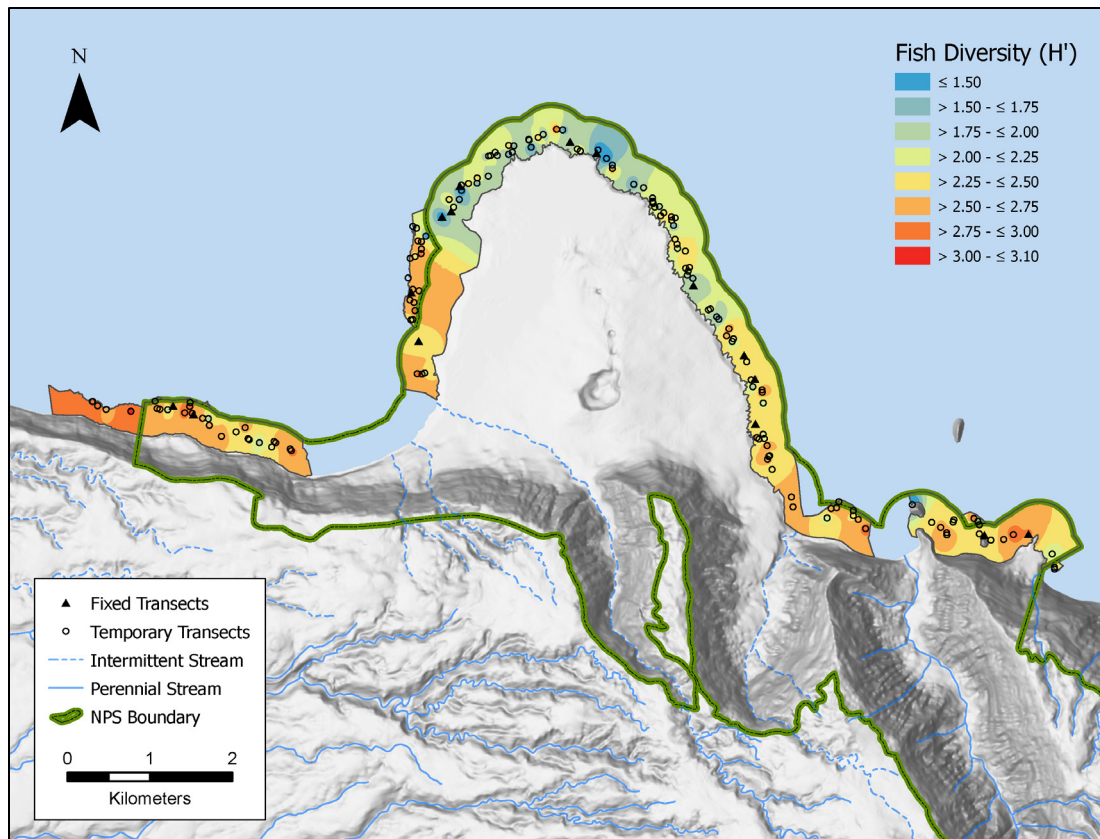


Figure 6. Fish diversity (H') at the 15 fixed sites (averaged over 10 years) and 150 temporary sites surveyed in Kalaupapa National Historical Park from 2006–2015 ($N = 300$ total transects represented by black dots). Contour plots include the hard-bottom sampling frame and other habitats to visually accentuate the spatial patterns and are not intended as realistic representations of actual distributions. The legend displays the range of species richness values at equally spaced intervals. Shoreline areas excluded are soft bottom habitats outside of the sampling frame.

Trophic Composition of the Fish Assemblage

The average trophic composition of the fish assemblage at Kalaupapa NHP from 2006 to 2015 varied in terms of numerical density and biomass. Secondary consumers accounted for approximately 74% of the fish numerical density observed during surveys from 2006–2015, with top predators accounting for 1%, and primary consumers making up the remaining 25% (Figure 7). Planktivores comprised 50% of the total numerical density with 24% as other secondary consumers. In comparison, the relative biomass of secondary consumers was only 28% (6% Planktivores, 22% Other secondary consumers), compared to 10% for top predators and 62% for primary consumers (Figure 7).

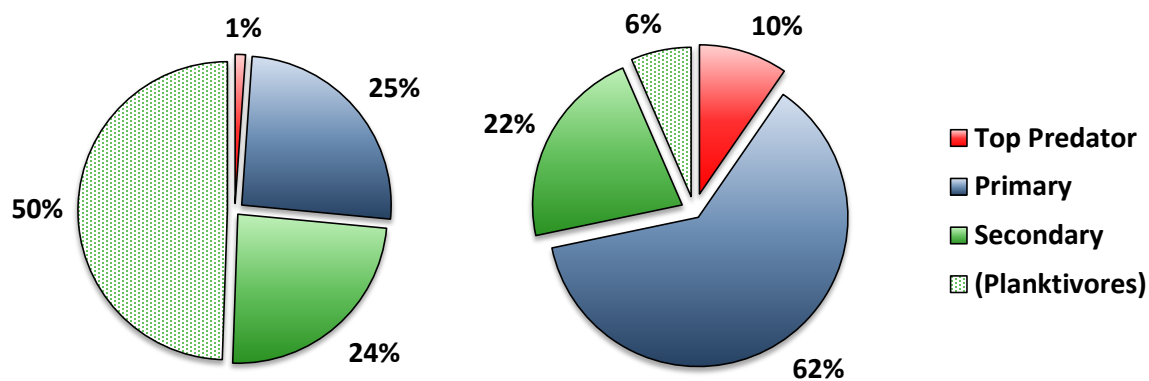


Figure 7. Percentage of fish consumer groups by numerical density (no. m^{-2}) (left) and biomass (g m^{-2}) (right) at Kalaupapa NHP averaged from 2006–2015. Note that Planktivores are broken out from the other Secondary Consumers.

Top Ten Fish Species

In terms of numerical density, *Chromis vanderbilti*, a small planktivorous damselfish, was by far the most abundant species found at Kalaupapa from 2006–2015 with 0.65 m^{-2} documented (Table 2). It was eight times more abundant than the next most common species in the park, the primary consumer *Kyphosus* spp (0.09 m^{-2}), a member of the rudderfish (Kyphosidae) family. The bulk of the biomass, however, was accounted for by *Kyphosus* spp. (53.4 g m^{-2}), a primary consumer, followed by the secondary consumer, the Hawaiian hogfish, *Bodianus alboteniatus* (12.6 g m^{-2}), and another primary consumer, the eye-stripe surgeonfish, *Acanthurus dussumieri* (11.5 g m^{-2}) (Table 3). Six of the top ten most abundant species by numerical density were secondary consumers, while four were primary consumers. The top ten most abundant species by biomass were composed of seven primary consumers, two secondary consumers, and one top predator.

Table 2. Top ten fish species by numerical density (no. m⁻²) at Kalaupapa National Historical Park averaged over the study period from 2006 to 2015. Common and Hawaiian names are from Randall (2010). Herbivore codes from Fishbase and other web-based sources: BR=browser, FA=farmer, GR=grazer, SC=scrapper.

Species	Common Name	Hawaiian Name	Consumer Group	Feeding Guild	Num. Density (no. m ⁻²)
<i>Chromis vanderbilti</i>	blackfin chromis	unknown	Secondary	Planktivore	0.65
<i>Kyphosus</i> spp.	rudderfish	nenu	Primary	Herbivore/GR	0.09
<i>Acanthurus leucopareius</i>	whitebar surgeonfish	māikoiko	Primary	Herbivore/BR	0.08
<i>Acanthurus nigrofusus</i>	brown surgeonfish	mā'i'i'i	Primary	Herbivore/GR	0.07
<i>Thalassoma duperrey</i>	saddle wrasse	hinālea lauili	Secondary	Mobile Invert	0.05
<i>Acanthurus triostegus</i>	convict surgeonfish	manini	Primary	Herbivore/GR	0.05
<i>Paracirrhites arcatus</i>	arc-eye hawkfish	piliko'a	Secondary	Mobile Invert	0.05
<i>Ctenochaetus strigosus</i>	goldring surgeonfish	kole	Secondary	Detritivore	0.05
<i>Chromis ovalis</i>	oval chromis	unknown	Secondary	Planktivore	0.04
<i>Naso hexacanthus</i>	sleek unicornfish	kala holo	Secondary	Planktivore	0.03

Table 3. Top ten fish species by biomass (g m⁻²) at Kalaupapa National Historical Park averaged over the study period from 2006 to 2015. Common and Hawaiian names are from Randall (2010). Herbivore codes from Fishbase and other web-based sources: BR=browser, FA=farmer, GR=grazer, SC=scrapper.

Species	Common Name	Hawaiian Name	Consumer Group	Feeding Guild	Biomass (g m ⁻²)
<i>Kyphosus</i> spp.	rudderfish	nenu	Primary	Herbivore/GR	53.4
<i>Bodianus albotaeniatus</i>	Hawaiian hogfish	'a'awa	Secondary	Mobile Invert	12.6
<i>Acanthurus dussumieri</i>	eye-stripe surgeonfish	Palani	Primary	Herbivore/BR	11.5
<i>Acanthurus olivaceus</i>	orangeband surgeonfish	na'ena'e	Primary	Herbivore/GR	9.8
<i>Scarus rubroviolaceus</i>	redlip parrotfish	palukaluka	Primary	Herbivore/SC	9.7
<i>Acanthurus leucopareius</i>	whitebar surgeonfish	māikoiko	Primary	Herbivore/BR	9.2
<i>Naso unicornis</i>	bluespine unicornfish	kala	Primary	Herbivore/BR	8.8
<i>Naso lituratus</i>	orangespine unicornfish	umaumalei	Primary	Herbivore/BR	8.3
<i>Naso hexacanthus</i>	sleek unicornfish	kala lōlō	Secondary	Planktivore	7.4
<i>Cephalopholis argus</i>	peacock hind	roi	Top	Piscivore	6.7

Trends in Fish Assemblage Characteristics

For the 30 transects (15 fixed and 15 temporary) surveyed annually from 2006 to 2015, trends varied by metric (Figure 8, Appendix C) and are summarized below. The Hausman test was >0.05 for each fish assemblage characteristic indicating that the random effects model was preferred.

- Mean fish species richness showed similar levels from 2006 (27.0 ± 6.7 SD species) to 2015 (27.3 ± 6.7 SE) but the overall trend increased significantly due to increases observed since 2009 ($r^2 = 0.68$, $z = 3.27$, $p = 0.001$) (Figure 8). Temporary transects had on average 3.3 more species on transect than fixed transects ($z = 2.12$, $p = 0.03$) (Figure 8).
- Mean fish numerical density varied considerably from 2006 to 2015 with a high of 2.3 ± 1.6 SD fish 125 m^{-2} in 2013 to a low of 1.0 ± 0.8 SD in 2009. The overall trend for this time period, however, was not significant ($r^2 = 0.48$, $z = -1.34$, $p = 0.18$, Figure 8). There was also no significant difference between temporary and fixed transects in terms of fish numerical density ($z = 0.73$, $p = 0.46$).
- Mean fish biomass increased significantly ($r^2 = 0.80$, $z = 2.67$, $p = 0.007$) from 2006 to 2015 with temporary transects on average recording nearly 90 g m^{-2} more than the fixed transects ($z = 3.79$, $p < 0.001$, Figure 8). Average annual biomass ranged from 186.4 ± 167.5 SD g m^{-2} in 2009 to 253.4 ± 203.5 SD g m^{-2} in 2011.
- Mean fish diversity (H') ranged between 1.92 ± 0.64 SD in 2008 to 2.56 ± 0.38 SD in 2014 with overall mean diversity 2.24 ± 0.53 SD (Figure 8). Diversity did show a significant increase ($r^2 = 0.68$, $z = 4.68$, $p < 0.001$) from 2006 to 2015 with no significant difference between fixed and temporary transects ($z = 1.25$, $p = 0.21$).

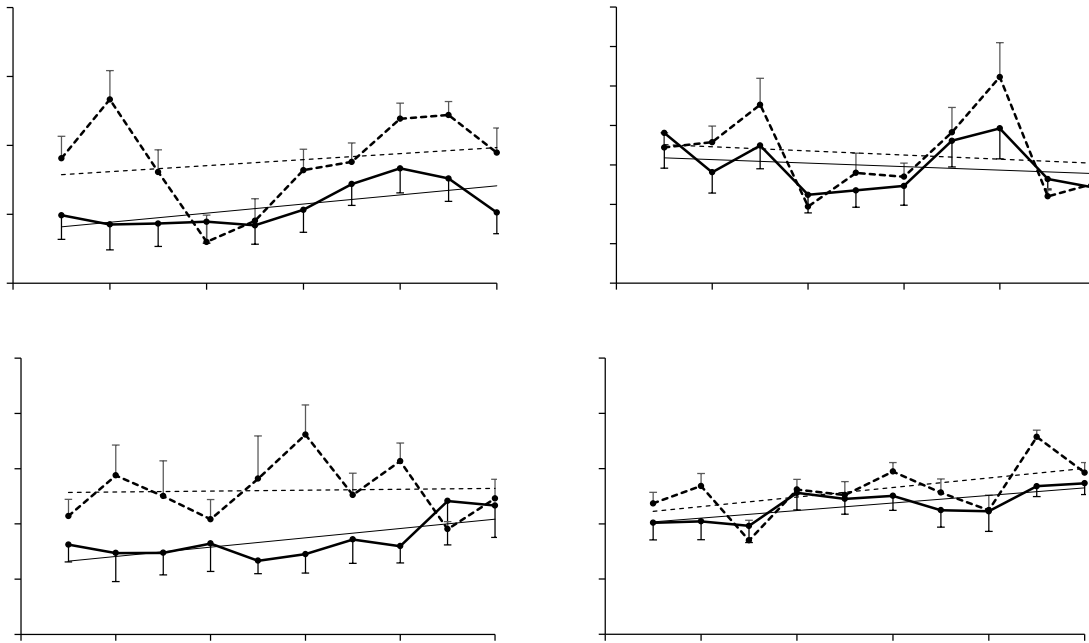


Figure 8. Trends in fish species richness (no. transect⁻¹) (top left), numerical density (no. m⁻²) (top right), biomass (g m⁻²) (bottom left), and diversity (H') (bottom right) at the 15 fixed sites (solid line) and 15 temporary sites (dashed lines) surveyed in each year at Kalaupapa NHP from 2006–2015. Error bars are one standard error of the mean with linear trend line and panel linear model z statistics displayed. The sign of the z statistic indicates whether it is a positive or negative trend.

Endemic Species

Endemic fish species ($N = 46$, 30% of the total number of fish species) accounted for 14.4% of the average density with 0.22 individuals m⁻² documented from 2006 to 2015. The most abundant endemic species was *Thalassoma duperrey* (saddle wrasse, 0.05 individuals m⁻²) followed by *Ctenochaetus stigosus* (goldring surgeonfish, 0.05 individuals m⁻²), and *Chromis ovalis* (oval chromis, 0.04 individuals m⁻²) (Table 2). Density for *T. duperrey* ($r^2 = 0.29$, $z = -2.12$, $p = 0.03$) and *C. ovalis* ($r^2 = 0.04$, $z = -2.09$, $p = 0.04$) decreased significantly from 2006–2015 (Figure 9). In contrast, *C. strigosus* density increased significantly over this same time period ($r^2 = 0.18$, $z = 2.16$, $p = 0.03$) (Figure 9). There were no significant differences between fixed and temporary transects for all three species.

Biomass of endemic species only comprised 6.4% of the total biomass of 64,684 g m⁻² for all fish species observed from 2006 to 2015. The top five endemic species included *Chlorurus perspicillatus* (spectacled parrotfish) with the highest total biomass values of 1,025 g m⁻² (1.6%) followed by *Ctenochaetus strigosus* (goldring surgeonfish, 649 g m⁻², 1.0 %), *Parupeneus porphyreus* (whitesaddle goatfish, 514 g m⁻², 0.8%), *Chromis verater* (threespot chromis, 313 g m⁻², 0.5%), and *Thalassoma duperrey* (saddle wrasse, 294 g m⁻², 0.4%). Biomass for four of the top five endemic species was relatively constant over the study period (Figure 10). The one exception was *T. duperrey* biomass, which increased significantly ($r^2 = 0.08$, $z = 3.27$, $p = 0.001$) from 2006 to 2015 (Figure 10).

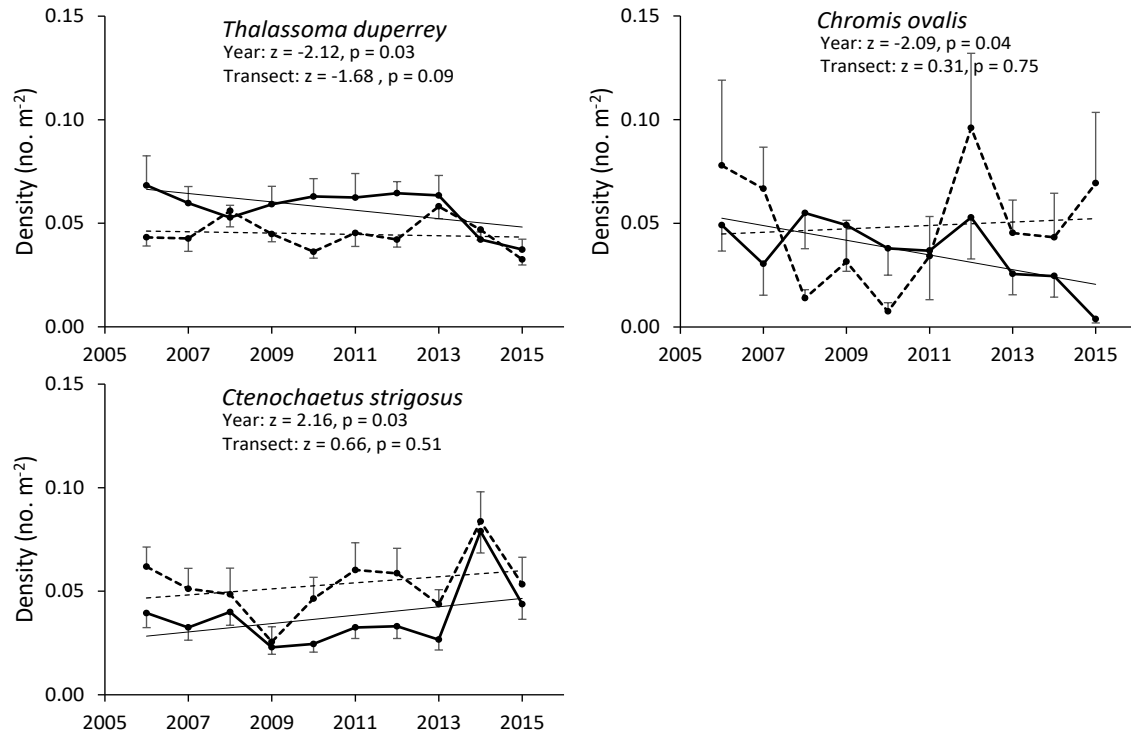


Figure 9. Trends in numerical density (no. m⁻²) of endemic fish species for *Thalassoma duperrey* (top left), *Chromis ovalis* (top right), and *Ctenochaetus strigosus* (bottom left) at the 15 fixed sites (solid line) and 15 temporary sites (dashed lines) surveyed in each year at Kalaupapa NHP from 2006–2015. Error bars are one standard error of the mean with linear trend line and panel linear model z statistics displayed. The sign of the z statistic indicates whether it is a positive or negative trend.

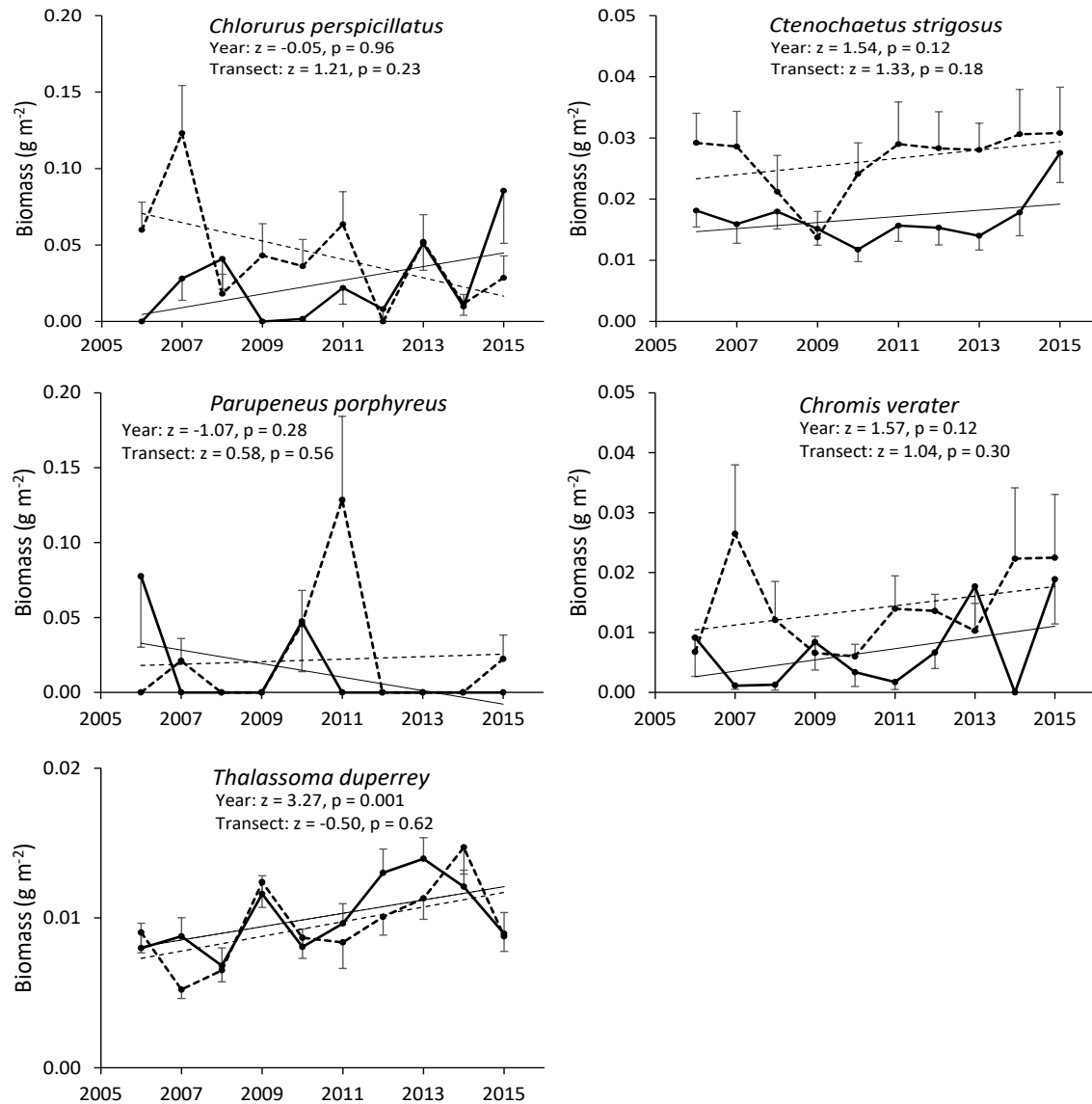


Figure 10. Trends in biomass (g m^{-2}) of endemic fish species for *Chlorurus perspicillatus* (top left), *Ctenochaetus strigosus* (top right), *Parupeneus porphyreus* (center left), *Chromis verater* (center right), and *Thalassoma duperrey* (bottom left) at the 15 fixed sites (solid line) and 15 temporary sites (dashed lines) surveyed in each year at Kalaupapa NHP from 2006–2015. Error bars are one standard error of the mean with linear trend line and panel linear model z statistics displayed. The sign of the z statistic indicates whether it is a positive or negative trend. Note different Y-axes.

Invasive Species

Four invasive species (<3% of the total number of fish species) accounted for 1.6 % of the average numerical density of 0.02 individuals m^{-2} . The primary invasive species, in terms of numerical density, was *Lutjanus kasmira* (bluestriped snapper) with a total of 0.02 individuals per m^2 documented from 2006–2015. This species accounted for 1.0% of the overall average fish numerical density. Over the 10-year period there was no statistically significant trend in numerical density ($r^2 = 0.08$, $z = -0.18$, $p = 0.86$) for this species with mean values ranging from 0.004 individuals per m^2 in 2008 and 2013 to 0.04 individuals per m^2 in 2009 (Figure 11). Variability for fixed and temporary transects was high (Appendix C) due to the schooling behavior of this species. The other three species were much less abundant and included *Cephalopholis argus* (bluespotted grouper, 0.006 individuals m^{-2}), *L. fulvus* (blacktail snapper, 0.0009 individuals m^{-2}), and *Abudefduf vaigiensis* (Indo-Pacific sergeant, 0.0006 individuals m^{-2}). These other species also had stable numerical density levels during the study period (Figure 11, Appendix C). There was a significant difference between fixed and temporary transects for *C. argus* and *L. fulvus* with higher numerical density levels documented on the temporary transects.

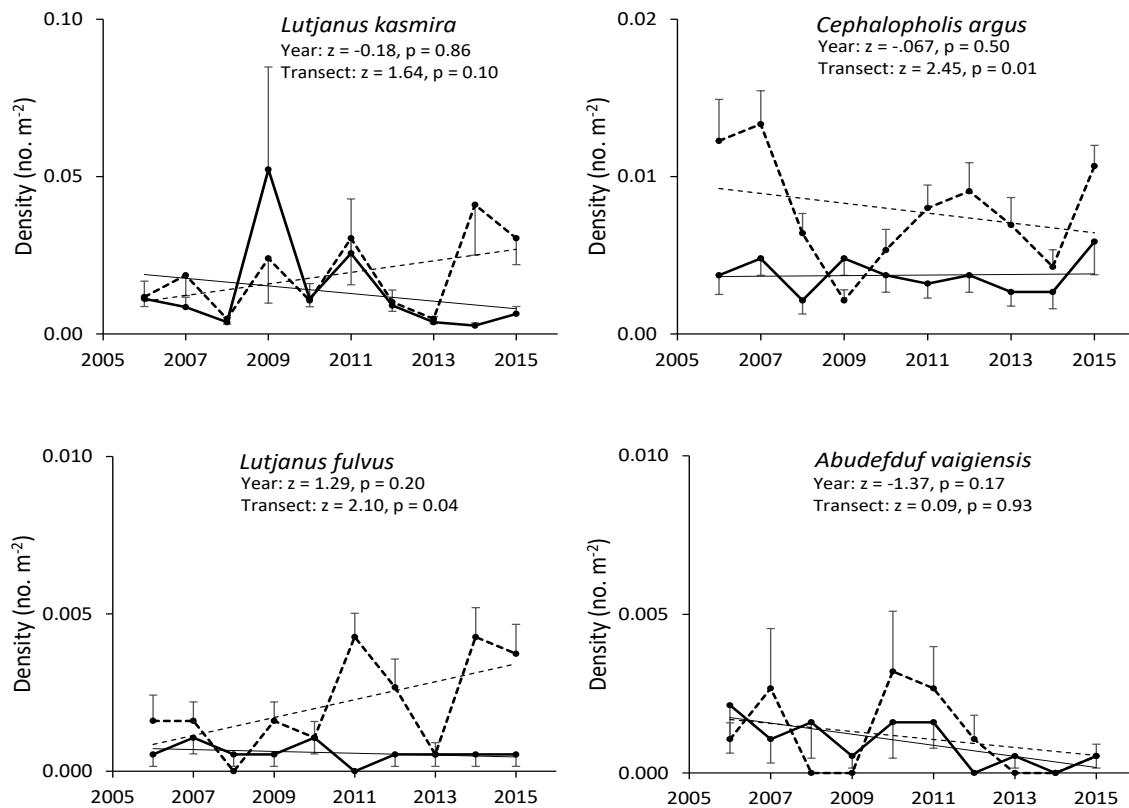


Figure 11. Trends in numerical density (no. m^{-2}) of invasive fish species for *Lutjanus kasmira* (top left), *Cephalopholis argus* (top right), *L. fulvus* (bottom left), and *Abudefduf vaigiensis* (bottom right) at the 15 fixed sites (solid line) and 15 temporary sites (dashed lines) surveyed in each year at Kalaupapa NHP from 2006–2015. Error bars are one standard error of the mean with linear trend line and panel linear model z statistics displayed. The sign of the z statistic indicates whether it is a positive or negative trend. Note different Y-axes.

Total biomass for all invasive species was over 6.2% of the total biomass of 64,684 g m⁻² observed from 2006 to 2015. The two primary invasive species (*Lutjanus kasmira* and *Cephalopholis argus*) accounted for 5.9% (*C. argus* – 3.1%, *L. kasmira* – 2.8%,) of the total biomass, with small contributions from *L. fulvus* (0.3%, blacktail snapper) and one recent colonizer, *Abudefduf vaigiensis* (0.03%, Indo-Pacific sergeant). Biomass values fluctuated dramatically for the schooling *L. kasmira* over the years compared to the more solitary *C. argus*, which was observed consistently from year to year (Figure 12). None of the four invasive species displayed a trend over the study period (Figure 12). There was a significant difference between fixed and temporary transects for *C. argus* with higher biomass levels documented on the temporary transects. The Hausman test, however rejected the null hypothesis of the random effects model and selected the alternative fixed effects model for both *L. kasmira* and *L. fulvus*. Therefore, no comparisons were conducted between fixed and temporary transects for these species. Numerical density and distribution of these invasive species as well as new introductions will be closely monitored as more data are collected.

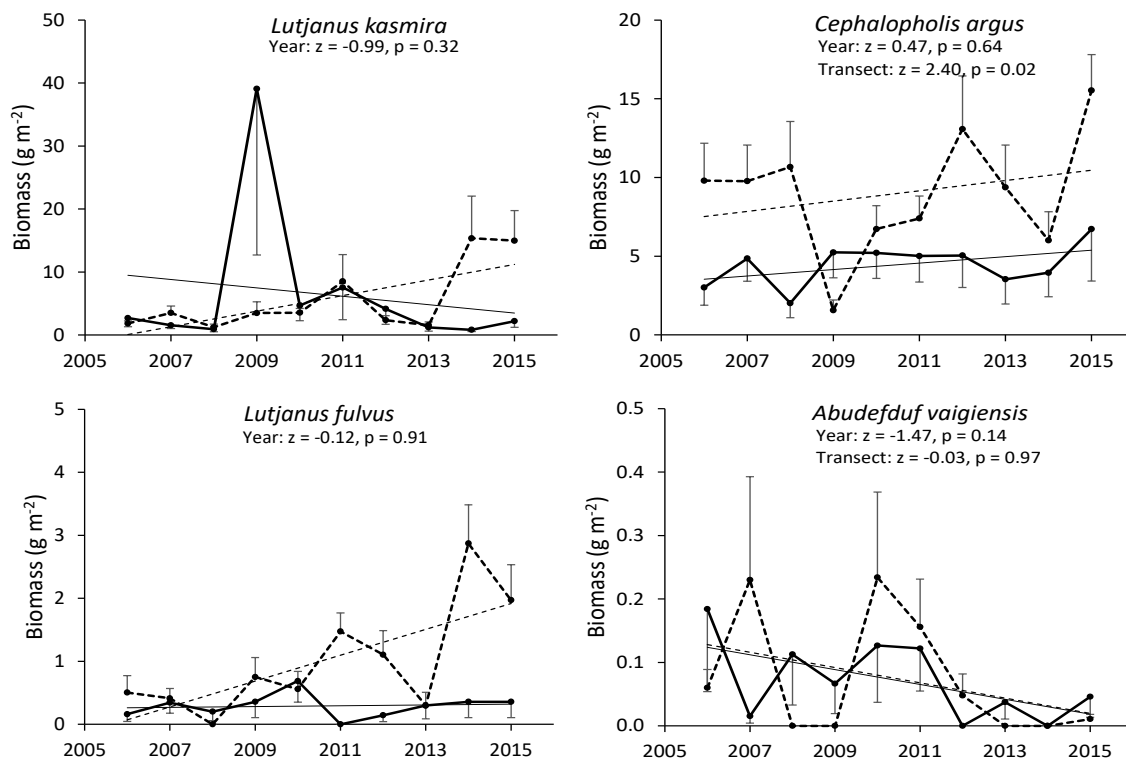


Figure 12. Trends in biomass (g m⁻²) of invasive fish species for *Lutjanus kasmira* (top left), *Cephalopholis argus* (top right), *L. fulvus* (bottom left), and *Abudefduf vaigiensis* (bottom right) at the 15 fixed sites (solid line) and 15 temporary sites (dashed line) surveyed in each year at Kalaupapa NHP from 2006–2015. Error bars are one standard error of the mean with linear trend line and panel linear model z statistics displayed. The sign of the z statistic indicates whether it is a positive or negative trend. Note different Y-axes.

Factors Influencing Fish Assemblage Characteristics

A number of factors explained a portion of the variability in each of the models and are listed in order of their contributions (Table 4, Appendix C). The direction of wave exposure at Kalaupapa was a significant factor in explaining the variation in the fish assemblage for species richness (Table 4). A higher average number of 5.5 species per transect were documented on the northern tip of the peninsula compared to sites on the northwestern side close to the human settlement. Fish density and biomass were also higher at the northernmost sites than at sites on the western side of the peninsula, but not statistically different from these sites or sites on the eastern side of the peninsula.

Table 4. Factors influencing fish assemblage characteristics for species richness, numerical density, biomass, and diversity using a Generalized Additive Mixed Model. Statistically significant parameters for the smoothed terms are ranked from most important to least important in explaining the variability in the model for each of the assemblage characteristics and separated out between the categorical factor (wave exposure) and the smoothed terms. Wave exposure is compared to the first level alphabetically entered into the model. E.g., The species richness estimate is for sites exposed to waves from the Northwest (NW) compared to sites exposed to waves from Both directions.

Parameter/ R ² Adjusted	Fixed Term	Estimate	<i>t</i>	<i>p</i>
Species richness (# spp. 125 m ⁻²)/ R ² Adj = 0.26	Waves from the NW	-5.40	-2.53	0.014
	Smoothed terms, <i>k</i> = 5	Edf	<i>F</i>	<i>p</i>
	Rugosity	1.0	12.63	<0.001
Density (# 125 m ⁻²)/ R ² Adj = 0.46	Waves from the NW	-0.16	-1.67	0.098
	Smoothed terms, <i>k</i> = 5	Edf	<i>F</i>	<i>p</i>
	Coral Cover	1.0	9.84	0.002
	Crustose Coralline Algae Cover	1.0	6.37	0.014
	pH	1.0	4.49	0.037
Biomass (g m ⁻²)/ R ² Adj = 0.08	Waves from the NW	-0.61	-1.72	0.089
	Smoothed terms, <i>k</i> = 5	Edf	<i>F</i>	<i>p</i>
	Rugosity	1.0	6.79	0.011
	pH	1.0	5.50	0.021
	Minimum Annual Temperature	1.0	4.22	0.043
Diversity (H')/ R ² Adj = 0.31	Waves from the NW	-0.002	-0.01	0.992
	Smoothed terms, <i>k</i> = 5	Edf	<i>F</i>	<i>p</i>
	Rugosity	1.0	6.48	0.013
	Benthic Species Richness	1.0	5.62	0.020
	Coral Cover	1.0	5.34	0.024

Rugosity (species richness, biomass, diversity), percent coral cover (density, diversity), pH (density, biomass), percent crustose coralline algae cover (density), minimum annual temperature (biomass), and benthic species richness (diversity) explained a portion of the variability in each of the models (Table 4). The rugosity of the substrate appeared to be the strongest predictor for most of the fish assemblage metrics due to the larger F statistics, with higher topographic complexity associated with higher values for species richness and biomass. Diversity had a parabolic response to rugosity with lower values at low and high levels of topographical complexity. Percent coral cover was another predictor that featured prominently in the fish assemblage with higher coral cover observed with higher fish species richness, but coral cover had a negative relationship with fish diversity. Other significant predictors that had positive relationships with the fish assemblage were crustose coralline algae cover, benthic pH, and minimum annual temperature. In the case of pH and minimum annual temperatures, the relationships were nonlinear with slightly lower fish density and biomass values at intermediate pH and minimum temperature levels. Benthic species richness had a negative relationship with diversity. Continuous predictors that did not appear to affect the fish assemblages were macroalgae cover, turf algae cover, depth, benthic temperature, benthic salinity, benthic turbidity, benthic dissolved oxygen, benthic chlorophyll, average annual temperature, and maximum annual temperature. The R^2 adjusted values were low for most of the models indicating that some important predictors (e.g., maximum significant wave height, fishing pressure) were missing from the model.

Discussion

Survey results from 2006 to 2015 indicated that transects with the highest fish species richness values, density, and biomass were concentrated near the northern tip and along the northeastern section of the peninsula coastline (Figures 3, 4, and 5). Fish diversity values, however, were evenly distributed throughout the park (Figure 6). In terms of biomass, three transects fell well outside the range found at all other transects (Figure 5). Fixed transect 6, located along the northwestern coast of the peninsula, had less than half of the biomass found at any other transect, while fixed transects 8 and 9, located near the northern tip of the peninsula, had more than four times the biomass found at any other transect. One notable exception was temporary transect 3, located on the western coast of the peninsula, which had almost twice the biomass as the remaining transects. Since surveys began in 2006, fixed transect 6 has had the lowest biomass of all transects every year.

Ecological factors influencing the spatial distribution of the fish assemblage characteristics within Kalaupapa NHP include variations in reproductive output from source populations (Claisse et al. 2009), post-settlement mortality (Hunt and Scheibling 1997), habitat extent (Caselle and Warner 1996) and complexity (Friedlander et al. 2007), physical disturbances (e.g., hurricanes, tsunamis), and currents. Overlaid on these natural elements are anthropogenic factors such as water quality, and fishing pressure that are influenced by human population levels at local and regional scales (Williams et al. 2015). Several of these factors (e.g., fish reproductive output and post-settlement mortality) are beyond the scope of this study so elements that have been directly measured will be addressed first, followed by factors that were assessed through the literature.

Habitat factors that could influence the fish assemblage structure around Kalaupapa include the spatial extent of shallow water habitat and complexity of the substrate. For the entire island of Moloka'i, the spatial extent (161.6 km²) of shallow water habitat (depth <20 m) that is suitable for coral reef development is less than on Kaua'i (178.8 km², 10% less), O'ahu (57%), Maui (2%), and Hawai'i (17%) (Rohmann et al. 2005). Examining habitat maps for only the wave exposed north shore sections of these islands, it is evident that the area around Kalaupapa has substantially less coral reef fish habitat available than the other islands, and this is restricted to a narrow band adjacent to the shoreline (NOAA – NCCOS 2007). This restricted range of suitable habitat should theoretically limit fish populations compared to other wave exposed north shore sites, as well as areas with extensive reef habitat around Hawai'i.

The rugosity or complexity of the substrate at Kalaupapa is different than other wave exposed north shore sites around the state. In the park, the substrate consists of large basalt boulders, which have numerous spaces for fish to hide (Brown et al. 2014) (Figure 13). In contrast, the more typical north shore coral reefs of Kaua'i, O'ahu, and Maui are relatively flat with encrusting coral communities (Jokiel et al. 2004) (Figure 13). Beets et al. (2010), reported that rugosity at Kalaupapa was higher than values reported at three other national parks (Pu'ukoholā Heiau National Historic Site, Kaloko-Honokōhau National Historical Park, Pu'uhoonua o Hōnaunau National Historical Park) on the leeward, wave protected coastline of Hawai'i Island. Friedlander et al. (2003) documented an average rugosity value of 1.60 at 60 sites around the MHI, which was similar to the overall mean

rugosity index value of 1.65 at Kalaupapa. Kalaupapa, however, had higher mean rugosity (1.64 versus 1.44) than other north shore reefs exposed to the northwest swells in the Friedlander et al. (2003) study. Friedlander et al. (2003) found the highest mean rugosity values in the MHI in sheltered areas such as Kāneʻohe Bay on Oʻahu (1.81) and along wave protected southern shorelines (1.71) with high coral cover. Therefore, even with a limited spatial extent of available habitat on a wave exposed shoreline, the high complexity of reef habitat at Kalaupapa coupled with the low fishing pressure has resulted in a high density and biomass of reef fish around the park.



Figure 13. Typical substrate profile at Kalaupapa NHP (top) and Hanalei Bay, Kauaʻi (bottom), which are both northern, wave-exposed coastlines around the MHI. Photos by a.) Sylvester Lee on September 24, 2014 and b.) Eric Brown on May 21, 2010.

Previous studies (e.g., Friedlander et al. 2007) have shown that complexity of the reef habitat explained a large percentage of the variability in fish species richness and biomass; higher complexity has higher fish assemblage metrics, although legal protection from fishing pressure also resulted in higher values for many fish assemblage characteristics (Friedlander et al. 2007). The results of this study concur with Friedlander et al. (2007) for reefs in Hawai‘i and helps explain why some transects with low rugosity (e.g., Fixed 6) had lower fish assemblage metrics than sites with more vertical relief and complexity (e.g., Fixed 8 and 9). The overall explanatory power of the model in this study, however, is lower. Several explanations exist for the difference. First, Friedlander et al. (2007) incorporated different management regimes in their model with more legal protection positively correlated with higher levels of all the fish assemblage characteristics. This factor clearly explained a significant portion of the variability in fish assemblages. Second, this study focused on a much narrower range of habitat types, wave exposure regimes, fishing pressure levels, and fish assemblage composition. Consequently, the metrics among sites in this study were more similar and therefore, more difficult to discern differences. Finally, this study incorporated a temporal component, which added a layer of variability not accounted for in the Friedlander et al. (2007) study.

Physical disturbances such as hurricanes/cyclones, tsunamis, and severe wave events have impacted the Hawaiian archipelago during the study period. No hurricanes have made landfall in the MHI since Hurricane Iniki in 1992, although numerous hurricanes and tropical storms have passed in close proximity to the MHI (National Hurricane Center 2021). Based on the results from this study, it does not appear that any of the storms had an impact on the fish assemblages at Kalaupapa. Previous studies from around the globe typically have either documented little impact from hurricanes (e.g., Greenwood et al. 2006) or a recovery of the fish assemblage after a major storm within two years (e.g., Walsh 1983). Walsh (1983) documented that a large segment of the fish assemblage at his study sites on the island of Hawai‘i moved to deeper water as a result of the habitat damage that occurred at the shallow sites during a severe storm. The fish moved back into the shallower water over a period of 16 months as the habitat stabilized.

There have been several tsunamis that have been documented in Hawai‘i from 2006 to 2015 (National Centers for Environmental Information 2021, NPS unpublished data). In chronological order, they include the tsunami from Chile resulting from an 8.8 magnitude earthquake on February 27, 2010, the Japan Tohoku tsunami from a 9.0 magnitude earthquake on March 11, 2011, and the Haida Gwaii tsunami that was generated by a 7.7 magnitude earthquake on October 27, 2012 off the coast of Canada. NPS water pressure loggers at Kalaupapa recorded the highest wave height of 1.0 m from the Haida Gwaii tsunami (NPS unpublished data, Table 5), but all of the tsunamis had minimal height compared to a runup of 16 m from the most significant tsunami to impact Waikolu valley in Kalaupapa in 1946 (National Centers for Environmental Information 2021). In terms of the fish assemblage, no detectable effects were documented within the National Park from any of these events. Other studies that have focused on tsunami impacts either recorded relatively few changes to the fish assemblage following the event (e.g., Campbell et al. 2007) or a relatively rapid recovery (e.g. Masuda et al. 2016). In the case of the massive 2011 tsunami in Japan, Masuda et al. (2016) estimated that it took approximately three years for the coastal reef fish assemblage to recover.

Table 5. Tsunamis documented at Kalaupapa harbor from 2006 to 2015 and listed in chronological order (NPS unpublished data). Tsunami height was estimated after removing the tide level.

Date	Origin	Earthquake Magnitude	Tsunami height (m)
February 27, 2010	Pelluhue, Chile	8.8	0.2
March 11, 2011	Tohoku, Japan	9.0	0.2
October 27, 2012	Haida Gwaii, Canada	7.7	1.0

The wave climate at Kalaupapa is dominated by northwest storm events during the fall/winter months from October to March and northeast tradewind swell that occurs throughout the year (Aucan 2006). In the Hawaiian archipelago, wave exposure is considered the predominant factor structuring coral reef communities (Grigg 1983) and in this study was a significant predictor for fish species richness. It also appeared important for fish density and biomass. All three metrics had higher average values off the northern tip and eastern coastline of the peninsula compared to sites on the western side of the park. These results suggest that sites with rougher conditions tend to harbor higher values for fish assemblage characteristics. Typically, wave exposure tends to have a negative relationship with fish assemblage organization in Hawai‘i (Friedlander and Parrish 1998, Friedlander et al 2003), but as Friedlander et al (2003) documented around the MHI, higher substrate complexity can provide spatial refugia resulting in higher values for many of the fish assemble metrics. This topic will be discussed in more detail below concerning the importance of rugosity as a predicator of the fish assemblage in this study.

Currents, which are the main mode of dispersal for planktonic larvae, have not been studied extensively around the park. Storlazzi et al. (2011) from one location documented that the predominant surface currents adjacent to the settlement were parallel to shore with rising/incoming tidal currents flowing to the northern end of the peninsula and falling tidal currents flowing south (Figure 14). There did not appear to be a prevailing direction at this location, which would limit larvae coming from outside sources. Additional current meters would need to be installed around the peninsula to clarify the net direction of current flow, especially during the spawning season. Lumpkin (1998) reported that, at a regional scale, the principal surface current flow around the Hawaiian archipelago was from east to west, which suggests that the peninsula would be a convergence zone for currents and ultimately an optimal area for larval recruitment (Figure 15). Fox et al. (2012), found that on the west coast of Hawai‘i Island fish recruitment was negatively correlated with eddy formation. When strong eddies developed that cycled the predominantly east to west currents back towards the coastline, recruitment was poor. In comparison, eddy formation around Kalaupapa could develop on the western side of the peninsula as easterly currents passed by the northern point of the peninsula. This current pattern has not been documented at Kalaupapa, although lower fish species richness and numerical density were found on the western side of the peninsula compared to the eastern side (Figures 3 and 4). Fox et al. (2012) also reported that other factors such as the El Niño Southern Oscillation, surface temperature, chlorophyll *a* concentration, sea surface height, and rainfall did not show any relationship with fish recruitment. Conklin et al. (2018) modeled larval connectivity for 11 species of fish and invertebrates around Moloka‘i and

found that the Kalaupapa peninsula served as a potential source of larval connections between islands. In addition, the west coast of the park acted as a net larval source for the majority of species in their study. Ultimately, additional methods (e.g., fish larval traps, tag and release, fish tracking, etc.) would need to be utilized to clarify whether Kalaupapa serves as a source or sink population of fish larvae.

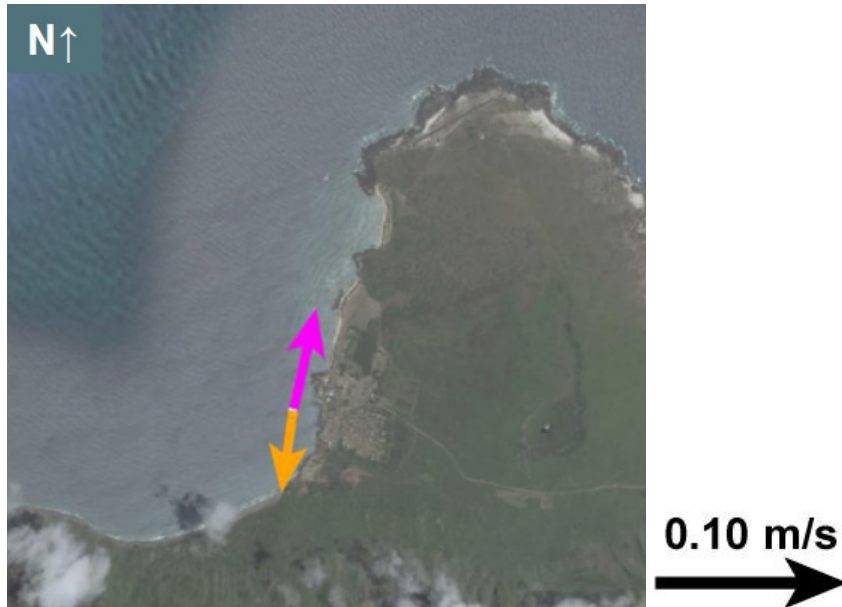


Figure 14. Map showing the relative magnitude and direction of near-surface tidal currents, in meters per second from true north. Magenta is flood tide and orange is ebb tide. A 0.10 m/s vector length is shown for scale. Figure from Storlazzi et al. (2011).

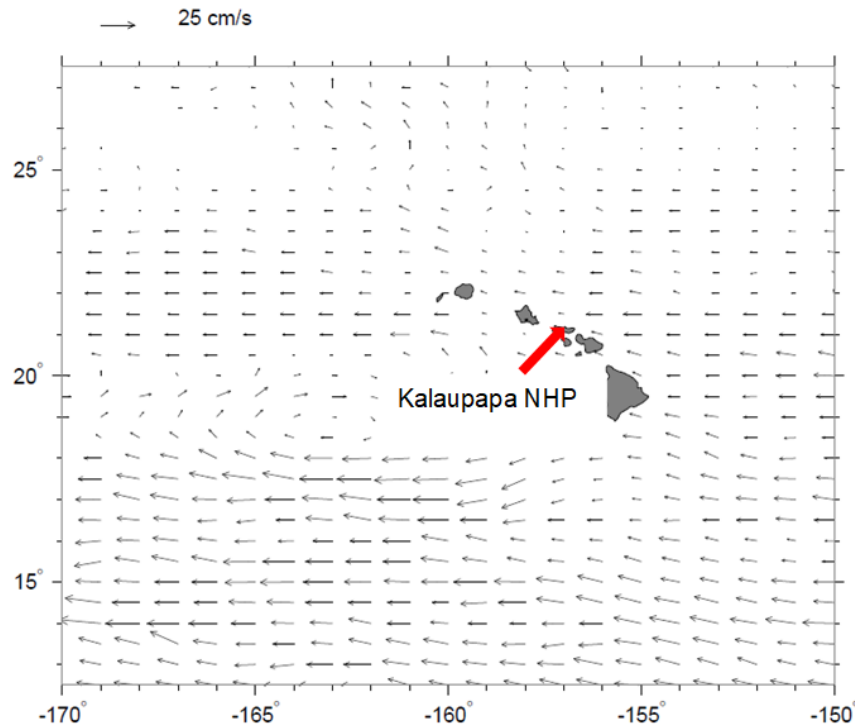


Figure 15. Average direction and strength of surface currents around Hawai'i. Units: cm/s (25 cm/s = 0.5 knot). Figure modified from <http://oos.soest.hawaii.edu/pacioos/outreach/oceanatlas/currents.php> (2015) and Lumpkin (1998).

The two primary local anthropogenic factors influencing the fish assemblage in the park are water quality and fishing pressure. The influence of water quality parameters on fish assemblages has only been recently evaluated for tropical estuaries (Duque et al. 2020) and tropical reef systems (e.g. Quimbayo et al. 2018). In general, studies have shown that anthropogenic factors such as poor water quality reduced levels of species richness, abundance, and biomass and the species composition shifted towards more tolerant species (Quimbayo et al. 2018). Adjacent to the Kalaupapa settlement, Beets et al (in review) did not detect anthropogenic sewage sources of nitrogen and documented lower concentrations of nitrate + nitrite ($\text{NO}_3^- + \text{NO}_2^-$) and phosphate (PO_4^{+}) compared to Kaloko-Honokōhau National Historical Park on the island of Hawai'i. Kalaupapa, however, did have significantly higher ammonium (NH_4^{+}) concentrations at benthic stations than Kaloko-Honokōhau, indicating submarine groundwater discharge west of the settlement. Around the entire park, PACN, documented low levels of total dissolved nitrogen with a ~25% decrease from 2013 to 2015. Total dissolved phosphorus was at non-detectable levels, salinity decreased 1–2 ‰, and temperatures increased ~1°C from 2008 to 2015. Raikow et al. (2021) partially attributed the changes in salinity and temperature to ENSO when the El Niño phase was at its peak. Overall, Raikow et al. (2021) considered marine water quality of Kalaupapa NHP to be in good condition with notable concerns. It should be noted that a subset of this data from 2008–2015 were used in the present study and two fish assemblage metrics (density, biomass) had a significant response to pH, with higher values at generally higher pH levels (Table 4). In either case, it does not appear that Kalaupapa is influenced

by significant sources of land-based nutrients based on the available data and consequently, the impact on the fish assemblage appears to be minimal.

Fishing pressure within the park is relatively light compared to other areas around Hawai‘i due to the geographic remoteness, seasonal weather patterns, and restricted access of Kalaupapa NHP (Tom 2011). Most of the fishing activity tends to be concentrated on the western side of the peninsula adjacent to the settlement. Tom (2011) noted, however, that the second highest cluster of shoreline segments with fishing pressure existed on the northern section of the peninsula. In most cases, fishing pressure consisted of rod and reel (64% of fishing effort observed) followed by throw net (10%), surround net (5%), three-prong (5%), and spear gun (1%). In the northern section, especially during the winter months, the water was generally too rough for in-water fishing techniques such as three-prong spears and spear guns, so effort shifted to rod and reel (75%) (Tom 2011). This fishing method has been shown to have the lowest catch per unit effort (CPUE) for reef fishes in Hawai‘i compared to all other techniques by at least an order of magnitude (McCoy et al. 2016). It is not likely that this inefficient gear type would have a significant impact on fish assemblages off the northern sector of the peninsula, although long-lived species can still be affected if population densities are low and recruitment is limited (Heppell et al. 2005).

The spatial distribution of human activities have been historically variable along the north shore of Moloka‘i (McCoy 2005, 2007, Flexner 2010). Most of the initial settlements prior to western contact occurred in the major valleys (Hālawā, Wailau, Pelekunu, and Waikolu) on the eastern side of the peninsula. Activities of the early Hawaiians were focused on fishing and taro farming (McCoy 2007). By the time the Hansen’s disease settlement was established in 1866 at Kalawao, on the east side of the peninsula, human habitation in the eastern valleys, with the exception of Hālawā, had largely disappeared (Flexner 2010). The human population at Kalawao later moved to Kalaupapa in the early 1900’s on the western side of the peninsula. These shifts in human occupation and associated activities, coupled with a decline of over 90% in the recorded human population on the peninsula over the last 100 plus years (Brown et al. 2011c), suggests that concomitant fishing pressure also declined over this time period. These declines would probably have offset any advancement in fishing technology over this time period, allowing the near shore fish assemblages to recover to the present-day levels and/or perhaps limiting the initial impact from resource extraction.

One of the most important metrics to examine from a resource manager’s perspective is total fish biomass. In comparison to other locations around the Pacific and Caribbean, total biomass at Kalaupapa approached levels seen in more remote and uninhabited island groups such as the Northwestern Hawaiian Islands (NWHI) (Figure 16). Friedlander et al. (2018) reported, in the largest and most comprehensive study to-date comparing fish assemblages across the MHI, that the two areas with the highest fish biomass in the state are the north shore of Moloka‘i, within the park boundaries, and around the island of Kaho‘olawe. These results are encouraging and suggest that fishing pressure at Kalaupapa is relatively light. Indeed, Tom (2011) reported that an “insignificant harvest effect was due to relatively small fishing effort at Kalaupapa”. Kaloko-Honokōhau National Historical Park, also in the MHI, had fish biomass levels that were only 33% of the biomass at Kalaupapa NHP even though the benthic habitat has much higher mean coral cover and similar

values for rugosity (Beets et al. 2010). It is important to note, however, that biomass of the top predators at Kalaupapa was still proportionally lower than levels documented in remote, uninhabited islands indicating some impact from fishing (Figure 16).

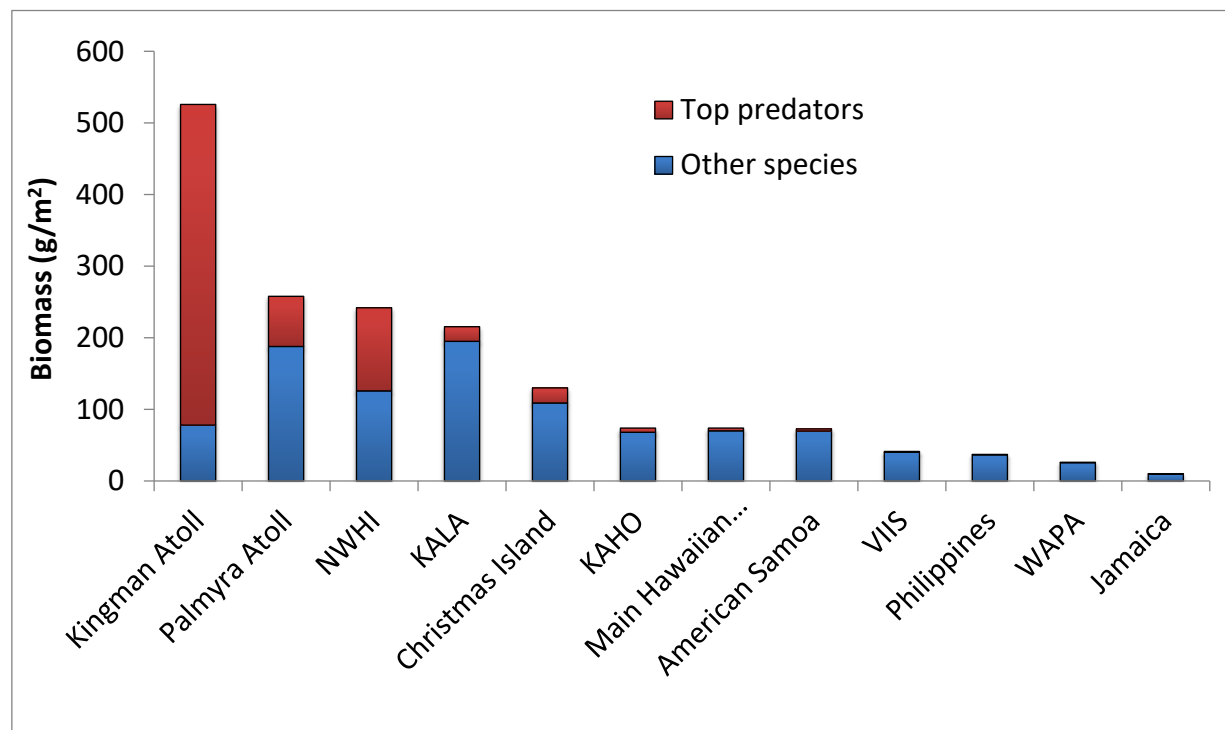


Figure 16. Mean fish biomass (g m^{-2}) for top predators and other consumer groups at various island locations in the Pacific and the Caribbean. Acronyms are as follows: NWHI = Northwestern Hawaiian Islands, KALA = Kalaupapa National Historical Park, KAHO = Kaloko-Honokohau National Historical Park, VIIS = Virgin Islands National Park, WAPA = War in the Pacific National Historical Park. Modified from Friedlander et al., (2008) and this study.

The trophic composition of the fish assemblage was dominated by planktivores (secondary consumers) and a few herbivores (primary consumers) in terms of fish density. The planktivore *Chromis vanderbilti* (blacktail chromis) was by far the most abundant species found at Kalaupapa (Table 2). The high density of this relatively small (up to about 7 cm, Hoover 2008) species also influenced the relative density versus biomass of the trophic groups. Secondary consumers (including *C. vanderbilti*) accounted for approximately 74% of the individual fish observed from 2006–2015 (Figure 7) yet made up only 28% of the biomass (Figure 8). These results suggest that Kalaupapa has a high abundance of plankton stemming from high primary productivity along the shoreline. Chlorophyll levels, which are typically used as a proxy for primary productivity (Huot et al. 2007), were not higher compared to other PACN parks (Raikow et al. 2021), even though planktivore numerical density and biomass levels at Kalaupapa NHP were higher than the PACN parks (NPS, unpublished data). Therefore, some other factor must explain the high planktivore levels. Sandin et al. (2008) noted that small plantivores numerically dominate reef assemblages in the absence of mesocarnivores and that pattern appears to hold for Kalaupapa NHP.

Biomass is considered a more sensitive metric for fishing pressure than numerical density (e.g., Edwards et al. 2013) and was also skewed towards primary (62%) and secondary (28%) consumers rather than top predators (10%), indicating fishing pressure had altered the fish assemblage at Kalaupapa NHP. Examining herbivore biomass using finer functional guilds revealed that the browsers were driving the temporal patterns for the entire assemblage (Figure 17). Edwards et al. (2013) documented that the browser functional group tended to be most susceptible to fishing with a higher biomass decline in fished areas versus inaccessible areas compared to other functional groups. In this study, it is difficult to determine if the browsers are being targeted preferentially over other herbivores because the only previous study on fisheries at Kalaupapa NHP (Tom 2011) did not partition out species in the catch statistics.

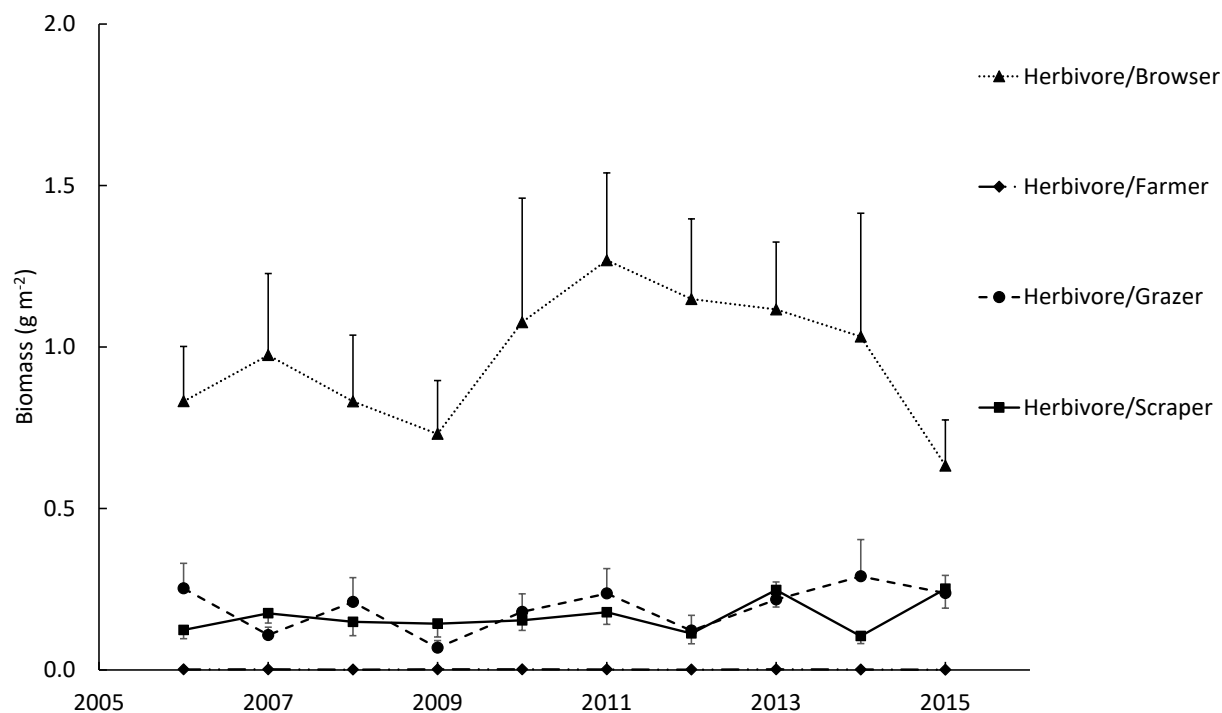


Figure 17. Mean herbivore fish biomass (g m⁻²) for the four functional guilds at the 30 transects surveyed in each year at Kalaupapa NHP from 2006–2015. Error bars are one standard error of the mean.

Of particular ecological importance are the top predators. Worldwide, large top predators have been on the decline with many, including sharks, disappearing at alarming rates due to intense fishing pressure (Worm et al. 2006, MacNeil et al. 2020). Even though many top predators have expansive ranges, the size-selective nature of fishing and modern equipment targets large, “trophy”-sized fish, resulting in a decrease of numerous populations (McClenachan 2008). These (typically) large predators are important to the reef because their absence can cause dramatic shifts in the species composition and dominant taxa of a reef (Sandin et al. 2008). Casey et al. (2017), however, found that on the outer Great Barrier Reef (GBR) where top predators had been removed but other confounding anthropogenic impacts (e.g., fishing of herbivorous fish and pollution) were minimal, top-down ecological forces were weak. Casey et al. (2017) concluded that “predator-mediated

trophic cascades are probably the exception rather than the rule in complex ecosystems” such as the GBR. At Kalaupapa NHP, trophic cascade effects may still occur, although they do not appear to be as evident as in heavily fished areas. As noted earlier, Tom (2011) documented relatively lighter fishing pressure at Kalaupapa, which partially explains the higher top predator biomass (10% of the total, Figure 7) compared to the rest of the MHI (Friedlander et al. 2018). In examining density and biomass of herbivorous fish and planktivores there does appear to be some level of predator release with higher relative levels of these trophic groups at Kalaupapa compared to other studies around Hawai‘i (e.g., Friedlander et al. 2003, Friedlander et al. 2007, Friedlander et al. 2018). These results suggest that the lighter fishing pressure has resulted in an intermediate reef assemblage at Kalaupapa NHP between a heavily fished area and a more pristine reef ecosystem. Consequently, fishing down the food web (e.g., Pauly et al. 1998) to target less desirable species such as herbivorous fish may be occurring at Kalaupapa, but biomass levels are still above the fishery benchmark of 100 g m^{-2} suggested by McClanahan et al. (2019). It is important to note, however, that in spite of the lighter fishing pressure the overall trophic structure and biomass level of 216 g m^{-2} at Kalaupapa more closely resembles fished reefs rather than unfished, wilderness reefs ($\sim 1900 \text{ g m}^{-2}$, McClanahan et al. 2019) where biomass is dominated by top predators and a trophic composition approximates an inverted pyramid (Sandin et al. 2008). Consequently, even minimal impacts are readily discernable.

From 2006 to 2015, the increasing trends in three of the fish assemblage characteristics (species richness, biomass, and diversity) indicated that the fish assemblage at Kalaupapa was improving over that time period (Figures 9, 11, 12). Only density remained relatively stable (Figure 10). An increase in biomass in recent years at the fixed transects was an encouraging sign and was driven primarily by the slight increase in herbivore biomass (Figure 17). Perhaps the most significant result is that the fish assemblage is not declining over the past 10 years as witnessed in other parts of the world (Pauly and Zeller 2016). Further monitoring in subsequent years will help us learn if these trends are ecologically significant, especially as the extended time sequence increases the statistical robustness of the data. The current temporal pattern may also simply be an artifact of natural variation in the system, however, the relatively low variance for each of the metrics across time compared to other reef areas in the Pacific suggests a relatively homogeneous fish assemblage across space and time.

Several factors likely contributed to the improvement in the fish assemblage structure. First, is the remoteness of the area. There are no roads leading into the settlement and the nearest harbor is more than 50 km from the western boundary of the park. Second, is the low level of human perturbation that occurs in the settlement. The human population at Kalaupapa has declined 92% from a peak of 1,177 in 1900 to 90 in 2010 (U.S. Census Bureau 2017). In addition, the population has been relatively stable for the past decade with light fishing and diving pressure (Tom 2011). There are also no major industries and no evidence of nutrient enrichment in the ocean from human sewage (Kalaupapa unpublished data, presented at 2012 International Coral Reef Symposium, Cairns, Australia). Third, is the seasonal refuge afforded by the strong winter storms (U.S. Naval Oceanographic 2010, NOAA 2015, Stormsurfing 2015), which restricts vessel traffic in the park and limits in-water (e.g., spearfishing) and even shoreline fishing during this time of year. Ultimately, all of these factors likely limit fishing activity in the park.

Endemic and invasive fish species were both significant components of the fish assemblage at Kalaupapa. Values for endemic species, however, were lower than fish assemblage metrics documented from elsewhere around the state. Friedlander et al. (2003) reported that endemics accounted for 35% (14% in this study) of the density and 22% (6% in this study) of the biomass from 60 stations from around the MHI. Their study sampled a wider array of habitats including reef areas dominated by endemic coral species such as *Porites compressa* (finger coral). This coral species appears to be a preferred substrate for many fish recruits, including *Ctenochaetus strigosus* (goldring surgeonfish), which is endemic to the Hawaiian Islands and Johnston Atoll (DeMartini and Anderson 2007). In comparison, Friedlander et al. (2003) found that invasive species at their study sites around the MHI accounted for <1% (3% in this study) of the total density and <3% (7.5% in this study) of the total biomass. Having a higher proportion of invasive fish species at Kalaupapa and similar to levels of endemic species might be a point of concern, but habitat differences and differing levels of resource extraction across the state could explain the observed patterns in the two groups of fishes. Indeed, DeMartini and Friedlander (2004) found that endemics comprised 52% of the total density and 37% of the total biomass in the NWHI, which has substantially different reef habitats than the MHI and no fishing. Invasive species were not an appreciable component of the fish assemblages in the NWHI. In addition, the most significant aspect of these results is that after 10 years of monitoring, the endemic species remain constant and the invasive species, especially the species considered most detrimental to native populations (i.e., *Lutjanus kasmira* [Gaither et al. 2013] and *Cephalopholis argus* [Dierking et al. 2009]) have not increased in numbers or size. Coles et al. (2006) found that the highest proportion of invasive species occurred at sites around the Hawaiian Islands that were isolated from the open ocean, which Kalaupapa is not. Therefore, it is possible that early spread of the invasive species to Kalaupapa from their release points on O‘ahu and Hawai‘i Island (Randall 1987) has stabilized and not increased in recent years. Endemic and invasive fish species will be closely monitored in the future because the proportion of these two components of the fish assemblage appears to be more similar at Kalaupapa than other nearshore habitats around the MHI.

Future changes in the fish assemblage should be evaluated in the context of temperature and ocean chemistry. It is anticipated that atmospheric changes in climate will have corresponding impacts on ocean temperatures and water chemistry. Sea surface ocean temperatures recorded by the National Marine Fisheries Service (1956–1992) and the Integrated Global Ocean Services System–National Meteorological Center (1992–2020) for Koko Head, O‘ahu indicate that overall temperatures have increased by almost 1° C since 1956 (Figure 18, see also Jokiel and Brown 2004). Several brief cooling periods have occurred during the intervening years, but the recent spike in temperatures in 2014 and 2015 along with the associated coral bleaching in these same years (Rodgers et al. 2015) indicate that the warming trend is continuing. From 2005 to 2015 temperatures rose almost 0.4° C yet minimal coral bleaching has been documented at Kalaupapa NHP (McCutcheon and McKenna In Press). Over a longer time period, ocean temperatures are expected to continue rising by 1.4–2.6 °C due to increased CO₂ emissions and the concomitant increase in atmospheric temperatures ([IPCC 2013](#)). Even though the impact of increasing temperature on coral reef fish communities has not been studied as well as temperature impacts on coral reef habitat, there are some recent studies that highlight potential issues. For example, Bellwood et al. (2012) reported that the cryptobenthic fish

assemblage in the central Great Barrier Reef failed to recover to pre-bleaching conditions following the 1998 El Niño bleaching event from prolonged high temperatures. This result was despite the fact that the coral community recovered fully and over 96 generations of these short-lived fish species had transpired. The authors did not attribute the lack of a recovery in the fish assemblage to the higher temperatures, but rather focused on the consequences of the bleaching event and the dynamic nature of reef recovery. Figueira and Booth (2010), Nakamura et al. (2013), and Feary et al. (2014) have identified 365 tropical reef fish species that have expanded their latitudinal ranges poleward in recent years as a result of warming ocean temperatures. Habary et al. (2016) examined a thermally sensitive damselfish (*Chromis viridis*) and found physiological impacts (e.g., weight loss, increase in basal metabolic requirements) as well as the lack of acclimation at warmer temperatures projected by 2100. This tropical species was only able to survive by moving to cooler temperatures. Given the recent increases in temperature, we anticipate more bleaching events and associated coral mortality, resulting in loss of fish habitat as well as potential shifts in assemblage composition at Kalaupapa NHP to more thermally tolerant species. The higher temperatures could also exert selection pressures on the existing fish species, which may have adverse impacts if the rate of change is higher than the adaptation rate of these fish species (e.g., Bell and Collins 2008).

Ocean chemistry is also expected to change with increasing CO₂ emissions ([IPCC 2013](#)). In particular, pH is expected to decrease, resulting in more acidic conditions and negatively impacting organisms (e.g., corals, mollusks, sea urchins, etc.) that secrete a calcium carbonate skeleton. Hoegh-Guldberg et al. (2007) projected that by 2050, coral reef ecosystems will reach a tipping point and corals will be unable to calcify and grow. Kalaupapa began monitoring ocean pH semi-annually along with other parameters in 2008 as part of the PACN I&M water quality protocol (Jones et al. 2011) and documented a mean pH of 8.07 on the substrate over that time (Raikow et al. 2021). Even though no trend was detected (Raikow et al. 2021), pH was an important predictor for fish density and biomass, displaying a nonlinear relationship with slightly lower fish density and biomass values at intermediate pH levels (Table 3). The overall relationship was positive with the highest fish density and biomass values at the higher pH levels suggesting that pH decreases due to climate change may also have a correlation with or impact the fish assemblage. Deploying pH loggers over longer time periods than what we currently utilize may help elucidate temporal patterns in ocean chemistry.

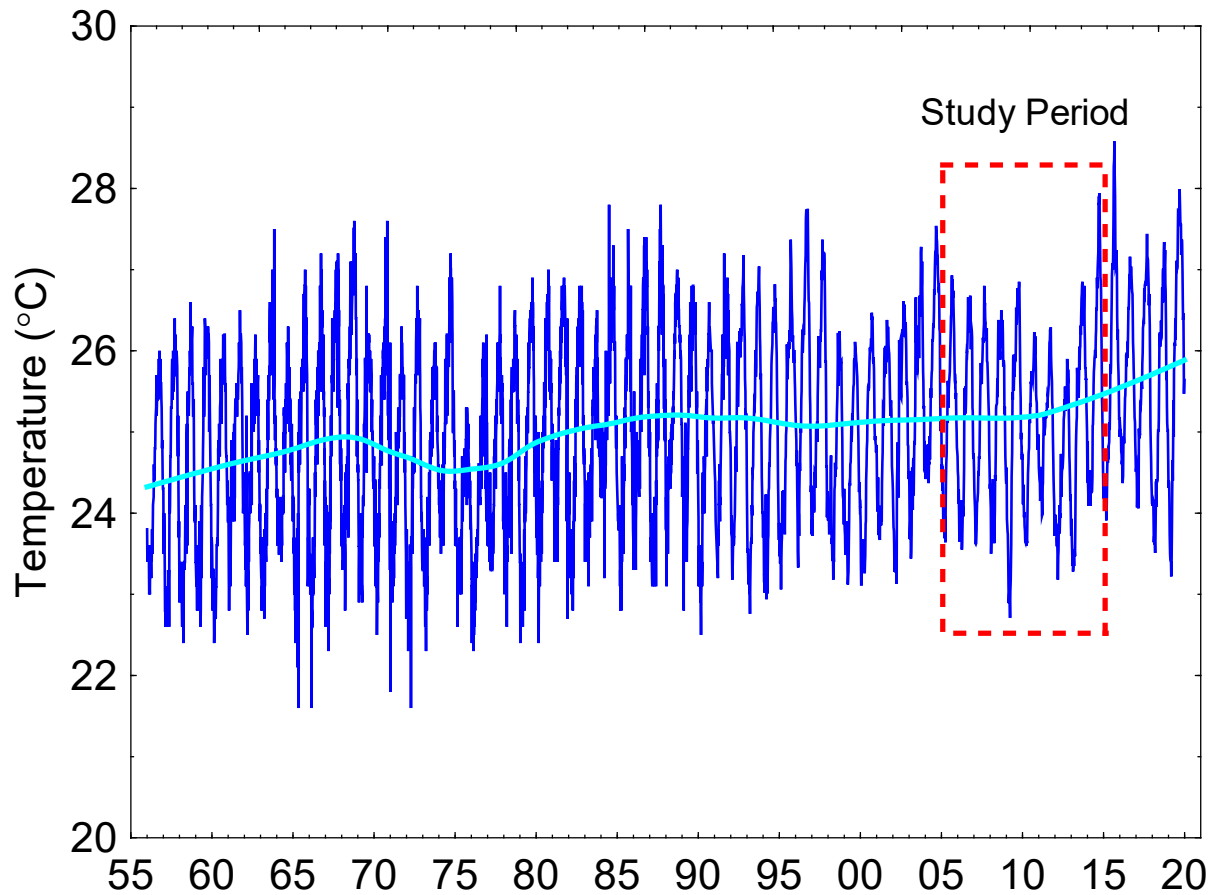


Figure 18. Combined sea surface temperature (SST) record using National Marine Fisheries Service (NMFS) data for Koko Head, Oahu (1956–1992) and corrected Integrated Global Ocean Services System–National Meteorological Center (IGOSS–NMC) temperature data (1992 to 2020; Modified from Jokiel and Brown 2004). The light blue line indicates a Lowess function fitted to the data. The study period for this report is outlined by the red dashed line.

Potential concerns with elevated CO₂ levels on coral reef fish include direct effects on internal calcifying structures such as otoliths (Ateweberhan et al. 2013), changes in fish predator-prey behavior (Cripps et al. 2011), changes in fish assemblage structure (e.g., loss of biodiversity) associated with declining coral reef habitat (Hixon 2011), and synergistic effects of stressors (Ateweberhan et al. 2013). The most widely studied aspect of these climate change impacts has focused on the negative effects of habitat decline on the related fish assemblage (Graham et al. 2009, Ateweberhan et al. 2013). At present, the increase in the fish assemblage metrics suggest that increases in temperatures or changes in pH have not negatively influenced the fish parameters measured in this study. In the short to medium time frame of this study, however, local impacts from the high wave energy environment and the concomitant low coral cover may have a greater potential influence on the fish assemblage at Kalaupapa than the longer term climate issues (e.g., Graham et al. 2014).

Further observations will be needed to determine whether these long-term trends of an increasing fish community are real or if natural fluctuations in fish assemblage characteristics, and/or measurement error associated with the methodology are masking the long-term pattern. Data collection and robust quantitative measures of uncertainty and associated factors will help us determine if the observed trends are ecologically significant, as long-term changes in the fish taxa or assemblages may be indicative of variation in certain environmental stressors or drivers. For example, a decrease in fish biomass has often been associated with increasing fishing pressure (Friedlander and DeMartini 2002) or a reduction in fish species richness corresponding to a degraded habitat such as high turbidity levels (Bejarano and Appeldoorn 2013). Co-location of this marine fish monitoring protocol with the benthic community monitoring protocol and the water quality monitoring protocol will allow us to clarify if any such associations exist at Kalaupapa. In addition, analyzing the fish assemblage using multivariate techniques in the future may also reveal more subtle changes not detected by the univariate approach.

In conclusion, the fish assemblage around Kalaupapa appears to be healthy and improving compared to the rest of the MHI, with continued monitoring needed to see how local, regional, and global factors are affecting these assemblages. It is important to note, however, that the fish assemblage has been impacted by fishing activities compared to areas that have not been overfished (e.g., Sandin et al. 2008, Friedlander et al. 2014). Consequently, continued monitoring of the assemblage but must be viewed in the context of a baseline that has shifted to an overfished state. To return the fish assemblage to a healthier state it is recommended that management actions include establishment of more marine protected or marine managed areas, banning certain gear types such as gill nets, and incorporating traditional knowledge and associated practices focused on spawning seasons and areas.

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Appendix A: Fish species documented in Kalaupapa National Historical Park

Table A-1. Fish species documented on transects in Kalaupapa NHP along with trophic information and length–mass fitting parameters used in the allometric growth equation. Feeding guild abbreviations are as follows: C = Coralivore, D = Detritivore, H/BR = Herbivore browser, H/FA = Herbivore farmer, H/GR = Herbivore grazer, H/SC = Herbivore scraper, MI = Mobile invertebrate feeder, O = Omnivore, P = Piscivore, Pk = Planktivore, SI = Sessile invertebrate feeder. Origin abbreviations are as follows: E = Endemic, I = Indigenous, X = Introduced or Exotic. The size conversion column represents the multiplication factor to convert total length (cm) to fork length.

Taxon	Consumer	Guild	Origin	a	b	Size Conversion
<i>Abudefduf abdominalis</i>	Secondary	Pk	E	0.02256218	3.13201768	0.865
<i>Abudefduf sordidus</i>	Primary	H/GR	I	0.02256218	3.13201768	0.930
<i>Abudefduf vaigiensis</i>	Secondary	Pk	X	0.02256218	3.13201768	0.870
<i>Acanthurus achilles</i>	Primary	H/GR	I	0.02803288	2.98288421	0.900
<i>Acanthurus blochii</i>	Primary	H/GR	I	0.02505596	3.03192925	0.930
<i>Acanthurus dussumieri</i>	Primary	H/BR	I	0.04256118	2.86826353	0.930
<i>Acanthurus guttatus</i>	Primary	H/BR	I	0.02803288	2.98288421	0.970
<i>Acanthurus leucopareius</i>	Primary	H/BR	I	0.02803288	2.98288421	0.953
<i>Acanthurus nigricans</i>	Primary	H/BR	I	0.02803288	2.98288421	0.980
<i>Acanthurus nigrofuscus</i>	Primary	H/BR	I	0.02637048	3.02836671	0.910
<i>Acanthurus nigroris</i>	Primary	H/BR	I	0.02803288	2.98288421	0.940
<i>Acanthurus olivaceus</i>	Primary	H/GR	I	0.02803288	2.98288421	0.890
<i>Acanthurus thompsoni</i>	Secondary	Pk	I	0.02803288	2.98288421	0.710
<i>Acanthurus triostegus</i>	Primary	H/GR	I	0.08306345	2.56968339	0.870
<i>Aetobatus ocellatus</i>	Secondary	MI	I	0.00465000	2.61350000	1.000
<i>Aluterus scriptus</i>	Primary	O	I	0.01222481	3.03275681	1.000
<i>Amblycirrhitus bimacula</i>	Secondary	MI	I	0.02984000	3.00000000	0.819
<i>Anampses chrysocephalus</i>	Secondary	MI	E	0.02260940	2.79271102	1.000
<i>Anampses cuvier</i>	Secondary	MI	E	0.02260940	2.79271102	1.000
<i>Aphareus furca</i>	Secondary	P	I	0.01673604	3.02215238	0.870
<i>Apolemichthys arcuatus</i>	Secondary	SI	E	0.05843515	2.71827770	1.000
<i>Aprion virescens</i>	Top	P	I	0.02296675	2.88626944	0.900
<i>Aulostomus chinensis</i>	Secondary	P	I	0.00021408	3.51443202	1.000

Table A-1 (continued). Fish species documented on transects in Kalaupapa NHP along with trophic information and length–mass fitting parameters used in the allometric growth equation. Feeding guild abbreviations are as follows: C = Coralivore, D = Detritivore, H/BR = Herbivore browser, H/FA = Herbivore farmer, H/GR = Herbivore grazer, H/SC = Herbivore scraper, MI = Mobile invertebrate feeder, O = Omnivore, P = Piscivore, Pk = Planktivore, SI = Sessile invertebrate feeder. Origin abbreviations are as follows: E = Endemic, I = Indigenous, X = Introduced or Exotic. The size conversion column represents the multiplication factor to convert total length (cm) to fork length.

Taxon	Consumer	Guild	Origin	a	b	Size Conversion
<i>Bodianus albotaeeniatus</i>	Secondary	MI	I	0.01081521	3.17305191	0.987
<i>Calotomus carolinus</i>	Primary	H/SC	I	0.02223697	2.97068234	1.000
<i>Calotomus zonarchus</i>	Primary	H/SC	E	0.02223697	2.97068234	1.000
<i>Cantherhines dumerilii</i>	Secondary	O	I	0.01222481	3.03275681	1.000
<i>Cantherhines sandwichiensis</i>	Primary	H/GR	I	0.01222481	3.03275681	1.000
<i>Canthigaster amboinensis</i>	Secondary	O	I	0.04237662	2.82202079	1.000
<i>Canthigaster coronata</i>	Secondary	SI	I	0.04237662	2.82202079	1.000
<i>Canthigaster jactator</i>	Secondary	MI	E	0.04237662	2.82202079	1.000
<i>Caracanthus typicus</i>	Secondary	MI	E	0.03372000	3.00000000	1.000
<i>Caranx ignobilis</i>	Top	P	I	0.01638314	3.05869327	0.890
<i>Caranx melampygus</i>	Top	P	I	0.02339817	2.91798706	0.890
<i>Caranx sexfasciatus</i>	Top	P	I	0.01983308	2.98604621	0.910
<i>Centropyge potteri</i>	Primary	H/GR	E	0.07448102	2.57693438	1.000
<i>Cephalopholis argus</i>	Top	P	X	0.00929300	3.18074251	1.000
<i>Chaetodon auriga</i>	Secondary	SI	I	0.04039709	2.82943061	1.000
<i>Chaetodon ephippium</i>	Secondary	SI	I	0.02248547	3.06092152	1.000
<i>Chaetodon fremblii</i>	Secondary	SI	E	0.04500811	2.81415860	1.000
<i>Chaetodon kleinii</i>	Secondary	Pk	I	0.04500811	2.81415860	1.000
<i>Chaetodon lineolatus</i>	Secondary	SI	I	0.06926482	2.62150684	1.000
<i>Chaetodon lunula</i>	Secondary	SI	I	0.04500811	2.81415860	1.000
<i>Chaetodon lunulatus</i>	Secondary	C	I	0.03110105	2.97565911	1.000
<i>Chaetodon miliaris</i>	Secondary	Pk	I	0.04500811	2.81415860	1.000
<i>Chaetodon multicinctus</i>	Secondary	C	E	0.04500811	2.81415860	1.000
<i>Chaetodon ornatissimus</i>	Secondary	C	I	0.04500811	2.81415860	1.000
<i>Chaetodon quadrimaculatus</i>	Secondary	C	I	0.04500811	2.81415860	1.000
<i>Chaetodon unimaculatus</i>	Secondary	C	I	0.05330290	2.83327856	1.000

Table A-1 (continued). Fish species documented on transects in Kalaupapa NHP along with trophic information and length–mass fitting parameters used in the allometric growth equation. Feeding guild abbreviations are as follows: C = Coralivore, D = Detritivore, H/BR = Herbivore browser, H/FA = Herbivore farmer, H/GR = Herbivore grazer, H/SC = Herbivore scraper, MI = Mobile invertebrate feeder, O = Omnivore, P = Piscivore, Pk = Planktivore, SI = Sessile invertebrate feeder. Origin abbreviations are as follows: E = Endemic, I = Indigenous, X = Introduced or Exotic. The size conversion column represents the multiplication factor to convert total length (cm) to fork length.

Taxon	Consumer	Guild	Origin	a	b	Size Conversion
<i>Cheilio inermis</i>	Secondary	MI	I	0.00349073	3.08156914	1.000
<i>Cheilodactylus vittatus</i>	Secondary	SI	I	0.00400000	3.36300000	0.910
<i>Chlorurus perspicillatus</i>	Primary	H/SC	E	0.02040000	3.00000000	1.000
<i>Chlorurus spilurus</i>	Primary	H/SI	I	0.02431142	2.96930628	1.000
<i>Chromis agilis</i>	Secondary	Pk	I	0.02285909	3.17522814	0.831
<i>Chromis hanui</i>	Secondary	Pk	E	0.02285909	3.17522814	0.796
<i>Chromis ovalis</i>	Secondary	Pk	E	0.09100000	2.41300000	0.758
<i>Chromis vanderbilti</i>	Secondary	Pk	I	0.02285909	3.17522814	0.860
<i>Chromis verater</i>	Secondary	Pk	E	0.02285909	3.17522814	0.937
<i>Cirrhitops fasciatus</i>	Secondary	MI	I	0.01700000	3.00000000	1.000
<i>Cirrhitus pinnulatus</i>	Secondary	MI	I	0.02140000	3.00000000	1.000
<i>Cirripectes vanderbilti</i>	Primary	H/GR	E	0.01304112	3.14965590	1.000
<i>Coris flavovittata</i>	Secondary	MI	E	0.00650084	3.25441380	1.000
<i>Coris gaimard</i>	Secondary	MI	I	0.00650084	3.25441380	1.000
<i>Coris venusta</i>	Secondary	MI	E	0.00650084	3.25441380	1.000
<i>Ctenochaetus hawaiiensis</i>	Primary	H/GR	I	0.02371233	3.05581445	0.960
<i>Ctenochaetus strigosus</i>	Secondary	D	E	0.02600000	2.93900000	0.783
<i>Decapterus macarellus</i>	Secondary	Pk	I	0.01392768	2.96377965	0.905
<i>Diodon hystrix</i>	Secondary	MI	I	0.19342648	2.47179069	1.000
<i>Echidna nebulosa</i>	Secondary	MI	I	0.00028206	3.35161078	1.000
<i>Evistias acutirostris</i>	Secondary	MI	I	0.03010000	2.94600000	0.966
<i>Exallias brevis</i>	Secondary	C	I	0.00217634	3.90064283	1.000
<i>Fistularia commersonii</i>	Secondary	P	I	0.00045958	3.04826935	1.000
<i>Forcipiger flavissimus</i>	Secondary	SI	I	0.04205095	2.84733177	1.000
<i>Forcipiger longirostris</i>	Secondary	MI	I	0.04205095	2.84733177	1.000

Table A-1 (continued). Fish species documented on transects in Kalaupapa NHP along with trophic information and length–mass fitting parameters used in the allometric growth equation. Feeding guild abbreviations are as follows: C = Coralivore, D = Detritivore, H/BR = Herbivore browser, H/FA = Herbivore farmer, H/GR = Herbivore grazer, H/SC = Herbivore scraper, MI = Mobile invertebrate feeder, O = Omnivore, P = Piscivore, Pk = Planktivore, SI = Sessile invertebrate feeder. Origin abbreviations are as follows: E = Endemic, I = Indigenous, X = Introduced or Exotic. The size conversion column represents the multiplication factor to convert total length (cm) to fork length.

Taxon	Consumer	Guild	Origin	a	b	Size Conversion
<i>Gomphosus varius</i>	Secondary	MI	I	0.02436678	2.70268809	1.000
<i>Gymnothorax eurostus</i>	Secondary	MI	I	0.00051794	3.30314261	1.000
<i>Gymnothorax flavimarginatus</i>	Secondary	P	I	0.00051794	3.30314261	1.000
<i>Gymnothorax melatremus</i>	Secondary	P	I	0.00051794	3.30314261	1.000
<i>Gymnothorax meleagris</i>	Secondary	P	I	0.00051794	3.30314261	1.000
<i>Halichoeres ornatissimus</i>	Secondary	MI	I	0.01601332	2.98741997	1.000
<i>Hemitaenichthys polylepis</i>	Secondary	Pk	I	0.04205095	2.84733177	1.000
<i>Kyphosus</i> sp	Primary	H/BR	I	0.01285290	3.15058869	0.940
<i>Labroides phthiophagus</i>	Secondary	MI	E	0.00731396	3.20293500	1.000
<i>Lutjanus fulvus</i>	Secondary	MI	X	0.02106145	2.97433152	0.960
<i>Lutjanus kasmira</i>	Secondary	MI	X	0.00842481	3.24696409	0.950
<i>Macropharyngodon geoffroy</i>	Secondary	MI	E	0.01066935	3.17764968	1.000
<i>Malacanthus brevirostris</i>	Secondary	SI	I	0.00490000	3.00000000	1.000
<i>Melichthys niger</i>	Secondary	H/Pk	I	0.00569644	3.39302801	1.000
<i>Melichthys vidua</i>	Primary	H/Pk	I	0.00569644	3.39302801	1.000
<i>Monotaxis grandoculis</i>	Secondary	MI	I	0.02295942	3.02223458	0.890
<i>Mulloidichthys flavolineatus</i>	Secondary	MI	I	0.01197390	3.10109252	0.920
<i>Mulloidichthys vanicolensis</i>	Secondary	MI	I	0.00742633	3.29343881	0.884
<i>Myripristis berndti</i>	Secondary	Pk	I	0.02769372	3.00336377	0.905
<i>Naso annulatus</i>	Secondary	Pk	I	0.05103242	2.71536954	0.950
<i>Naso brevirostris</i>	Primary	H/BR	I	0.01064945	3.24297329	1.000
<i>Naso caesioides</i>	Secondary	Pk	I	0.00848066	3.24964416	0.960
<i>Naso hexacanthus</i>	Secondary	Pk	I	0.02016519	2.95582519	0.950
<i>Naso lituratus</i>	Primary	H/BR	I	0.00848066	3.24964416	0.970
<i>Naso unicornis</i>	Primary	H/BR	I	0.01788029	3.03545410	0.960
<i>Neoniphon sammara</i>	Secondary	MI	I	0.02761540	2.88835358	0.920

Table A-1 (continued). Fish species documented on transects in Kalaupapa NHP along with trophic information and length–mass fitting parameters used in the allometric growth equation. Feeding guild abbreviations are as follows: C = Coralivore, D = Detritivore, H/BR = Herbivore browser, H/FA = Herbivore farmer, H/GR = Herbivore grazer, H/SC = Herbivore scraper, MI = Mobile invertebrate feeder, O = Omnivore, P = Piscivore, Pk = Planktivore, SI = Sessile invertebrate feeder. Origin abbreviations are as follows: E = Endemic, I = Indigenous, X = Introduced or Exotic. The size conversion column represents the multiplication factor to convert total length (cm) to fork length.

Taxon	Consumer	Guild	Origin	a	b	Size Conversion
<i>Oplegnathus punctatus</i>	Secondary	MI	I	0.02030000	3.00000000	0.968
<i>Ostracion meleagris</i>	Secondary	SI	I	0.12882216	2.51949459	1.000
<i>Oxycheilinus bimaculatus</i>	Secondary	MI	I	0.06784618	2.31728229	1.000
<i>Oxycheilinus unifasciatus</i>	Secondary	P	I	0.01550828	3.05791695	1.000
<i>Paracirrhites arcatus</i>	Secondary	MI	I	0.00927327	3.26840110	1.000
<i>Paracirrhites forsteri</i>	Secondary	P	I	0.00927327	3.26840110	1.000
<i>Parupeneus cyclostomus</i>	Secondary	P	I	0.01444606	3.12991984	0.957
<i>Parupeneus insularis</i>	Secondary	MI	I	0.01690000	3.10000000	0.896
<i>Parupeneus multifasciatus</i>	Secondary	MI	I	0.01135854	3.21081918	0.865
<i>Parupeneus pleurostigma</i>	Secondary	MI	I	0.01444606	3.12991984	0.894
<i>Parupeneus porphyreus</i>	Secondary	MI	E	0.13100000	3.15300000	0.896
<i>Pervagor aspricaudus</i>	Secondary	O	I	0.01222481	3.03275681	1.000
<i>Pervagor spilosoma</i>	Primary	O	E	0.01222481	3.03275681	1.000
<i>Plagiotremus ewaensis</i>	Secondary	P	E	0.00180493	3.58055900	0.950
<i>Plagiotremus goslinei</i>	Secondary	P	E	0.00180493	3.58055900	0.983
<i>Plectroglyphidodon imparipennis</i>	Secondary	MI	I	0.02090877	3.19080029	0.940
<i>Plectroglyphidodon johnstonianus</i>	Secondary	C	I	0.02090877	3.19080029	0.945
<i>Plectroglyphidodon sindonis</i>	Primary	H/GR	E	0.02090877	3.19080029	0.911
<i>Priacanthus meeki</i>	Secondary	Pk	E	0.02968104	2.80379073	1.000
<i>Pristiapogon kallopterus</i>	Secondary	MI	I	0.01009672	3.31415542	0.920
<i>Pseudocheilinus evanidus</i>	Secondary	MI	I	0.01066935	3.17764968	1.000
<i>Pseudocheilinus octotaenia</i>	Secondary	MI	I	0.01066935	3.17764968	1.000
<i>Pseudocheilinus tetrataenia</i>	Secondary	MI	I	0.01066935	3.17764968	1.000
<i>Pseudojuloides cerasinus</i>	Secondary	MI	I	0.01066935	3.17764968	1.000
<i>Pterois sphex</i>	Secondary	P	E	0.03580728	2.69658801	1.000
<i>Rhinecanthus rectangulus</i>	Secondary	MI	I	0.00569644	3.39302801	1.000

Table A-1 (continued). Fish species documented on transects in Kalaupapa NHP along with trophic information and length–mass fitting parameters used in the allometric growth equation. Feeding guild abbreviations are as follows: C = Coralivore, D = Detritivore, H/BR = Herbivore browser, H/FA = Herbivore farmer, H/GR = Herbivore grazer, H/SC = Herbivore scraper, MI = Mobile invertebrate feeder, O = Omnivore, P = Piscivore, Pk = Planktivore, SI = Sessile invertebrate feeder. Origin abbreviations are as follows: E = Endemic, I = Indigenous, X = Introduced or Exotic. The size conversion column represents the multiplication factor to convert total length (cm) to fork length.

Taxon	Consumer	Guild	Origin	a	b	Size Conversion
<i>Sargocentron spiniferum</i>	Secondary	MI	I	0.01540585	3.11881111	0.948
<i>Sargocentron xantherythrum</i>	Secondary	MI	E	0.02190000	3.04700000	0.940
<i>Scarus dubius</i>	Primary	H/SC	E	0.02337388	2.95646312	0.970
<i>Scarus psittacus</i>	Primary	H/SC	I	0.01045090	3.31870889	0.905
<i>Scarus rubroviolaceus</i>	Primary	H/SC	I	0.02337388	2.95646312	0.910
<i>Scarus</i> sp	Primary	H/SC	I	0.02337388	2.95646312	0.963
<i>Scorpaenopsis cacopsis</i>	Secondary	P	E	0.02460000	2.90800000	1.000
<i>Scorpaenopsis diabolus</i>	Secondary	P	I	0.01305184	3.26066400	1.000
<i>Seriola dumerili</i>	Top	P	I	0.03250000	2.87000000	0.890
<i>Sphyræna barracuda</i>	Top	P	I	0.00617076	3.01095083	0.886
<i>Stegastes fasciolatus</i>	Primary	H/FA	I	0.00281307	4.06294312	0.884
<i>Stethojulis balteata</i>	Secondary	MI	I	0.01908391	2.87625764	1.000
<i>Sufflamen bursa</i>	Secondary	MI	I	0.03244088	2.92911541	1.000
<i>Sufflamen fraenatum</i>	Secondary	MI	I	0.02865176	2.96582773	1.000
<i>Synodus</i> sp	Secondary	P	I	0.00847755	3.07770000	0.940
<i>Taenianotus triacanthus</i>	Secondary	P	I	0.02458744	2.90752613	1.000
<i>Thalassoma ballieui</i>	Secondary	MI	E	0.01230595	3.09702036	0.980
<i>Thalassoma duperrey</i>	Secondary	MI	E	0.01230595	3.09702036	0.900
<i>Thalassoma purpureum</i>	Secondary	MI	I	0.01230595	3.09702036	0.940
<i>Thalassoma trilobatum</i>	Secondary	MI	I	0.01230595	3.09702036	1.000
<i>Triaenodon obesus</i>	Top	P	I	0.00179736	3.34393360	0.822
<i>Wetmorella albofasciata</i>	Secondary	MI	I	0.01066935	3.17764968	1.000
<i>Zanclus cornutus</i>	Secondary	SI	I	0.01470374	3.36990807	0.960
<i>Zebrasoma flavescens</i>	Primary	H/BR	I	0.03783369	2.85676740	1.000
<i>Zebrasoma veliferum</i>	Primary	H/GR	I	0.03425216	2.86580578	1.000

Appendix B: Database queries used to generate data for figures, tables, and statistical analyses

Table B-1. Fish Assemblage Spatial Patterns.

Data	Database Query
Fish species richness	qs_j043_Fish_Summary_totals_per_transect
Fish numerical density	qs_j043_Fish_Summary_totals_per_transect
Fish biomass	qs_j043_Fish_Summary_totals_per_transect
Fish diversity	qs_j043_Fish_Summary_totals_per_transect

Table B-2. Trophic Composition.

Data	Database Query
Trophic composition by numerical density	qs_j133_Fish_Consumer_Abundance(#/m2)_per_transect_xtab
Trophic composition by biomass	qs_j153_Fish_Consumer_Biomass_per_transect_xtab

Table B-3. Top Ten Fish Species.

Data	Database Query
Fish top ten species by numerical density	qs_j053_Fish_Top_25_Density_per_park_all_years
Fish top ten species by biomass	qs_j063b_Fish_Top_25_Biomass_per_park_all_years

Table B-4. Trend Line Graphs.

Data	Database Query
Fish species richness	qs_j253_Fish_Trend_Stat_Setup
Fish numerical density	qs_j253_Fish_Trend_Stat_Setup
Fish biomass	qs_j253_Fish_Trend_Stat_Setup
Fish diversity	qs_j253_Fish_Trend_Stat_Setup

Table B-5. Endemic and Invasive Species.

Data	Database Query
Endemic and Invasive Fish by density	qs_j083_Fish_Endemic-Invasive_Species_Density_per_park_per_year
Endemic and Invasive Fish by biomass	qs_j103_Fish_Endemic-Invasive_Species_Biomass_per_park_year

Table B-6. Factors Influencing Fish Assemblage Characteristics.

Data	Database Query
Fish assemblage metrics	qs_j253_Fish_Trend_Stat_Setup
Benthic community metrics	qs_f041_Benthic_Cover_type_percent_per_transect_xtab

Appendix C: R code used in trend analysis (panel linear model) and analysis of influential predictors (generalized additive mixed model) along with interpretative plots

```
# Species Richness Trend Analysis
# Load the required packages

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lmerTest)      # This package contains the linear mixed
model (lmer) used for diagnostics
library(lmtest)        # This package contains the Breusch-Pagan
test (bptest) for homoskedascity
library(ggplot2)
library(doBy)
library(plm)           # This package contains the panel linear
model (plm) program

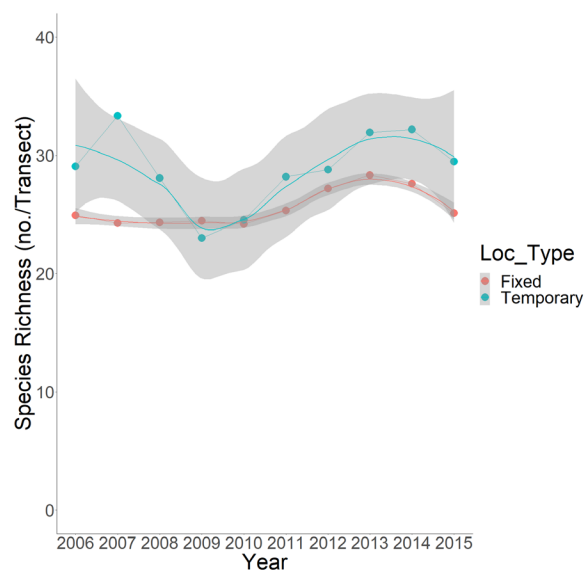
getwd()                # Returns the working directory
setwd("D:/Transfer/I&M/Fish") # Sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Fish_Data_06-15.txt", header=TRUE, sep="\t")
# Imports the data file into the object Fish
head(Fish)             # Prints out the first six rows of the
data set
  Park Year Loc_Type Transect1 Transect2 Richness Density Biomass
Diversity Evenness
1 KALA 2006   Fixed         1         1      20    0.448   56.98
2.63      0.88
2 KALA 2006   Fixed         2         2      23    1.352   77.12
1.73      0.55
3 KALA 2006   Fixed         3         3      24    1.792  470.07
2.06      0.65
4 KALA 2006   Fixed         4         4      30    0.944  150.43
2.88      0.85
5 KALA 2006   Fixed         5         5      20    7.416  159.33
0.86      0.29
6 KALA 2006   Fixed         6         6      11    0.456    5.34
1.68      0.70
```

```
meanse<-summaryBy(Richness~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Generates table of Count,
Mean, SD, SE of Richness X Year X Transect type
```

```
print(meanse)
```

```
p <-ggplot(meanse, aes(x=Year, y=Richness.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(0,40)
+ labs(y="Species Richness (no./Transect)") #Plots 2
loess regression lines on the same plot for Richness X Year X
transect type with 95% confidence interval error bands. One can
substitute "lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2005,2015,1)) #Adds chart elements such as text=50 points
and an x-scale from 2005 to 2015 at 1 year intervals.
```



```
fit1<-plm(Richness~Year + Loc_Type, data=Fish, index="Transect2",
model="within") # Runs the plm program for the fixed effects
model
```

```
summary(fit1) # Prints the output of the fixed effects model
```

```

fit2<-plm(Richness~Year + Loc_Type, data=Fish, index="Transect2",
model="random")      # Runs the plm program for the random effects
model

summary(fit2)        # Prints the output of the random effects model

phtest(fit1,fit2)     # Runs hausman test to compare the within or
fixed effects model to the random effects model. If the null
hypothesis (random model) is rejected at the p<0.5 level then
accept the results of the within/fixed effects model.

fit3<-lmer(Richness ~ Year*Loc_Type + (1|Transect2), data=Fish)  #
Runs the linear mixed effects model

summary(fit3)        # Prints the output of the linear mixed effect
model

ResidDiagnostic<-function(fit) {  # Examine residuals of raw data
fit
  par(mfrow=c(2,2))
  plot(fitted(fit), resid(fit))
  qqnorm(resid(fit))
  hist(resid(fit))}
ResidDiagnostic(fit3)

pbgtest(fit2)        # Testing for serial or auto correlation. If
p<0.05 then yes.

bptest(Richness~Year + Loc_Type, data=Fish, studentize=F)      #
Testing for homoskedasticity (homogeneity of variance). If p<0.05
then no.

# Numerical Density Trend Analysis
# Load the required packages

Sys.setenv(TZ="US/Hawaii")

```

```

Sys.getenv("TZ")
Sys.time()
library(lmerTest)      # This package contains the linear mixed
model (lmer) used for diagnostics
library(lmtest)        # This package contains the Breusch-Pagan
test (bptest) for homoskedascity
library(ggplot2)
library(doBy)
library(plm)           # This package contains the panel linear
model (plm) program

getwd()                # Returns the working directory
setwd("D:/Transfer/I&M/Fish")    # Sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Fish_Data_06-15.txt", header=TRUE, sep="\t")
# Imports the data file into the object Fish
head(Fish)             # Prints out the first six rows of the
data set

  Park Year Loc_Type Transect1 Transect2 Richness Density Biomass
Diversity Evenness
1 KALA 2006    Fixed          1          1        20    0.448    56.98
2.63      0.88
2 KALA 2006    Fixed          2          2        23    1.352    77.12
1.73      0.55
3 KALA 2006    Fixed          3          3        24    1.792   470.07
2.06      0.65
4 KALA 2006    Fixed          4          4        30    0.944   150.43
2.88      0.85
5 KALA 2006    Fixed          5          5        20    7.416   159.33
0.86      0.29
6 KALA 2006    Fixed          6          6        11    0.456     5.34
1.68      0.70

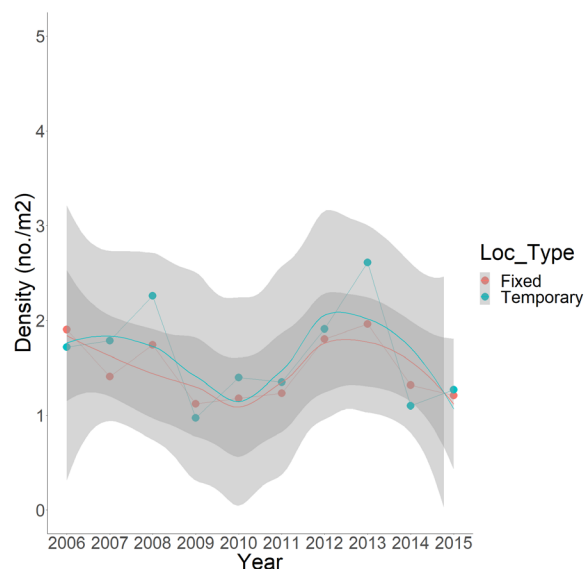
meanse<-summaryBy(Density~Year*Loc_Type, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))    # Generates table of Count,
Mean, SD, SE of Richness X Year X Transect type

print(meanse)

```

```
p <-ggplot(meanse, aes(x=Year, y=Density.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(0,5)
+ labs(y="Density (no./m2)") #Plots 2 loess
regression lines on the same plot for Density X Year X transect
type with 95% confidence interval error bands. One can substitute
"lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2005,2015,1)) #Adds chart elements such as text=50 points
and an x-scale from 2005 to 2015 at 1 year intervals.
```



```
logit<-function(x) return(sqrt(x)) # Transform the data
if it is right skewed. Better than log
```

```
Fish$LogitDensity<- logit((Fish$Density)) # Creates a variable
called LogitDensity, which is the square-root of the density.
```

```
fit1<-plm(LogitDensity~Year + Loc_Type, data=Fish,
index="Transect2", model="within") # Runs the plm program for
the fixed effects model
```

```
summary(fit1) # Prints the output of the fixed effects model
```

```

fit2<-plm(LogitDensity~Year + Loc_Type, data=Fish,
index="Transect2", model="random")      # Runs the plm program for
the random effects model

summary(fit2)      # Prints the output of the random effects model

phtest(fit1,fit2)      # Runs hausman test to compare the within or
fixed effects model to the random effects model. If the null
hypothesis (random model) is rejected at the p<0.5 level then
accept the results of the within/fixed effects model.

fit3<-lmer(Density ~ Year*Loc_Type + (1|Transect2), data=Fish)  #
Runs the linear mixed effects model

summary(fit3)      # Prints the output of the linear mixed effect
model

ResidDiagnostic<-function(fit) {      # Examine residuals of raw data
fit
  par(mfrow=c(2,2))
  plot(fitted(fit), resid(fit))
  qqnorm(resid(fit))
  hist(resid(fit))}
ResidDiagnostic(fit3)

pbgtest(fit2)      # Testing for serial or auto correlation. If
p<0.05 then yes.

bptest(Density~Year + Loc_Type, data=Fish, studentize=F)      #
Testing for homoskedasticity (homogeneity of variance). If p<0.05
then no.

# Biomass Trend Analysis
# Load the required packages

Sys.setenv(TZ="US/Hawaii")

```

```

Sys.getenv("TZ")
Sys.time()
library(lmerTest)      # This package contains the linear mixed
model (lmer) used for diagnostics
library(lmtest)        # This package contains the Breusch-Pagan
test (bptest) for homoskedascity
library(ggplot2)
library(doBy)
library(plm)           # This package contains the panel linear
model (plm) program

getwd()                # Returns the working directory
setwd("D:/Transfer/I&M/Fish")    # Sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Fish_Data_06-15.txt", header=TRUE, sep="\t")
# Imports the data file into the object Fish
head(Fish)             # Prints out the first six rows of the
data set

  Park Year Loc_Type Transect1 Transect2 Richness Density Biomass
Diversity Evenness
1 KALA 2006    Fixed          1          1        20    0.448    56.98
2.63      0.88
2 KALA 2006    Fixed          2          2        23    1.352    77.12
1.73      0.55
3 KALA 2006    Fixed          3          3        24    1.792   470.07
2.06      0.65
4 KALA 2006    Fixed          4          4        30    0.944   150.43
2.88      0.85
5 KALA 2006    Fixed          5          5        20    7.416   159.33
0.86      0.29
6 KALA 2006    Fixed          6          6        11    0.456     5.34
1.68      0.70

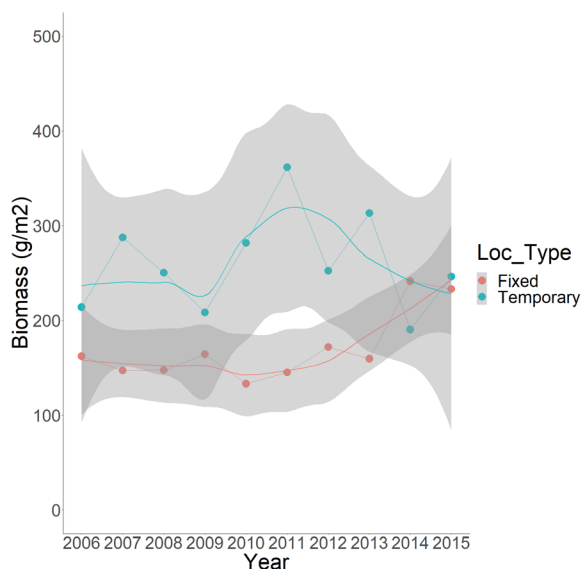
meanse<-summaryBy(Biomass~Year*Loc_Type, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))    # Generates table of Count,
Mean, SD, SE of Richness X Year X Transect type

print(meanse)

```

```
p <-ggplot(meanse, aes(x=Year, y=Biomass.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() +
ylim(0,500) + labs(y="Biomass (g/m2)") #Plots 2 loess
regression lines on the same plot for Biomass X Year X transect
type with 95% confidence interval error bands. One can substitute
"lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2005,2015,1)) #Adds chart elements such as text=50 points
and an x-scale from 2005 to 2015 at 1 year intervals.
```



```
logit<-function(x) return(log(x+1)) # Transform the data
if it is strongly right skewed.
```

```
Fish$LogitBiomass<- logit((Fish$Biomass)) # Better
transformation than sqrt.
```

```
fit1<-plm(LogitBiomass~Year + Loc_Type, data=Fish,
index="Transect2", model="within") # Runs the plm program for
the fixed effects model
```

```
summary(fit1) # Prints the output of the fixed effects model
```

```

fit2<-plm(LogitBiomass~Year + Loc_Type, data=Fish,
index="Transect2", model="random")      # Runs the plm program for
the random effects model

summary(fit2)      # Prints the output of the random effects model

phtest(fit1,fit2)

fit3<-lmer(Biomass ~ Year*Loc_Type + (1|Transect2), data=Fish)  #
Runs the linear mixed effects model

summary(fit3)      # Prints the output of the linear mixed effect
model

ResidDiagnostic<-function(fit) {      # Examine residuals of raw data
fit
  par(mfrow=c(2,2))
  plot(fitted(fit), resid(fit))
  qqnorm(resid(fit))
  hist(resid(fit))}
ResidDiagnostic(fit3)

pbgtest(fit2)      # Testing for serial or auto correlation. If
p<0.05 then yes.

bptest(LogitBiomass~Year + Loc_Type, data=Fish, studentize=F)
# Testing for homoskedasticity (homogeneity of variance). If p<0.05
then no.

# Diversity Trend Analysis
# Load the required packages

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()

```

```

library(lmerTest)          # This package contains the linear mixed
model (lmer) used for diagnostics
library(lmtest)            # This package contains the Breusch-Pagan
test (bptest) for homoskedascity
library(ggplot2)
library(doBy)
library(plm)               # This package contains the panel linear
model (plm) program

getwd()                    # Returns the working directory
setwd("D:/Transfer/I&M/Fish") # Sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Fish_Data_06-15.txt", header=TRUE, sep="\t")
# Imports the data file into the object Fish
head(Fish)                 # Prints out the first six rows of the
data set
  Park Year Loc_Type Transect1 Transect2 Richness Density Biomass
Diversity Evenness
1 KALA 2006   Fixed          1          1      20   0.448   56.98
2.63      0.88
2 KALA 2006   Fixed          2          2      23   1.352   77.12
1.73      0.55
3 KALA 2006   Fixed          3          3      24   1.792  470.07
2.06      0.65
4 KALA 2006   Fixed          4          4      30   0.944  150.43
2.88      0.85
5 KALA 2006   Fixed          5          5      20   7.416  159.33
0.86      0.29
6 KALA 2006   Fixed          6          6      11   0.456    5.34
1.68      0.70

meanse<-summaryBy(Diversity~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Generates table of Count,
Mean, SD, SE of Richness X Year X Transect type

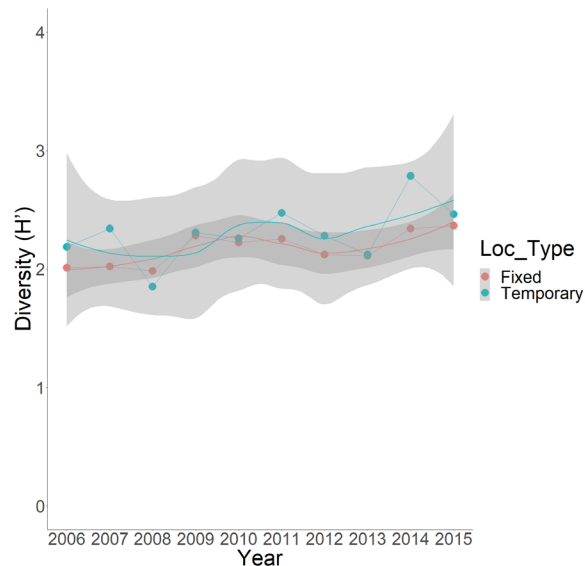
print(meanse)

p <-ggplot(meanse, aes(x=Year, y=Diversity.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+

```

```
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(0,4)
+ labs(y="Diversity (H')") #Plots 2 loess regression
lines on the same plot for Diversity X Year X transect type with
95% confidence interval error bands. One can substitute "lm" for
"loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2005,2015,1)) #Adds chart elements such as text=50 points
and an x-scale from 2005 to 2015 at 1 year intervals.
```



```
fit1<-plm(Diversity~Year + Loc_Type, data=Fish, index="Transect2",
model="within") # Runs the plm program for the fixed effects
model
```

```
summary(fit1) # Prints the output of the fixed effects model
```

```
fit2<-plm(Diversity~Year + Loc_Type, data=Fish, index="Transect2",
model="random") # Runs the plm program for the random effects
model
```

```
summary(fit2) # Prints the output of the random effects model
```

```
phtest(fit1,fit2)
```

```

fit3<-lmer(Diversity ~ Year*Loc_Type + (1|Transect2), data=Fish)
# Runs the linear mixed effects model

summary(fit3)      # Prints the output of the linear mixed effect
model

ResidDiagnostic<-function(fit) {  # Examine residuals of raw data
fit
  par(mfrow=c(2,2))
  plot(fitted(fit), resid(fit))
  qqnorm(resid(fit))
  hist(resid(fit))}
ResidDiagnostic(fit3)

pbgtest(fit2)      # Testing for serial or auto correlation. If
p<0.05 then yes.

bptest(Diversity~Year + Loc_Type, data=Fish, studentize=F)      #
Testing for homoskedasticity (homogeneity of variance). If p<0.05
then no.

# Numerical Density Trend Analysis - Endemic Species
# Fish Density-THDU

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lmerTest)
library(lattice)
library(ggplot2)
library(doBy)
library(plm)

getwd()            # returns the working directory
setwd("D:/Transfer/I&M/Fish")      # sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Endemic_Fish_Data_06-15.txt", header=TRUE,
sep="\t")

```

```

head(Fish)
  Year Park Loc_Type Transect Transect2 CAJA_Den CHOV_Den CHVE_Den
CTST_Den THDU_Den CAJA_DenT CHOV_DenT CHVE_DenT CTST_DenT
THDU_DenT CHPE_Bio CTST_Bio PAPO_Bio CHVE_Bio THDU_Bio CHPE_BioT
CTST_BioT PAPO_BioT CHVE_BioT THDU_BioT
1 2006 KALA Fixed 1 1 0.008 0.000 0
0.000 0.008 0.08944272 0.0000000 0 0.00000000 0.08944272
0 0.0000 0 0 0.0025 0 0.000000000
0 0 0.001084381
2 2006 KALA Fixed 2 2 0.000 0.104 0
0.000 0.080 0.00000000 0.3224903 0 0.00000000 0.28284271
0 0.0000 0 0 0.0082 0 0.000000000
0 0 0.003546693
3 2006 KALA Fixed 3 3 0.024 0.096 0
0.032 0.072 0.15491933 0.3098387 0 0.17888544 0.26832816
0 0.0155 0 0 0.0099 0 0.006679928
0 0 0.004278372
4 2006 KALA Fixed 4 4 0.024 0.112 0
0.040 0.048 0.15491933 0.3346640 0 0.20000000 0.21908902
0 0.0204 0 0 0.0029 0 0.008770450
0 0 0.001257631
5 2006 KALA Fixed 5 5 0.008 0.000 0
0.008 0.336 0.08944272 0.0000000 0 0.08944272 0.57965507
0 0.0003 0 0 0.0348 0 0.000130269
0 0 0.014856420
6 2006 KALA Fixed 6 6 0.008 0.000 0
0.000 0.080 0.08944272 0.0000000 0 0.00000000 0.28284271
0 0.0000 0 0 0.0009 0 0.000000000
0 0 0.000390689

```

```

meanse<-summaryBy(THDU_Den~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE of Coral
X Year BEST

```

```

print(meanse)

```

```

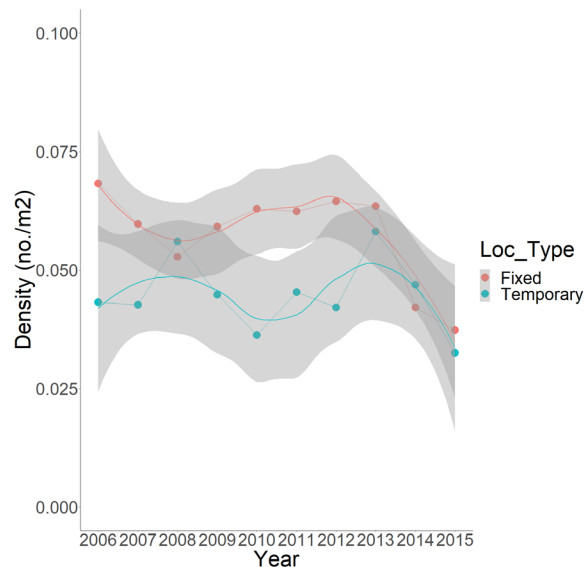
meanse1<-summaryBy(THDU_Den~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE of Coral
X Year BEST

```

```
print(meanse1)
```

```
p <-ggplot(meanse, aes(x=Year, y= THDU_Den.mean, col=Loc_Type)) +
  geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
  geom_smooth(method="loess", se=TRUE) + theme_classic() +
  ylim(0,0.1) + labs(y="Density (no./m2)" ) #Plots 2
  loess regression lines on the same plot for Richness X Year X
  transect type with 95% confidence interval error bands. One can
  substitute "lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
  seq(2006,2015,1)) #Adds chart elements such as text=50 points
  and an x-scale from 2008 to 2020 at 1 year intervals.
```



```
fit1<-plm(THDU_DenT~Year + Loc_Type, data=Fish, index="Transect2",
  model="within")
```

```
summary(fit1)
```

```
fit2<-plm(THDU_DenT~Year + Loc_Type, data=Fish, index="Transect2",
  model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that  
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2  
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and  
site effects
```

```
fit3<-lmer(THDU_DenT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),  
data=Fish)
```

```
summary(fit3)
```

```
ResidDiagnostic<-function(fit) { # Examine residuals of  
transformed data fit
```

```
par(mfrow=c(2,2))  
plot(fitted(fit), resid(fit))  
qqnorm(resid(fit))  
hist(resid(fit))}  
ResidDiagnostic(fit3)
```

```
=====  
# Fish Density-CTST
```

```
meanse<-summaryBy(CTST_Den~Year*Loc_Type, data=Fish,  
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),  
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE of Coral  
X Year BEST
```

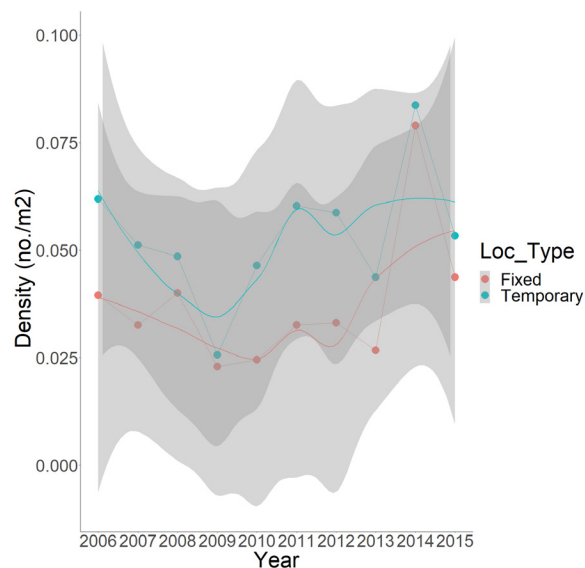
```
print(meanse)
```

```
meanse1<-summaryBy(CTST_Den~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST
```

```
print(meanse1)
```

```
p <-ggplot(meanse, aes(x=Year, y= CTST_Den.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.01,0.1) + labs(y=" Density (no./m2) ")          #Plots 2
loess regression lines on the same plot for Richness X Year X
transect type with 95% confidence interval error bands. One can
substitute "lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))      #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.
```



```
fit1<-plm(CTST_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(CTST_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(CTST_DenT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```
summary(fit3)
```

```
ResidDiagnostic<-function(fit) { # Examine residuals of
transformed data fit
```

```
par(mfrow=c(2,2))
```

```
plot(fitted(fit), resid(fit))
```

```
qqnorm(resid(fit))
```

```
hist(resid(fit))}
```

```
ResidDiagnostic(fit3)
```

```
=====
# Fish Density-CHOV
```

```
meanse<-summaryBy(CHOV_Den~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE of Coral
X Year BEST
```

```
print(meanse)
```

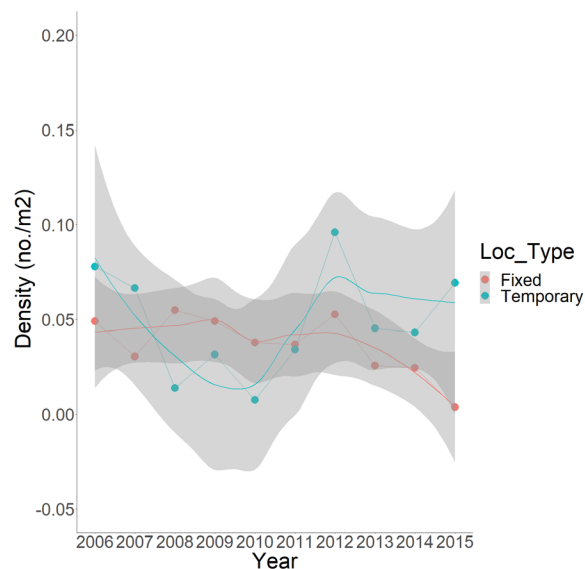
```
meanse1<-summaryBy(CHOV_Den~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
```

```
se=sd(x)/sqrt(length(x))) # Count, Mean, SD, SE of Coral
X Year BEST
```

```
print(meanse1)
```

```
p <-ggplot(meanse, aes(x=Year, y= CHOV_Den.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.05,0.2) + labs(y=" Density (no./m2) ") #Plots 2
loess regression lines on the same plot for Richness X Year X
transect type with 95% confidence interval error bands. One can
substitute "lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1)) #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.
```



```
fit1<-plm(CHOV_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(CHOV_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```

summary(fit2)

phptest(fit1,fit2)

Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
fit3<-lmer(CHOV_DenT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
summary(fit3)

ResidDiagnostic<-function(fit) { # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

# Biomass Trend Analysis - Endemic Species
# Fish Biomass-CHPE

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lmerTest)
library(lattice)
library(ggplot2)
library(doBy)
library(plm)

getwd() # returns the working directory

setwd("D:/Transfer/I&M/Fish") # sets the working directory to
C:\transfer\I&M\Fish

```

```

Fish<-read.table("KALA_Endemic_Fish_Data_06-15.txt", header=TRUE,
sep="\t")
head(Fish)

meanse<-summaryBy(CHPE_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse)

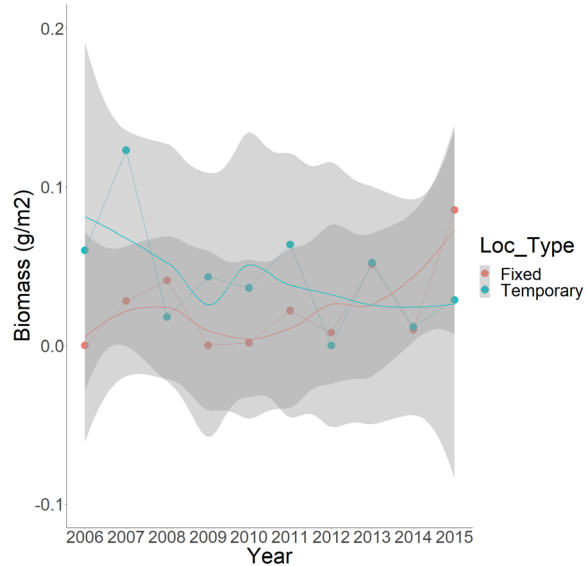
meanse1<-summaryBy(CHPE_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= CHPE_Bio.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.1,0.2) + labs(y="Biomass (g/m2)")          #Plots 2 loess
regression lines on the same plot for Richness X Year X transect
type with 95% confidence interval error bands. One can substitute
"lm" for "loess" to get a simple linear trend.

p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))          #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.

```



```
fit1<-plm(CHPE_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(CHPE_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phptest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(CHPE_Bio ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```

summary(fit3)

ResidDiagnostic<-function(fit) {  # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

=====
# Fish Biomass-CTST

meanse<-summaryBy(CTST_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse)

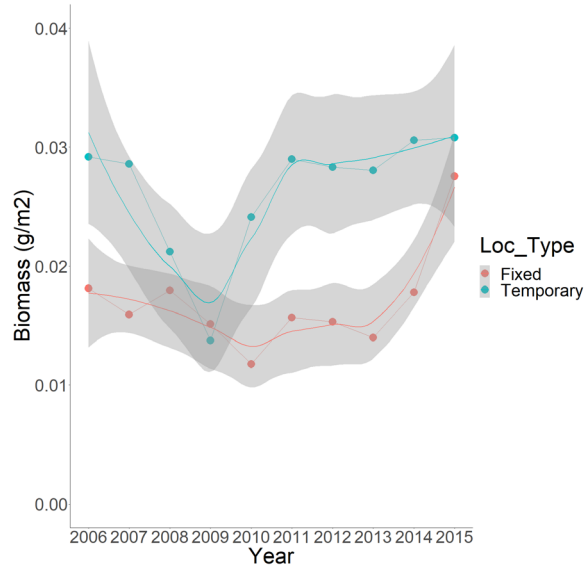
meanse1<-summaryBy(CTST_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= CTST_Bio.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() +
ylim(0,0.04) + labs(y="Biomass (g/m2)")          #Plots 2
loess regression lines on the same plot for Richness X Year X
transect type with 95% confidence interval error bands. One can
substitute "lm" for "loess" to get a simple linear trend.

p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))      #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.

```



```
fit1<-plm(CTST_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(CTST_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(CTST_BioT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```

summary(fit3)

ResidDiagnostic<-function(fit) {  # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

=====
# Fish Biomass-PAPO

meanse<-summaryBy(PAPO_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse)

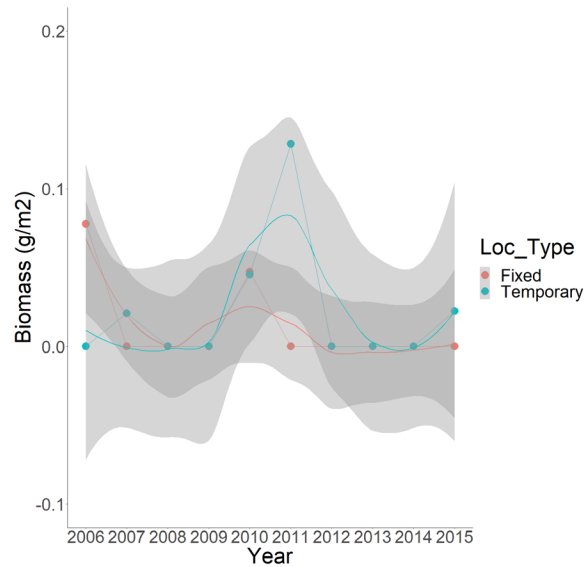
meanse1<-summaryBy(PAPO_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= PAPO_Bio.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.1,0.2) + labs(y="Biomass (g/m2)")          #Plots 2 loess
regression lines on the same plot for Richness X Year X transect
type with 95% confidence interval error bands. One can substitute
"lm" for "loess" to get a simple linear trend.

p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))          #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.

```



```
fit1<-plm(PAPO_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(PAPO_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(PAPO_Bio ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```

summary(fit3)

ResidDiagnostic<-function(fit) {  # Examine residuals of
transformed data fit

par(mfrow=c(2,2))

plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

=====
# Fish Biomass-CHVE

meanse<-summaryBy(CHVE_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse)

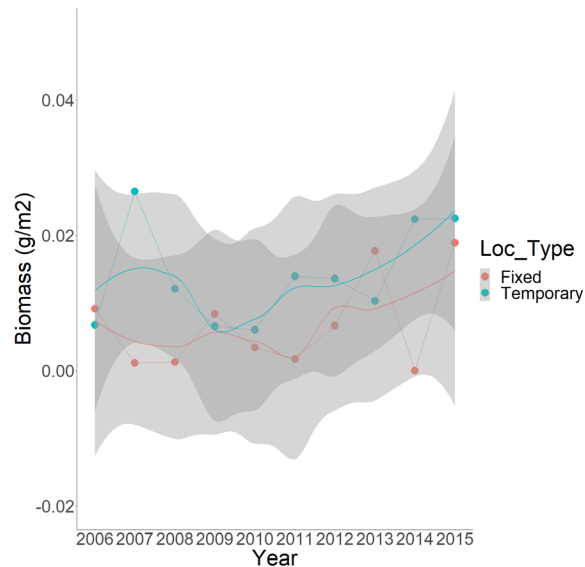
meanse1<-summaryBy(CHVE_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= CHVE_Bio.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.02,0.05) + labs(y="Biomass (g/m2)")          #Plots 2 loess
regression lines on the same plot for Richness X Year X transect
type with 95% confidence interval error bands. One can substitute
"lm" for "loess" to get a simple linear trend.

```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1)) #Adds chart elements such as text=50 points
and an x-scale from 2006 to 2015 at 1 year intervals.
```



```
fit1<-plm(CHVE_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(CHVE_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phptest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
fit3<-lmer(CHVE_Bio ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
summary(fit3)
```

```

ResidDiagnostic<-function(fit) {  # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

=====
# Fish Biomass-THDU

meanse<-summaryBy(THDU_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse)

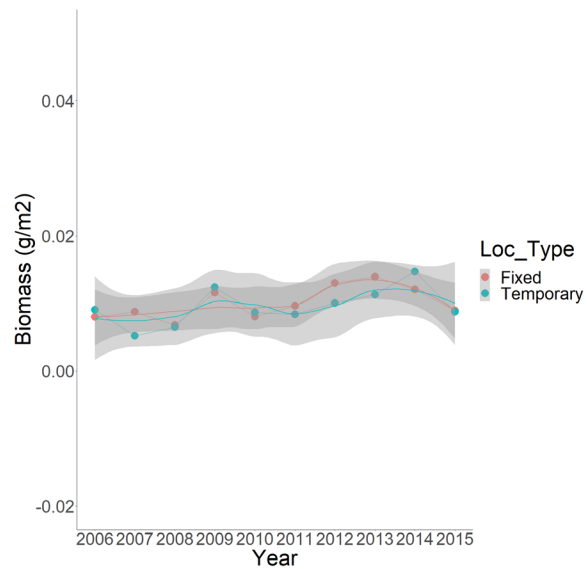
meanse1<-summaryBy(THDU_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE of Coral
X Year BEST

print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= THDU_Bio.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.02,0.05) + labs(y="Biomass (g/m2)")          #Plots 2 loess
regression lines on the same plot for Richness X Year X transect
type with 95% confidence interval error bands. One can substitute
"lm" for "loess" to get a simple linear trend.

p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))      #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.

```



```
fit1<-plm(THDU_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(THDU_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(THDU_Bio ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```
summary(fit3)
```

```

ResidDiagnostic<-function(fit) {  # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

```

Numerical Density Trend Analysis - Invasive Species

```
# Fish Density-ABVA
```

```

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lmerTest)
library(lattice)
library(ggplot2)
library(doBy)
library(plm)

```

```

getwd() # returns the working directory
setwd("D:/Transfer/I&M/Fish") # sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Invasive_Fish_Data_06-15.txt", header=TRUE,
sep="\t")
head(Fish)
  Year Park Loc_Type Transect Transect2 ABVA_Den CEAR_Den LUFU_Den
LUKA_Den ABVA_DenT CEAR_DenT LUFU_DenT  LUKA_DenT ABVA_Bio CEAR_Bio
LUFU_Bio LUKA_Bio ABVA_BioT CEAR_BioT LUFU_BioT LUKA_BioT
1 2006 KALA Fixed      1          1          0          0          0
0.000      0          0          0 0.00000000          0          0
0      0.00          0          0          0 0.00000000
2 2006 KALA Fixed      2          2          0          0          0
0.000      0          0          0 0.00000000          0          0
0      0.00          0          0          0 0.00000000
3 2006 KALA Fixed      3          3          0          0          0
0.008      0          0          0 0.08944272          0          0
0      0.96          0          0          0 0.2922561

```

```

4 2006 KALA      Fixed      4      4      0      0      0
0.008      0      0      0 0.08944272      0      0
0      2.85      0      0      0 0.5854607
5 2006 KALA      Fixed      5      5      0      0      0
0.000      0      0      0 0.00000000      0      0
0      0.00      0      0      0 0.00000000
6 2006 KALA      Fixed      6      6      0      0      0
0.000      0      0      0 0.00000000      0      0
0      0.00      0      0      0 0.00000000

```

```

meanse<-summaryBy(ABVA_Den~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))      # Count, Mean, SD, SE
print(meanse)
meanse1<-summaryBy(ABVA_Den~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))      # Count, Mean, SD, SE
print(meanse1)

```

```

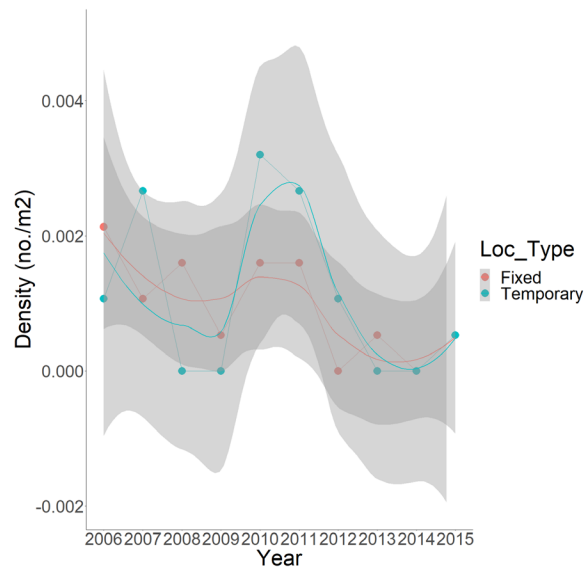
p <-ggplot(meanse, aes(x=Year, y= ABVA_Den.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.002,0.005) + labs(y="Density (no./m2)")      #Plots 2
loess regression lines on the same plot for Richness X Year X
transect type with 95% confidence interval error bands. One can
substitute "lm" for "loess" to get a simple linear trend.

```

```

p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))      #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.

```



```
fit1<-plm(ABVA_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(ABVA_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(ABVA_DenT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```
summary(fit3)
```

```

ResidDiagnostic<-function(fit) {  # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

=====
# Fish Density-CEAR

meanse<-summaryBy(CEAR_Den~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE

print(meanse)

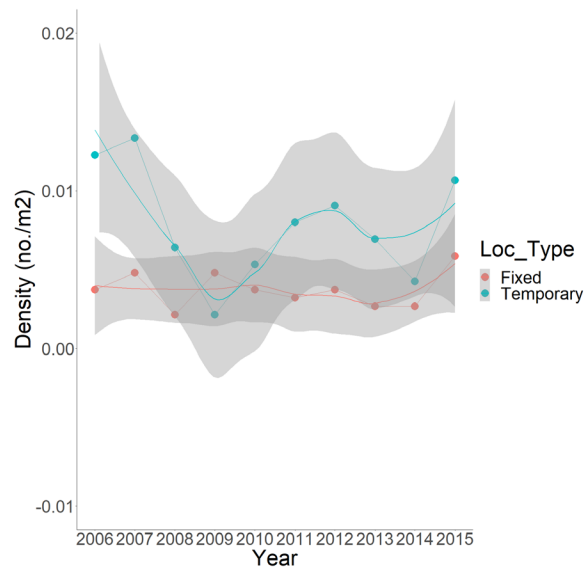
meanse1<-summaryBy(CEAR_Den~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE

print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= CEAR_Den.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.01,0.02) + labs(y="Density (no./m2)")          #Plots 2
loess regression lines on the same plot for Richness X Year X
transect type with 95% confidence interval error bands. One can
substitute "lm" for "loess" to get a simple linear trend.

p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))      #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.

```



```
fit1<-plm(CEAR_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(CEAR_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(CEAR_DenT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```
summary(fit3)
```

```
ResidDiagnostic<-function(fit) { # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
```

```
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)
```

```
=====
# Fish Density-LUFU
```

```
meanse<-summaryBy(LUFU_Den~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE
```

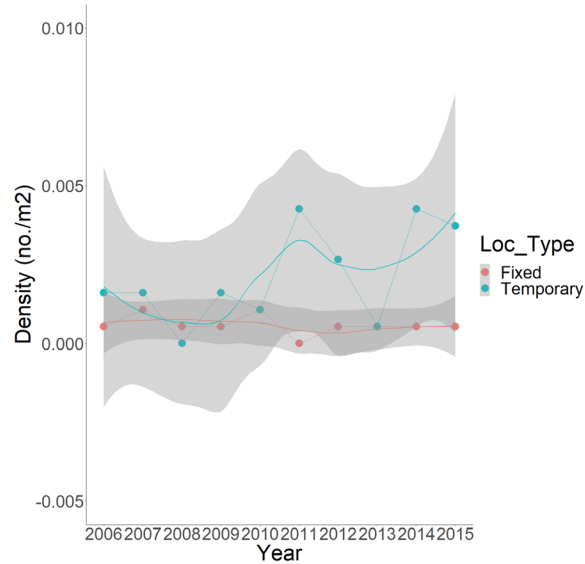
```
print(meanse)
```

```
meanse1<-summaryBy(LUFU_Den~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE
```

```
print(meanse1)
```

```
p <-ggplot(meanse, aes(x=Year, y= LUFU_Den.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.005,0.01) + labs(y="Density (no./m2)")          #Plots 2
loess regression lines on the same plot for Richness X Year X
transect type with 95% confidence interval error bands. One can
substitute "lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))          #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.
```



```
fit1<-plm(LUFU_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(LUFU_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(LUFU_DenT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```
summary(fit3)
```

```
ResidDiagnostic<-function(fit) { # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
```

```
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)
```

```
=====
# Fish Density-LUKA
```

```
meanse<-summaryBy(LUKA_Den~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE
```

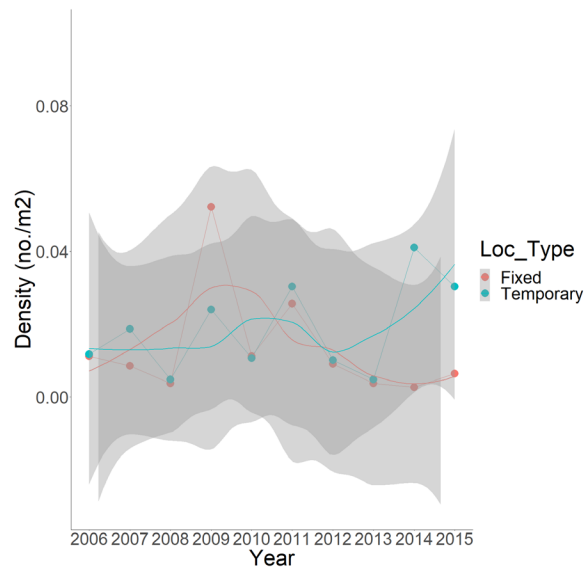
```
print(meanse)
```

```
meanse1<-summaryBy(LUKA_Den~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE
```

```
print(meanse1)
```

```
p <-ggplot(meanse, aes(x=Year, y= LUKA_Den.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
0.03,0.1) + labs(y="Density (no./m2)")          #Plots 2 loess
regression lines on the same plot for Richness X Year X transect
type with 95% confidence interval error bands. One can substitute
"lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))          #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.
```



```
fit1<-plm(LUKA_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(LUKA_DenT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(LUKA_DenT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```
summary(fit3)
```

```
ResidDiagnostic<-function(fit) { # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
```

```

plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))
ResidDiagnostic(fit3)

```

Biomass Trend Analysis - Invasive Species

```
# Fish Biomass-ABVA
```

```

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lmerTest)
library(lattice)
library(ggplot2)
library(doBy)
library(plm)

```

```

getwd() # returns the working directory
setwd("D:/Transfer/I&M/Fish") # sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Invasive_Fish_Data_06-15.txt", header=TRUE,
sep="\t")
head(Fish)

```

```

meanse<-summaryBy(ABVA_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE

```

```
print(meanse)
```

```

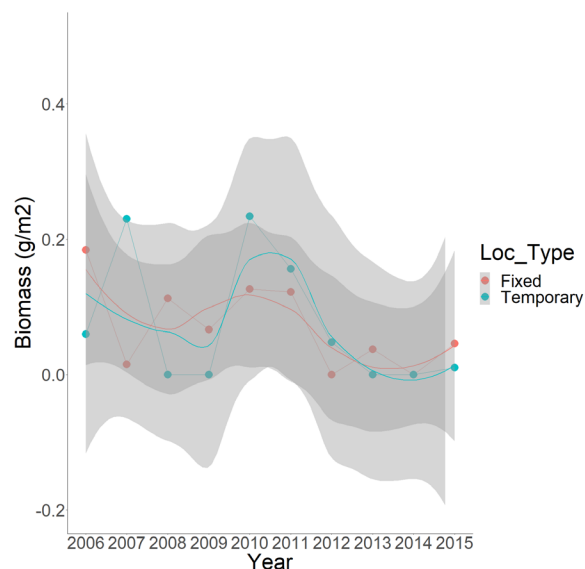
meanse1<-summaryBy(ABVA_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE

```

```
print(meanse1)
```

```
p <-ggplot(meanse, aes(x=Year, y= ABVA_Bio.mean, col=Loc_Type)) +
  geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
  geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
  0.2,0.5) + labs(y="Biomass (g/m2)") #Plots 2 loess
  regression lines on the same plot for Richness X Year X transect
  type with 95% confidence interval error bands. One can substitute
  "lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
  seq(2006,2015,1)) #Adds chart elements such as text=50 points
  and an x-scale from 2008 to 2020 at 1 year intervals.
```



```
fit1<-plm(ABVA_BioT~Year + Loc_Type, data=Fish, index="Transect2",
  model="within")
```

```
summary(fit1)
```

```
fit2<-plm(ABVA_BioT~Year + Loc_Type, data=Fish, index="Transect2",
  model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```

Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects

fit3<-lmer(ABVA_Bio ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)

summary(fit3)

ResidDiagnostic<-function(fit) { # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

=====
# Fish Biomass-CEAR

meanse<-summaryBy(CEAR_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE

print(meanse)

meanse1<-summaryBy(CEAR_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE

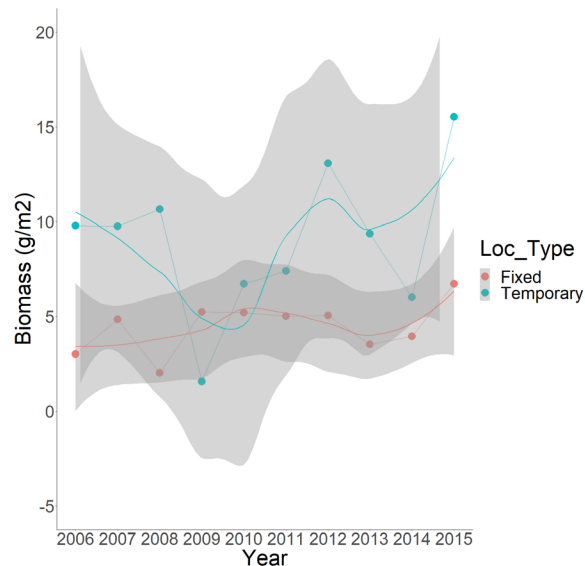
print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= CEAR_Bio.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+

```

```
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-5,20) + labs(y="Biomass (g/m2)") #Plots 2 loess regression lines on the same plot for Richness X Year X transect type with 95% confidence interval error bands. One can substitute "lm" for "loess" to get a simple linear trend.
```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks = seq(2006,2015,1)) #Adds chart elements such as text=50 points and an x-scale from 2006 to 2015 at 1 year intervals.
```



```
fit1<-plm(CEAR_BioT~Year + Loc_Type, data=Fish, index="Transect2", model="within")
```

```
summary(fit1)
```

```
fit2<-plm(CEAR_BioT~Year + Loc_Type, data=Fish, index="Transect2", model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that begins at year 0
```

```

Fish$Year<-as.factor(Fish$Year)  # Change Year and Transect2
covariates to factors.
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
fit3<-lmer(CEAR_BioT ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
summary(fit3)

ResidDiagnostic<-function(fit) {  # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

=====
# Fish Biomass-LUFU

meanse<-summaryBy(LUFU_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE

print(meanse)

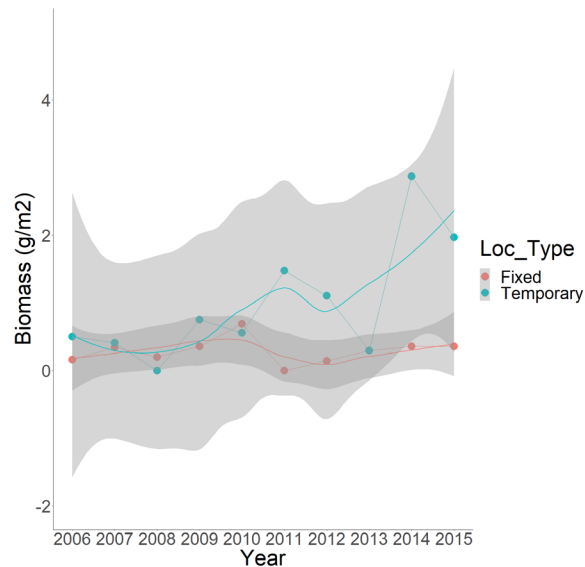
meanse1<-summaryBy(LUFU_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE

print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= LUFU_Bio.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-2,5)
+ labs(y="Biomass (g/m2)")          #Plots 2 loess regression
lines on the same plot for Richness X Year X transect type with 95%
confidence interval error bands. One can substitute "lm" for
"loess" to get a simple linear trend.

```

```
p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1)) #Adds chart elements such as text=50 points
and an x-scale from 2006 to 2020 at 1 year intervals.
```



```
fit1<-plm(LUFU_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(LUFU_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
fit3<-lmer(LUFU_Bio ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
summary(fit3)
```

```

ResidDiagnostic<-function(fit) {  # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
plot(fitted(fit), resid(fit))
qqnorm(resid(fit))
hist(resid(fit))}
ResidDiagnostic(fit3)

=====
# Fish Biomass-LUKA

meanse<-summaryBy(LUKA_Bio~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE

print(meanse)

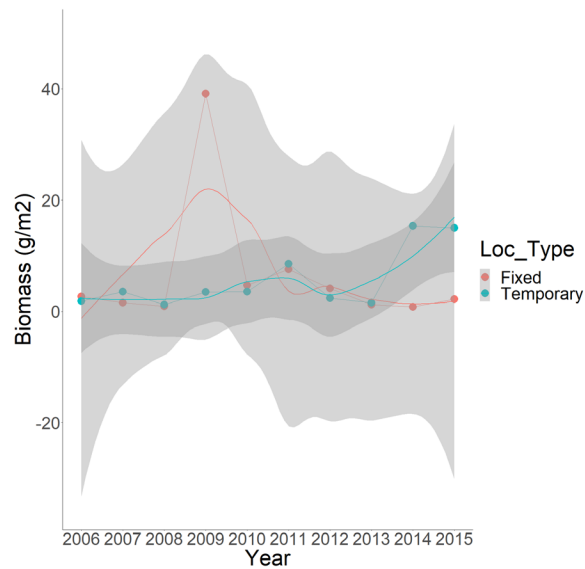
meanse1<-summaryBy(LUKA_Bio~Year, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))          # Count, Mean, SD, SE

print(meanse1)

p <-ggplot(meanse, aes(x=Year, y= LUKA_Bio.mean, col=Loc_Type)) +
geom_line(aes(colour=Loc_Type)) + geom_point(size=8)+
geom_smooth(method="loess", se=TRUE) + theme_classic() + ylim(-
30,50) + labs(y="Biomass (g/m2)")          #Plots 2 loess
regression lines on the same plot for Richness X Year X transect
type with 95% confidence interval error bands. One can substitute
"lm" for "loess" to get a simple linear trend.

p + theme(text=element_text(size=50)) + scale_x_continuous(breaks =
seq(2006,2015,1))          #Adds chart elements such as text=50 points
and an x-scale from 2008 to 2020 at 1 year intervals.

```



```
fit1<-plm(LUKA_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="within")
```

```
summary(fit1)
```

```
fit2<-plm(LUKA_BioT~Year + Loc_Type, data=Fish, index="Transect2",
model="random")
```

```
summary(fit2)
```

```
phtest(fit1,fit2)
```

```
Fish$WYear<-Fish$Year-2006 # Create a time covariate, WYear, that
begins at year 0
```

```
Fish$Year<-as.factor(Fish$Year) # Change Year and Transect2
covariates to factors.
```

```
Fish$Transect2<-as.factor(Fish$Transect2) # Model random year and
site effects
```

```
fit3<-lmer(LUKA_Bio ~ WYear*Loc_Type + (1|Transect2) + (1|Year),
data=Fish)
```

```
summary(fit3)
```

```
ResidDiagnostic<-function(fit) { # Examine residuals of
transformed data fit
par(mfrow=c(2,2))
```

Influential predictors on species richness using gamm with raw y variable and transformed predictors

```
Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lattice)
library(ggplot2)
library(scales)
library(doBy)
library(mgcv)      # This is the package that contains the
generalized additive mixed model (gamm) program
```

Year	Loc_Type	Survey_Date	Transect1	Transect2	Richness	Density	DensityT	Biomass	BiomassT	Diversity	Wave	Depth	Algae	Coral	CCA	Turf	AlgaeT	CoralT	CCAT	Turft	Rugosity	Brichness	AvgTemp	MinTemp	MaxTemp	Temp	pH	Salinity	Turbidity	DO	Chl	
1	2006	Fixed	8/2/2006	1	1	20	0.448	0.37	56.98	4.06	2.63	NW	17.8	11.31	0.62	1.23	81.92	0.343	0.079	0.111	1.132	1.41	15	24.65689	22.21158	26.9791	NA	NA	NA	NA	NA	NA
2	2006	Fixed	8/2/2006	2	2	23	1.352	0.86	77.12	4.36	1.73	NW	12.8	16.62	5.08	2.77	72.92	0.420	0.227	0.167	1.024	1.45	22	24.65689	22.21158	26.9791	NA	NA	NA	NA	NA	NA

```

3 2006      Fixed    8/10/2006          3          3          24    1.792
1.03 470.07        6.15        2.06  NW  14.2 20.62  5.31 4.00 68.92
0.471 0.232 0.201 0.979        1.72          13 24.65689 22.21158
26.9791  NA NA        NA        NA NA NA  NA
4 2006      Fixed    8/2/2006          4          4          30    0.944
0.66 150.43        5.02        2.88  NW  18.4 36.62  4.69 2.00 56.15
0.650 0.218 0.142 0.847        1.42          14 24.65689 22.21158
26.9791  NA NA        NA        NA NA NA  NA
5 2006      Fixed    8/8/2006          5          5          20    7.416
2.13 159.33        5.08        0.86  NW  11.5 4.46  9.85 5.38 79.77
0.213 0.319 0.234 1.104        1.43          9 24.65689 22.21158
26.9791  NA NA        NA        NA NA NA  NA
6 2006      Fixed    7/24/2006         6          6          11    0.456
0.38  5.34        1.85        1.68  NW  12.7 4.69  8.00 2.38 84.62
0.218 0.287 0.155 1.168        1.30          15 24.65689 22.21158
26.9791  NA NA        NA        NA NA NA  NA

```

```

meanse<-summaryBy(Richness~Year*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Generates table of Count,
Mean, SD, SE of Richness X Year X Transect type

```

```

meanse<-summaryBy(Richness~Wave*Loc_Type, data=Fish,
FUN=function(x) c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Generates table of Count,
Mean, SD, SE of Richness X Wave X Transect type

```

```

print(meanse)

```

```

fit1<-
gamm(Richness~Wave+s(Depth,k=5)+s(AlgaeT,k=5)+s(CoralT,k=5)+s(CCAT,
k=5)+s(TurfT,k=5)+s(Rugosity,k=5)+
s(Brichness,k=5)+s(AvgTemp,k=5)+s(MinTemp,k=5)+s(MaxTemp,k=5)+s(Tem
p,k=5)+s(pH,k=5)
+s(Salinity,k=5)+s(Turbidity,k=5)+s(DO,k=5)+s(Chl,k=5), data=Fish,
random=list(Year=~1,Transect2=~1))

```

```

summary(fit1$lme)
summary(fit1$gam)

```

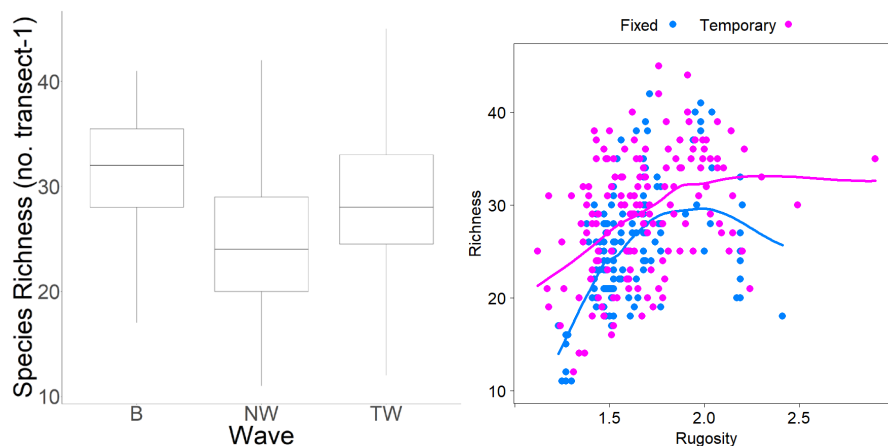
```
plot(fit1$gam,pages=1) #examines all of the smoothed independent
variables
gam.check(fit1$gam,pch=16) #checks residuals and normality. Also
examines if k values are too low (i.e. EDF close to k-1 and p-value
is significant). Solution is to increase k for that variable.
```

```
# Plot out the significant relationships using the raw data.
```

```
p1<-ggplot(Fish, aes(x=Wave, y=Richness)) + geom_boxplot() +
theme_classic()+ labs(y="Species Richness (no. transect-1)") +
theme(text=element_text(size=75)) #Plots a boxplot with text=75
points.
```

```
p2<-xyplot(Richness~Rugosity, groups=Loc_Type,
auto.key=list(points=TRUE, columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish) #Scatterplot of Richness by CCA X Transect type with
lowess line.
```

```
p1
print(p2, position=c(0,0.5,0.5,1),more=FALSE)
```



#Influential predictors on numerical density using gamm with transformed y variable and transformed predictors

```
# Load the required packages
```

```

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lattice)
library(ggplot2)
library(scales)
library(doBy)
library(mgcv)      # This is the package that contains the
generalized additive mixed model (gamm) program

getwd()              # Returns the working directory
setwd("D:/Transfer/I&M/Fish")  # Sets the working directory to
D:\Transfer\I&M\Fish
Fish<-read.table("KALA_Fish_Data_06-15_Predictor.txt", header=TRUE,
sep="\t")           # Imports the data file in the Fish object
head(Fish)          # Prints out the first six rows of the
data set

meanse<-summaryBy(Density~Year*Loc_Type, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))      # Generates table of Count,
Mean, SD, SE of Density X Year X Transect type

meanse<-summaryBy(Density~Wave*Loc_Type, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x))))      # Generates table of Count,
Mean, SD, SE of Density X Wave X Transect type

print(meanse)

fit1<-
gamm(DensityT~Wave+s(Depth,k=5)+s(AlgaeT,k=5)+s(CoralT,k=5)+s(CCAT,
k=5)+s(TurfT,k=5)+s(Rugosity,k=5)+
s(Brichness,k=5)+s(AvgTemp,k=5)+s(MinTemp,k=5)+s(MaxTemp,k=5)+s(Tem
p,k=5)+s(pH,k=5)
+s(Salinity,k=5)+s(Turbidity,k=5)+s(DO,k=5)+s(Chl,k=5), data=Fish,
random=list(Year=~1,Transect2=~1))

summary(fit1$lme)

```

```

summary(fit1$gam)

plot(fit1$gam,pages=1)  #examines all of the smoothed independent
variables
gam.check(fit1$gam,pch=16)  #checks residuals and normality. Also
examines if k values are too low (i.e. EDF close to k-1 and p-value
is significant). Solution is to increase k for that variable.

plot(fit1$gam,pages=1)  #examines all of the smoothed independent
variables
gam.check(fit1$gam,pch=16)  #checks residuals and normality. Also
examines if k values are too low (i.e. EDF close to k-1 and p-value
is significant). Solution is to increase k for that variable.
close to k-1 and p-value is significant). Solution is to increase k
for that variable.

# Plot out the significant relationships using the raw data.

p1<-ggplot(Fish, aes(x=Wave, y=Density)) + geom_boxplot() +
theme_classic()+ labs(y="Species Density (no./m2)") +
theme(text=element_text(size=75)) #Plots a boxplot with text=75
points.

p2<-xyplot(Density~Coral, groups=Loc_Type,
auto.key=list(points=TRUE, columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)  #Scatterplot of Density by Coral X Transect type with
lowess line.

p3<-xyplot(Density~CCA, groups=Loc_Type, auto.key=list(points=TRUE,
columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)  #Scatterplot of Density by CCA X Transect type with
lowess line.

```

```

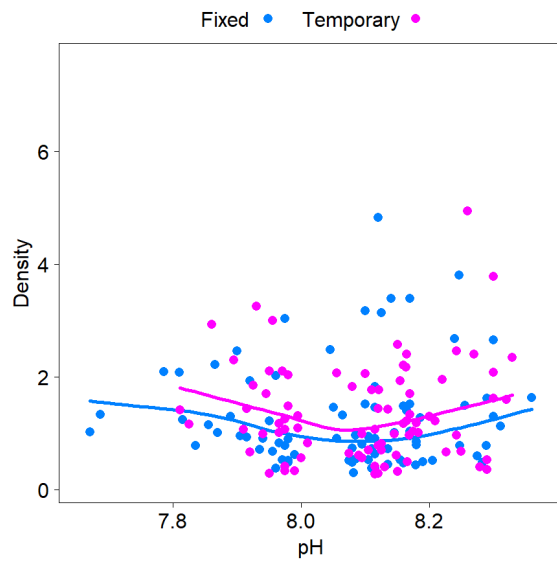
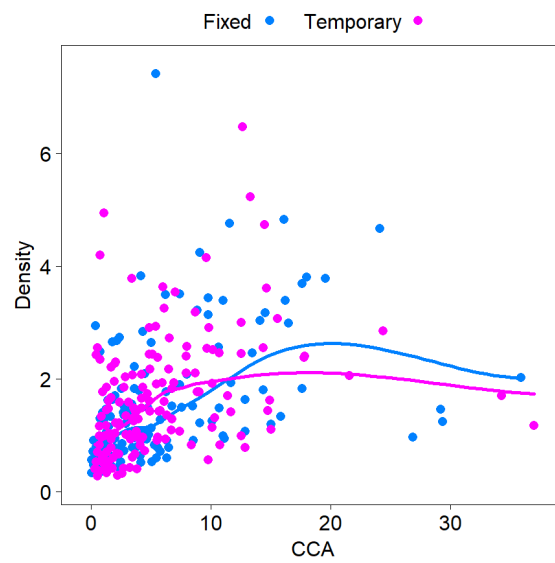
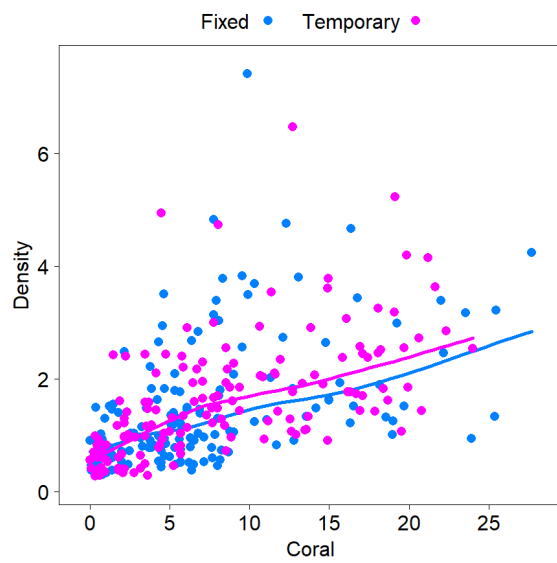
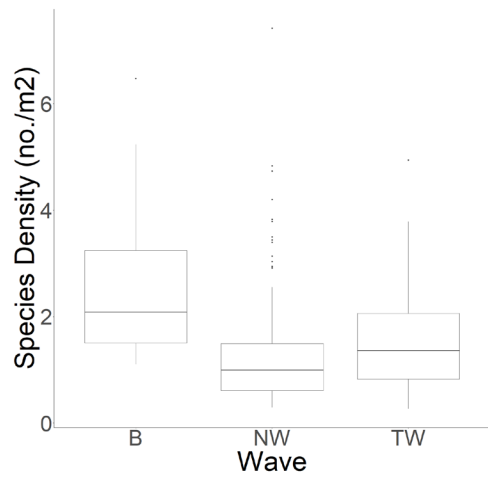
p4<-xyplot(Density~pH, groups=Loc_Type, auto.key=list(points=TRUE,
columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)    #Scatterplot of Density by Turf with lowess line.

```

```

p1
print(p2, position=c(0,0.5,0.5,1),more=TRUE)
print(p3, position=c(0.5,0.5,1,1),more=TRUE)
print(p4, position=c(0,0,0.5,0.5),more=FALSE)

```



#Influential predictors on biomass using gamm with transformed y variable and transformed predictors

```

# Load the required packages

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lattice)
library(ggplot2)
library(scales)
library(doBy)
library(mgcv)

getwd() # returns the working directory
setwd("D:/Transfer/I&M/Fish") # sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Fish_Data_06-15_Predictor.txt", header=TRUE,
sep="\t")
head(Fish) # Examine the first six rows of the data
set

summaryBy(Biomass~Year*Loc_Type, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE of Coral
X Year BEST

meanse<-summaryBy(Biomass~Wave*Loc_Type, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Generates table of Count,
Mean, SD, SE of Biomass X Wave X Transect type

print(meanse)

fit1<-
gamm(BiomassT~Wave+s(Depth,k=5)+s(AlgaeT,k=5)+s(CoralT,k=5)+s(CCAT,
k=5)+s(TurfT,k=5)+s(Rugosity,k=5)+
s(Brichness,k=5)+s(AvgTemp,k=5)+s(MinTemp,k=5)+s(MaxTemp,k=5)+s(Tem
p,k=5)+s(pH,k=5)
+s(Salinity,k=5)+s(Turbidity,k=5)+s(DO,k=5)+s(Chl,k=5), data=Fish,
random=list(Year=~1,Transect2=~1))

```

```
summary(fit1$lme)
summary(fit1$gam)
```

```
plot(fit1$gam,pages=1)  #examines all of the smoothed independent
variables
gam.check(fit1$gam,pch=16)  #checks residuals and normality. Also
examines if k values are too low (i.e. EDF close to k-1 and p-value
is significant). Solution is to increase k for that variable.
# Plot out the significant relationships using the raw data.
```

```
p1<-ggplot(Fish, aes(x=Wave, y=Biomass)) + geom_boxplot() +
theme_classic()+ labs(y="Biomass (g/m2)") +
theme(text=element_text(size=75)) #Plots a boxplot with text=75
points.
```

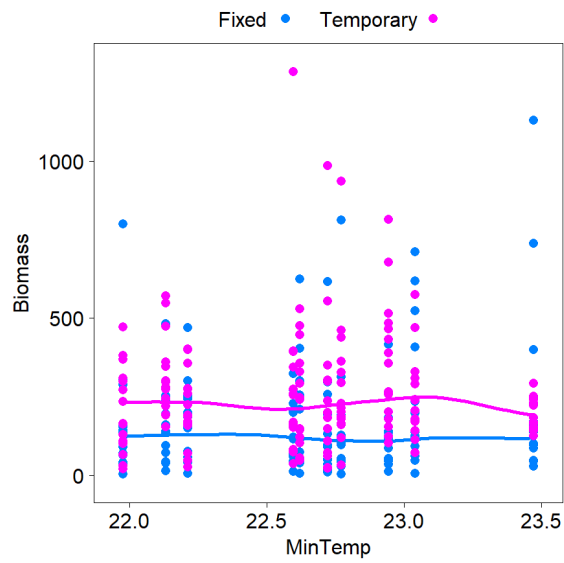
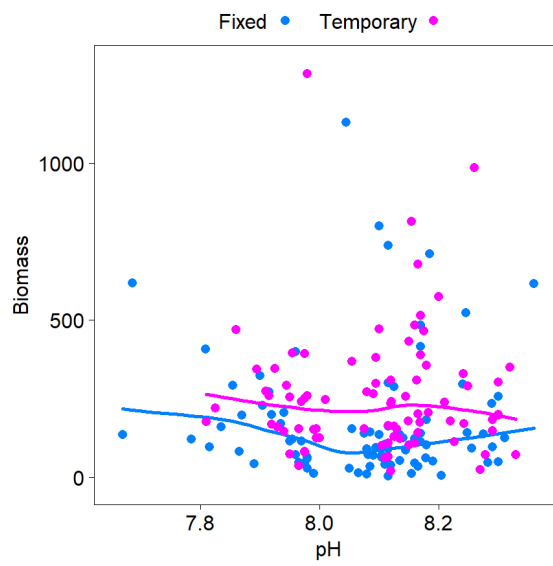
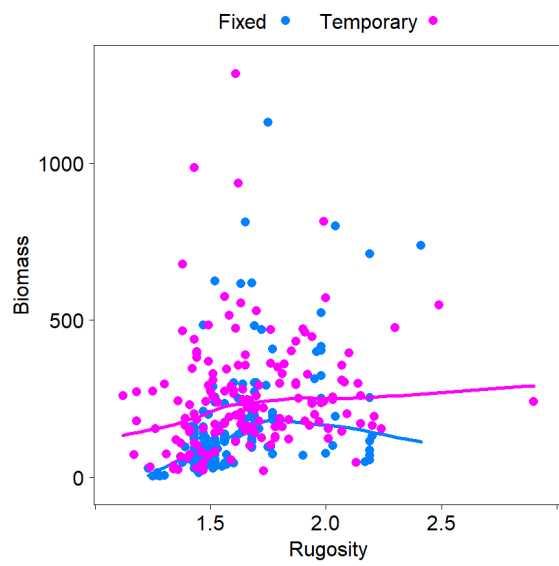
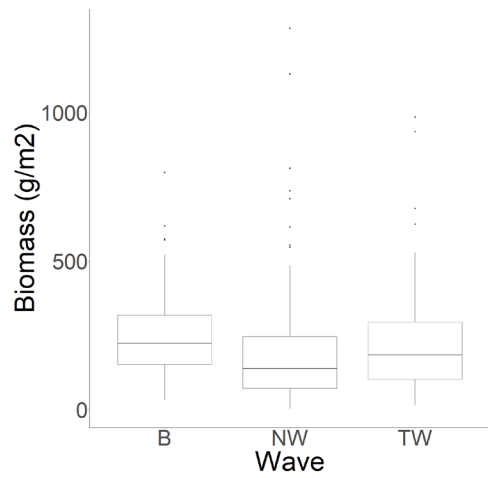
```
p2<-xyplot(Biomass~Rugosity, groups=Loc_Type,
auto.key=list(points=TRUE, columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)  #Scatterplot of Biomass by CCA X Transect type with
lowess line.
```

```
p3<-xyplot(Biomass~pH, groups=Loc_Type, auto.key=list(points=TRUE,
columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)  #Scatterplot of Biomass by Turf with lowess line.
```

```
p4<-xyplot(Biomass~MinTemp, groups=Loc_Type,
auto.key=list(points=TRUE, columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)  #Scatterplot of Biomass by Coral X Transect type with
lowess line.
```

```
p1
```

```
print(p2, position=c(0,0.5,0.5,1),more=TRUE)
print(p3, position=c(0.5,0.5,1,1),more=TRUE)
print(p4, position=c(0,0,0.5,0.5),more=FALSE)
```



#Influential predictors on diversity using gamm with raw y variable and transformed predictors

```

# Load the required packages

Sys.setenv(TZ="US/Hawaii")
Sys.getenv("TZ")
Sys.time()
library(lattice)
library(ggplot2)
library(scales)
library(doBy)
library(mgcv)

getwd() # returns the working directory
setwd("D:/Transfer/I&M/Fish") # sets the working directory to
C:\transfer\I&M\Fish
Fish<-read.table("KALA_Fish_Data_06-15_Predictor.txt", header=TRUE,
sep="\t")
head(Fish) # Examine the first six rows of the data
set

summaryBy(Div~Year*Loc_Type, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Count, Mean, SD, SE of Coral
X Year BEST

meanse<-summaryBy(Div~Wave*Loc_Type, data=Fish, FUN=function(x)
c(count=length(x), mean=mean(x), sd=sd(x),
se=sd(x)/sqrt(length(x)))) # Generates table of Count,
Mean, SD, SE of Div X Wave X Transect type

print(meanse)

fit1<-
gamm(Diversity~Wave+s(Depth,k=5)+s(AlgaeT,k=5)+s(CoralT,k=5)+s(CCAT
,k=5)+s(TurfT,k=5)+s(Rugosity,k=5)+
s(Brichness,k=5)+s(AvgTemp,k=5)+s(MinTemp,k=5)+s(MaxTemp,k=5)+s(Tem
p,k=5)+s(pH,k=5)
+s(Salinity,k=5)+s(Turbidity,k=5)+s(DO,k=5)+s(Chl,k=5), data=Fish,
random=list(Year=~1,Transect2=~1))

```

```

summary(fit1$lme)
summary(fit1$gam)

plot(fit1$gam,pages=1,pch=16)  #examines all of the smoothed
independent variables
gam.check(fit1$gam,pch=16)  #checks residuals and normality. Also
examines if k values are too low (i.e. EDF close to k-1 and p-value
is significant). Solution is to increase k for that variable.

# Plot out the significant relationships using the raw data.

p1<-ggplot(Fish, aes(x=Wave, y=Diversity)) + geom_boxplot() +
theme_classic()+ labs(y="Diversity (H')") +
theme(text=element_text(size=75)) #Plots a boxplot with text=75
points.

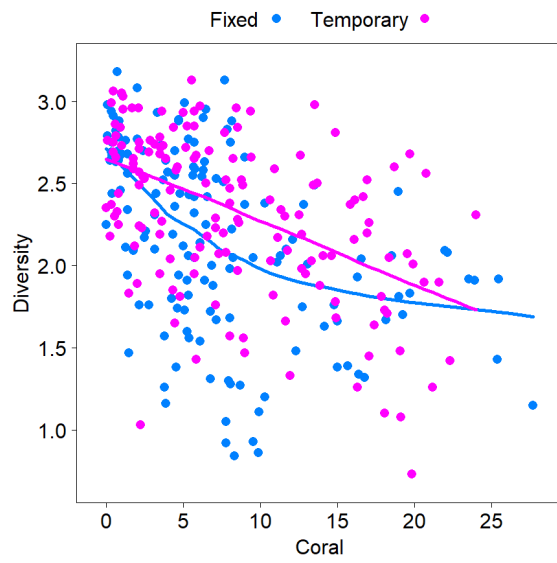
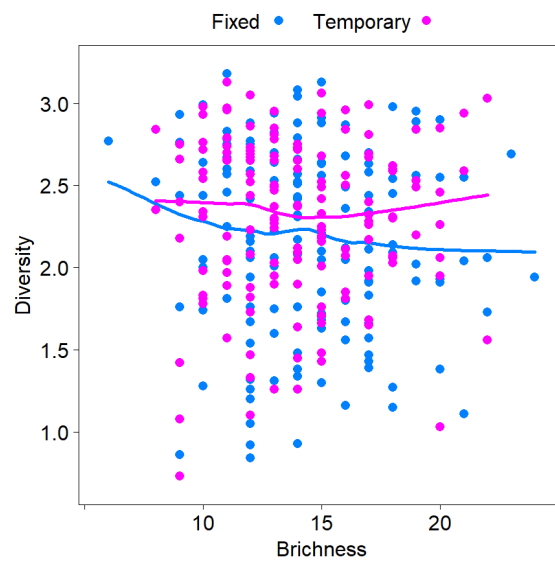
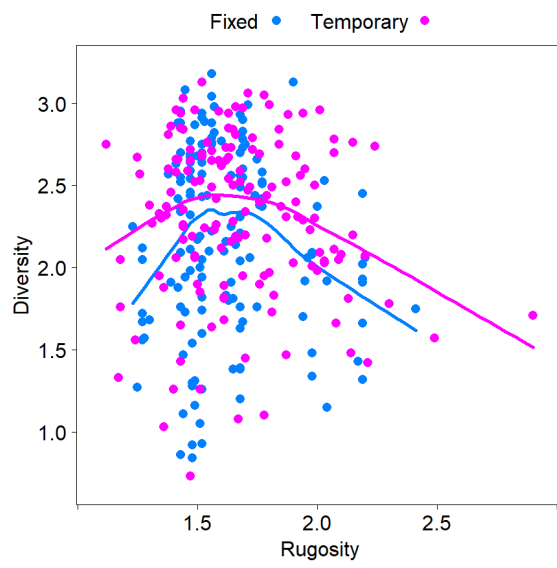
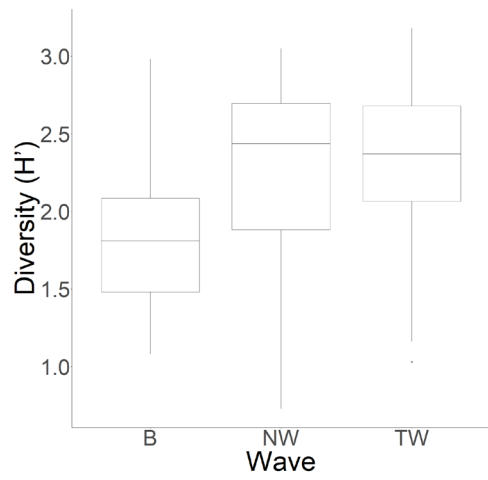
p2<-xyplot(Diversity~Rugosity, groups=Loc_Type,
auto.key=list(points=TRUE, columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)  #Scatterplot of Div by CCA X Transect type with lowess
line.

p3<-xyplot(Diversity~Brichness, groups=Loc_Type,
auto.key=list(points=TRUE, columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)  #Scatterplot of Div by Turf with lowess line.

p4<-xyplot(Diversity~Coral, groups=Loc_Type,
auto.key=list(points=TRUE, columns=2, cex=2),
par.settings=list(superpose.symbol=list(pch=16,cex=1.7)),
scales=list(tck=c(1,0), x=list(cex=2), y=list(cex=2)),
xlab=list(cex=2), ylab=list(cex=2), lwd=5, type=c("p","smooth"),
data=Fish)  #Scatterplot of Div by Coral X Transect type with
lowess line.

```

```
p1
print(p2, position=c(0,0.5,0.5,1),more=TRUE)
print(p3, position=c(0.5,0.5,1,1),more=TRUE)
print(p4, position=c(0,0,0.5,0.5),more=FALSE)
```



The Department of the Interior protects and manages the nation's natural resources and cultural heritage; provides scientific and other information about those resources; and honors its special responsibilities to American Indians, Alaska Natives, and affiliated Island Communities.

NPS 491/179660, March 2022

National Park Service
U.S. Department of the Interior



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1201 Oakridge Drive, Suite 150
Fort Collins, CO 80525