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A Habitat Analysis of Estuarine Fishes and Invertebrates, with Observations on the Effects of Habitat-Factor Resolution

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A Habitat Analysis of Estuarine Fishes and Invertebrates, with Observations on the Effects of Habitat-Factor Resolution

by

Brianna Michaud

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science with a concentration in Marine Resource Assessment College of Marine Science University of South Florida

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Abstract

Between 1988 and 2014, otter trawls, seine nets, and plankton nets were deployed along the salinity gradients of 18 estuaries by the University of South Florida and the Florida Fish and Wildlife Research Institute (FWRI, a research branch of the Florida Fish and Wildlife Conservation Commission). The purpose of these surveys was to document the responses of aquatic estuarine biota to variation in the quantity and quality of freshwater inflows that were being managed by the Southwest Florida Water Management District (SWFWMD).

In the present analyses, four community types collected by these gears were compared with a diversity of habitat factors to identify the factors with the greatest influence on beta diversity, and also to identify the factors that were most influential to important prey species and economically important species. The four community types were (1) plankton-net invertebrates, (2) plankton-net ichthyoplankton, (3) seine nekton, and (4) trawl nekton. The habitat factors were (1) vertical profiles of salinity, dissolved oxygen, pH, and water temperature taken at the time of the biological collections, (2) various characterizations of local habitat associated with seine and trawl deployments, (3) chlorophyll \( a \), color, and turbidity data obtained from the STORET database (US Environmental Protection Agency), and (4) data that characterize the effects of freshwater inflow on different estuarine zones, including factors for freshwater inflow, freshwater turnover time, and temporal instability in freshwater inflow (flashiness). Only 13 of the 18 estuaries had data that were comprehensive enough to allow habitat-factor analysis.

An existing study had performed distance-based redundancy analysis (dbRDA) and principle component analysis (PCA) for these data within 78 estuarine survey zones that were
composited together (i.e., regardless of estuary of origin). Based on that study’s findings, the communities of primarily spring-fed and primarily surface-fed estuaries were analyzed separately in the present study. Analysis was also performed with the habitat factors grouped into three categories (water management, restoration, and water quality) based on their ability to be directly modified by different management sectors.

For an analysis of beta diversity interactions with habitat factors, dbRDA (called distance-based linear modeling (DistLM) in the PRIMER software) was performed using PRIMER 7 software (Quest Research Limited, Auckland, NZ). The dbRDA indicated pH, salinity, and distance to the Gulf of Mexico (distance-to-GOM) usually explained the most variation in the biotic data. These results were compared with partial dbRDA using the Akaike Information Criterion (AIC) as the model selection criterion with distance-to-GOM held as a covariate to reduce the effect of differences in the connectivity of marine-derived organisms to the different estuaries; distance-to-GOM explained between 8.46% and 32.4% of the variation in beta diversity. Even with the variation from distance-to-GOM removed, salinity was still selected as most influential factor, explaining up to an additional 23.7% of the variation in beta diversity. Factors associated with the water-management sector were most influential (primarily salinity), followed by factors associated with the restoration sector (primarily factors that describe shoreline type and bottom type).

For the analysis of individual species, canonical analysis of principal coordinates (CAP) was performed to test for significant difference in community structure between groups of sites that represented high and low levels of each factor. For those communities that were significantly different, an indicator value (IndVal) was calculated for each species for high and low levels of each factor. Among species with significant IndVal for high or low levels of at least
one factor, emphasis was given to important prey species (polychaetes, copepods, mysids, shrimps, bay anchovy juveniles, and gammaridean amphipods) and to species of economic importance, including adults, larvae and juveniles of commercial and recreational fishes, pink shrimp, and blue crab. Shrimps, copepods and mysids were all associated with estuarine zones that had low percentages of wooded or lawn-type shoreline, a factor that may serve as a proxy for flood conditions, as lawns or trees were usually only sampled with seines at high water elevations and in the freshwater reaches of the estuaries. Many copepod and shrimp species were strongly associated with high flushing times, which suggests that if flushing times were too short in an estuarine zone, then these species or their prey would be flushed out.

Multiple regression analysis was performed on each of the selected indicator species, using AIC as a selection criterion and distance-to-GOM as a covariate. As might be expected, the apparent influences of different habitat factors varied from species to species, but there were some general patterns. For prey species in both spring-fed and surface-fed estuaries, pH and flushing time explained a significant amount of variation. In surface-fed estuaries, the presence of oysters on the bottom also had a positive effect for many prey species. For economically important species, depth was important in both spring-fed and surface-fed estuaries. This suggested the importance of maintaining large, shallow areas, particularly in surface-fed estuaries. Another important factor in spring-fed estuaries was the percent coverage of the bottom with sand; however, a mixture of positive and negative coefficients on this factor suggested the importance of substrate variety. In surface-fed estuaries, flashiness also often explained substantial variation for many economically important species, usually with positive coefficients, possibly due to the importance of alternation between nutrient-loading and high-
primary-productivity periods. When comparing the three management sectors, the restoration sector was the most explanatory.

Several factors were averaged over entire estuaries due to data scarcity or due to the nature of the factors themselves. Specifically, the STORET data for chlorophyll, color, and turbidity was inconsistently distributed with in the survey areas and was not collected at the same time as the biological samples. Moreover, certain water-management factors such as freshwater-inflow rate and flashiness are inherently less dimensional than other factors, and could only be represented by a single observation (i.e., no spatial variation) at any point in time. Due to concern that reduced spatiotemporal concurrence/dimensionality was masking the influence of habitat factors, the community analysis was repeated after representing each estuary with a single value for each habitat factor. We found that far fewer factors were selected in this analysis; salinity was only factor selected from the water-management factors.

Overall, the factor that explained the most variation most often was the presence of emergent vegetation on the shoreline. This factor is a good proxy for urban development (more developed areas have lower levels of emergent vegetation on the shoreline). Unlike the previous analysis, the restoration sector overwhelmingly had the highest $R^2$ values compared with other management sectors. In general, these results indicate the seeming importance of salinity in the previous analysis was likely because it had a higher resolution compared with many other factors, and that the lack of resolution homogeneity did influence the results.

Of the habitat factors determined to be most influential with the analysis of communities and individual species (salinity, pH, emergent vegetation and lawn-and-trees shoreline types, oyster and sand bottom types, depth, flashiness, and flushing time) most were part of an estuarine gradient with high values at one end of the estuary with a gradual shift to low values at the other
end. Since many of the analyzed species also showed a gradient distribution across the estuary, the abundance and community patterns could be explained by any of the habitat factors with that same gradient pattern. Therefore, there is a certain limitation to determining which factors are most influential in estuaries using this type of regression-based analysis. Three selected factors that do not have a strong estuarine gradient pattern are the sand bottom type, depth, and flashiness. In particular, flashiness has a single value for each estuary so it is incapable of following the estuarine gradient. This suggests that flashiness has an important process-based role that merits further investigation of its effect on estuarine species.
Chapter 1 - Literature Review and a Brief History of Multivariate Community Analysis:

The study of community ecology began over 200 years ago with the work of Alexander Von Humboldt (1807). Von Humboldt’s work was largely descriptive and focused on land-based vegetation communities. In particular, Von Humboldt noted that certain plants were commonly associated and that plants experiencing similar environmental conditions (i.e., tropical climate) tended to have similar physical characteristics. He proposed that the habitat effects of climate, soil, and vegetation should have similar effects on vegetation communities worldwide. His work was followed by similar work throughout the beginning of the 19th century by other botanists such as Joachim Schouw, Franz Meyen, Oswald Heer, and August Grisebach. By the mid-19th century, these same principles were being applied to oceanic communities. Notable contributors include Karl Möbius, who described the interactions of organisms in oyster beds (1893), Ernst Haeckel, who defined the term “ecology” in 1870, Carl Semper, who discussed interactions such as competition, parasitism, and mimicry, and Edward Forbes (1844), who divided the Aegean Sea into eight biological zones and discussed the influence of climate and depth on these zones. Towards the end of the century, entomologist Lorenzo Camerano published the first known food-web diagrams and discussed how perturbations would affect the food-web system as a whole (English version, Camerano, 1994).

At the end of the 19th century, Karl Pearson started his work on linear regression. Regression had previously been conceived by Sir Francis Galton in his work on genetics in pea plants (Galton, 1889), but the first mathematically rigorous treatment of correlation and regression was published by Pearson in 1896. In this work, Pearson demonstrated how to
calculate the optimal slope and correlation coefficient from the product moment. Galton also wrote a vague conception of multiple regression when he realized that multiple prior generations of pea plants could have an effect on the phenotype of the newest generation (i.e., the effect of the mother, the grandmother, and the great grandmother) and that these effects would not be equal (Galton, 1898). Pearson later refined this idea into the form of multiple regression that is well-known today (Pearson, 1938). Other contributions of Pearson include chi distance, p-values, and principle component analysis (Pearson, 1900, Pearson, 1901).

At the beginning of the 20th century, several schools of thought emerged in regard to how biological communities functioned. The first was posited by Frederic Clements (1916, 1920). Based on his study of Nebraska vegetation and previous studies on succession, such as those by Henry Cowles, Clements developed the theory that vegetation communities change over time until they reach a "climax state" with a community that is most perfectly suited for that particular environment. Under Clements’ theory, the community behaved much like a single organism, with species acting like “organs” that depended on one another, and the entire community could be considered a single evolutionary unit. Clements was also influential in his development of methods for the study of community ecology such as using quadrats, transects, and removal and transplant experiments (1905). These methods were some of the first attempts to make community ecology a quantitative, rather than descriptive, science. He also wrote about using certain species as indicators of early- or late-stage communities.

Clements’ theory on communities was challenged by Henry Gleason in 1917. Then, in 1926, Gleason proposed his “individualistic concept” of plant communities. Gleason argued that Clements’ theory assumed too much homogeneity, and that the associations were far less structured than Clements suggested. Instead, Gleason posited that the abundance of each species
changes independently in response to environmental gradients. Therefore, communities that arise in different areas are more or less coincidental. In this case, the community would not be considered its own evolutionary unit, since each species in the community may be responding to different environmental conditions, and populations would change at different rates. It should be noted that the present study does not follow the dogma of either of these theories, and a range of options exists between the two extremes (Fuller, 1918).

While plant community ecology was developing new theories, animal community ecology was also taking steps forward. In 1927, Charles Elton wrote the now classic book *Animal Ecology*. In this book, he outlined many of the concepts that integrated population ecology and community ecology and opened the door for the study of trophic dynamics. These concepts included niches, the food chain/web, and the pyramid of numbers where many smaller animals are needed to support a few larger animals. Sir Aruthur Tansley wrote "The use and abuse of vegetational terms and concepts" in 1935 which coined the term “ecology” and emphasized the importance of the transfer of materials from the physical environment to the biotic one. The new idea of ecology was further married to trophic dynamics and succession with the work of Raymond Lindeman (1942) on lake ecosystems which included elements of biogeochemistry and mathematical models of energy flow.

Around the same time as these developments, there were efforts being made to describe ecological interactions mathematically. One of the earliest examples is the Lotka-Volterra model of predator-prey interactions. The model was originally proposed by Alfred Lotka in 1910 in relation to the theory of autocatalytic chemical reactions. He later extended the use of this equation to organic systems, first with an herbivorous species as an example and later with predators and prey (Lotka, 1920, Lotka, 1925). The same equations were published by Vito
Volterra in 1926 to explain the observation of Umberto D'Ancona that there were a higher percentage of predatory fish caught in the Adriatic Sea after fishing effort had decreased during World War I. Though this model represents a very basic system and makes many simplifying assumptions that are now not commonly held as being true, it provided a starting point for many other scientists to build more complex equations.

Another major contributor at the time was Ronald Fischer. In 1912, Fischer developed the maximum likelihood method which is used to find ideal values for parameters in equations, a method that is essential to many types of statistical analysis. In 1918, in a paper on quantitative genetics, he first introduced the term “variance” and suggested that it be formally analyzed. He followed this paper with the creation of Analysis of Variance (ANOVA) in 1921, a method that is widely used today. In 1924, he created the $F$ distribution, which is the null distribution used to test the significance of ANOVA and multiple regression. Further statistical methods were published in 1932, including techniques for meta-analysis and using a standard $p$-value of 0.05, which represents a 1-in-20 rate of error.

Much of the early development of non-parametric statistics was far removed from the realm of ecology, though many were aware of the work of Fischer and others. In the psychology field, Charles Spearman developed the Spearman rank correlation, a version of the Pearson correlation that did not require the population to have a normal distribution (1904). Spearman also coined the term “factor analysis,” which refers to the description many correlated factors with a few latent uncorrelated factors. One form of factor analysis, canonical correlation, was developed in the realm of economics by Harold Hotelling in 1936.

The integration of ecology and mathematics continued through the middle of the 20th century. George Hutchinson, along with his student, Raymond Lindeman (1942), developed the
idea of trophic levels as a way to numerically evaluate the efficiency of energy transfer in different ecosystems. Hutchinson also built on Elton’s niche theory, related biological productivity to nutrient availability, and discussed the presence of feedback loops in ecosystems (Slobodkin, 1993). Another important innovation was the dissimilarity measure created by J. Roger Bray and John Curtis (1957) for the ordination of Wisconsin forest communities. The Bray-Curtis dissimilarity measure is calculated by summing all the absolute differences in abundance for every species between the two sites and then dividing that sum by the sum of the total abundance for both sites. This results in a value between 0 and 1 where 0 is when the sites are identical in species abundance and composition and 1 is when the sites share no species in common; it can also be represented as a percentage that ranged from 0% (all species present in the same proportions) to 100% (no species in common). The Bray-Curtis dissimilarity measure can be viewed as a measure of the difference in species abundance and composition between samples or beta diversity and has also been determined to be the best dissimilarity measure to use for the ordination of ecological abundance data (Kessell and Whittaker, 1976). Even though Bray-Curtis dissimilarity can be viewed as a measure of beta diversity, the term was not coined until 1960 by Robert Whittaker. Whittaker also developed gradient analysis on vegetation by comparing the logarithm of sample similarity and environmental separation (Whittaker and Niering, 1965, Whittaker 1973). This kind of analysis could be seen as a precursor to modern techniques such as distance-based redundancy analysis, though Whittaker’s method only works with one habitat factor at a time (e.g., elevation or soil moisture). Multi-dimensional scaling (MDS) was undergoing similar development in the realm of psychology. Most notably, Shepard (1962) and Kruskal (1964) were developing non-metric MDS which would later be used by ecologists (Anderson, 1971).
Wolfowitz first used the term “nonparametric” in 1942 to mean “where the functional forms of the distributions are unknown.” In many other statistical methods (e.g., ANOVA, redundancy analysis, etc), it is assumed that the data have a normal distribution; however, with organism abundance data, this is rarely the case. Therefore, using these types of tests to analyze or partition variance would be inappropriate. Some early forms of non-parametric statistics include the aforementioned Spearman’s r (Spearman, 1904), Friedman’s use of ranks in analysis of variance (Friedman, 1937), and Cochran’s Q test (Cochran, 1950). Several non-parametric methods were used in the present study, including indicator values (IndVal), distance-based redundancy analysis (db-RDA), canonical analysis of principal coordinates (CAP), and biological-environmental analysis (BEST).

The indicator value method used in the present study was created by Dufrene and Legendre (1997). This new approach combined a species’ relative abundance with its relative frequency of occurrence in different groups of sites to give a value that is independent of the relative abundance of other species. The indicator value will be close to 0 if the species is not strongly associated with one group over the others and close to 100 if the species is strongly associated with one group over the others. Before this method was developed, there were several other proposed ways of selecting indicator species. Macnaughton-Smith (1965) used information analysis, which is a symmetric approach that considers joint absences and joint presences equally, yet this is not usually appropriate for abundance data (Field, 1969). Later, Field (1969) created information statistic tests which assumed the probability of observing a given species in a given group has a chi-square distribution, and thus the probabilities of two groups can be obtained from a chi-square table to determine significant difference (Field, 1969, 1982). Another technique that has been used is to calculate the $F$-value for each species in order to determine
which species had the greatest contribution to each group (Shin, 1982). Finally, Hill (1979) created the two-way indicator species analysis (TWINSPAN) procedure, which sequentially divides all of the sites into subsets, and at each division gives each species an attribute that describes its preference for one subset. The species are then compared to pseudo-species with pre-defined relative abundances in order to determine which of the original species had a preference for a subgroup of sites. In the case of using the chi-square test, abundance data does not always meet the assumptions of the chi-square distribution, and thus it is not always appropriate. In the case of using the F-value, the species are ordered by relative contribution to between-group variation, but there is no test to determine which of these contributions are significant. Two main problems with TWINSPAN are its assumption that a strong gradient dominates the data structure, which may cause it to fail to identify other structures or patterns in the data, and its somewhat arbitrary nature in separating subgroups (Belbin and McDonald, 1993). In contrast, indicator values are independent of the relative abundance of other species and use a randomization procedure rather than pseudo-species to define species’ preference.

Distance-based redundancy analysis, which was developed by Legendre and Anderson (1999), is a form of multivariate multiple regression that uses principle component analysis (PCoA) to create a Euclidean embedding of non-metric or semi-metric dissimilarity measures (such as Bray-Curtis dissimilarity). Since PCoA embedding will only include the Euclidean portion of the data, the dissimilarity matrix can be corrected to account for the non-Euclidean portion, using the method of Gower and Legendre (1986). Distance-based redundancy analysis was originally designed so that abundance data could be analyzed using parametric methods such as ANOVA and MANOVA, but it also lends itself to variance partitioning among multiple continuous explanatory variables (multivariate multiple regression). Examples of previous
attempts to solve this problem of partitioning variance for community data include the efforts of Pillar and Orlóci (1996), who partitioned the multivariate sums of squares in a multifactorial linear model, which replaces traditional squared straight-line distances with squared dissimilarities. However, this method requires the use of a Euclidean dissimilarity metric which would only work for abundance data with very few zeros/rare species (so the double-zero effect would be negligible). The development of db-RDA would not have been possible without the past work of Rao (1964, 1973), who first described parametric redundancy analysis (RDA), and Gower (1966), who first described principle component analysis.

Canonical analysis of principal coordinates (CAP) analysis is primarily used to perform a constrained ordination based on a dissimilarity measure of multivariate data, and regresses the original variables with patterns in the ordination. CAP analysis was first described by Anderson and Willis (2003). The method is somewhat similar to non-metric multidimensional scaling, which was developed by Shepard (1962) and later by Kruskal (1964). Their work was, in turn, based on the work of Torgerson (1958), who developed metric multidimensional scaling. However, both of these methods, while still based on a dissimilarity measure, are unconstrained ordination procedures, and as such draw new orthogonal axes with the objective of maximizing the total variation depicted, whereas constrained ordination (such as CAP) draws the new orthogonal axes to maximize the depiction of variation between groups that have been specified a priori. Other early forms of canonical ordination include canonical discriminant analysis (CDA), which focused on between-group variation, and canonical correlation analysis (CCorA), which maximized the correlation with linear combinations of some quantitative predictor variables (James and Wilkinson, 1971; Gittins, 1985). The downside of both of these techniques is that each is based on a particular, metric distance measure (Mahalanobis distances for CDA
and chi-square distances for CCorA), whereas CAP analysis is flexible and can use any
dissimilarity measure, including those most suitable for ecological data (e.g. Bray-Curtis
dissimilarity). Simply put, the procedure for CAP analysis is to first perform principal coordinate
analysis on the Y data, using the dissimilarity measure of choice. Then, canonical analysis (either
CDA or CCorA as appropriate) is performed on a subset \((m)\) of the principal coordinate axes.
The subset \((m)\) is determined by minimizing the misclassification error (i.e., how often a new
data point is assigned to the wrong group), which is determined by the leave-one-out approach of
Lachenbruch and Mickey (1968). In this approach, one sample is left out of the dataset and CAP
analysis is run on the remainder of the data. The left-out data point is then placed back into
canonical space and classified into one of the groups. This is repeated for each data point to
derive the overall misclassification rate. Then, the misclassification rate is calculated for each
potential value of \(m\) to determine which subset is ideal for the CAP analysis. New points are
placed into canonical space using the interpoint distances between the point in question and all
other points, as described by Gower (1968). This contrasts with previous canonical analyses,
which could use Fisher’s discriminant rule since they are in Euclidean space (Fisher, 1936). This
reduction of dimensionality provides a check on the potential arbitrariness of the canonical
results that can result if large amounts of within-group variation is contained in the data. CAP
analysis also allows the testing of the hypothesis that there is no significant difference in
multivariate location among groups or the hypothesis that there is no significant relationship with
quantitative environmental or other factors by calculating the sum of canonical eigenvalues
(trace statistic), which is the total among group variation, and then using permutations to derive a
p-value (e.g., Anderson, 2001).
Biota-environmental analysis (BEST) was created by Clarke and Ainsworth (1993), and was further tested and developed by Clarke et al. (2008) in an effort to provide a method for determining which habitat factors best match the pattern of variation in biological communities. Previous methods attempting to explain biological community variation with habitat factors include the method by Field et al. (1982). In their study, Field et al. analyzed nematode data from the Exe estuary (United Kingdom) by creating non-metric MDS plots of the abundance data and comparing that to habitat factors by superimposing the values for each habitat factor over the MDS plot. The dissatisfactory aspect of this method is that it only allows the comparison of one factor at a time, which will not elucidate how much variation in the community is explained by the full suite of habitat factors (or subsets of factors), nor which factors may be redundant or covarying. Another previous method is to use Procrustes analysis on the two ordinations from the biological data and the habitat data (Gower, 1971). This technique minimizes ‘squared distance apart’ between the two ordinations by rotating, reversing, and shrinking one plot in relation to the other. This has the disadvantage of operating only in either 2 or 3 dimensions, and the resulting best subset of habitat factors may change based on how many dimensions are used.

BEST global analysis works by creating two distance matrices, one for the biological data and one for the habitat data, using whichever dissimilarity metric is most appropriate (e.g., Bray Curtis for the biological data and Euclidean distance for the habitat data). Next, a Mantel test (Mantel and Valand, 1970) is performed, which measures the correlation between the two resemblance matrices. Since the two matrices may use different dissimilarity metrics with different ranges of values (e.g., 0 to 100 for Bray Curtis and 0 to infinity for Euclidean distance) and using a linear relationship is often not appropriate, BEST analysis performs the Mantel test using the value ranks (Spearman correlation) rather than the original values. This is repeated for
every possible subset of habitat factors until the largest correlation coefficient is found. The significance of the correlation is tested by shuffling the subset of habitat data to simulate conditions under the null hypothesis that there is no true relationship between the habitat and biological data, and then calculating the correlation coefficient. This is repeated many times to obtain a p-value. Advantages of BEST analysis compared with other methods include the ability to use the appropriate dissimilarity measure for each data set and the lack of assumptions about the nature of the relationship between biota and the environment. In contrast, many classical methods, such as canonical correlation, assume a linear relationship between the two datasets.

Applications to Estuarine Community Structure

Though most recent studies involving multivariate analysis of biological communities and habitat factors concern benthic communities (e.g., Ysebaert et al., 2003; Gaston et al., 1998; Warwick et al., 1991; Ellingsen, 2002), there are still many studies that involve zooplankton or fish communities. One example for a fish community is that of Marshall and Elliott (1998). This study compared the fish community gathered by a beam trawl at 14 stations in the Humber Estuary (United Kingdom) with salinity, temperature, turbidity, depth, tidal state, and dissolved oxygen to determine which were most influential. The samples were grouped by species composition using the TWINSpan method. These groupings were then compared with a PCA of the normalized habitat data. Based on this somewhat qualitative analysis, the TWINSpan groupings appeared to be mostly defined by salinity. The biological data were also analyzed using CCA. The first two axes explained 73.5% of the variability, and vectors created via Spearman rank correlation indicated salinity and temperature were the most important habitat factors. The significance of all factors was assessed using the Monte Carlo routine within the
CANOCO software package. Mid-water salinity, mid-water temperature, and bottom dissolved oxygen were each determined to have significant influences on the fish community. When partial correlations were performed to control for salinity, sole had a negative relationship with dissolved oxygen, gobies, plaice and stickleback had positive relationships with temperature, and herring had a negative relationship with depth. Interestingly, it appeared that turbidity had very little effect on the fish community. The authors attributed this to the fact that Humber is a highly turbid estuary, and variation in turbidity probably doesn’t matter at levels above 80 NTU.

An example of a study comparing zooplankton communities to habitat factors is the paper by Schallenberg and Burns (2003). In this study, zooplankton community data from two tidal-lake estuaries (Lake Waihola and Lake Waihori, New Zealand) were compared with suspended particulate organic matter, suspended particulate matter, suspended particulate inorganic matter, organic content of suspended particulate matter, specific conductivity, turbidity, chlorophyll $a$, total phosphorus, total nitrogen, ammonia, and filterable reactive phosphorus. First, these water-quality factors were correlated with hydrological and meteorological factors, and it was found that wind-driven sediment resuspension had the largest effect on overall water quality. CCA was used to compare the zooplankton data to the water-quality data. Altogether, the water-quality factors explained 53% of the variation in zooplankton abundance. For Lake Waihola, the first two CCA axes explained 72% of the abundance-environment relationship. The first axis explained 46% and was strongly influenced by salinity. The second axis explained 26% and was strongly influenced by total nitrogen, total phosphorus, and filterable reactive phosphorus. The authors suggested the second axis represented a gradient of nutrient enrichment or trophic state. Even though Lake Waihola experienced periods of high turbidity, neither turbidity nor suspended particulate matter significantly affected zooplankton
community structure. For Lake Waihori, the first three CCA axes explained 52%, 29%, and 6% of the variation in zooplankton abundance data respectively. Much like Lake Waihola, the first axis corresponded to the salinity gradient (conductivity and chloride) and the second axis corresponded to productivity/trophic-state gradient (chlorophyll $a$ and ammonia depletion). Suspended particulate matter was weakly loaded on the third axis. Though the salinity gradient was found to be the most influential factor in both lakes, the authors recognized that, besides affecting species ability to osmoregulate, salinity may influence inter-specific competition or zooplankton predator species. The authors also noted that other studies observed negative effects of suspended particulate matter on zooplankton communities, and the lack of that effect in the two tidal lakes may be due to the high organic content of the sediment in these lakes providing a food source for zooplankton.

One important habitat factor to consider is that the presence or absence of different habitat types is likely to play a significant role in both fish and zooplankton communities. Estuaries with a variety of substrates and submerged aquatic vegetation tend to have higher overall diversity than more uniform estuaries (Whitfield, 1983). Explanations for this pattern have ranged from increased prey availability to predator avoidance. For instance, Heck and Crowder (1991) found that juvenile fish experienced lower predation rates in structurally complex seagrass beds than in less complex habitat. In the Kosi estuary (South Africa), a certain subset of fish was only associated with a rocky outcrop, and this subset would presumably be absent without the structure (Blaber, 1978). Another study by Connolly (1994) found that communities were grouped in relation to either eelgrass or unvegetated sites. An example of a shift in habitat leading to a change in species composition is in the Swartvlei estuary (South Africa), where the decline of the macrophyte *Potamogeton pectinatus* and an increase in benthic
algal mats led to an increase in mugilid fishes (Whitfield, 1986). Bell et al. (1988) found that the particular location of complex habitat within an estuary can be an important factor for communities. They suggested seagrass beds that are closer to the mouths of estuaries are more likely to recruit fish larvae and therefore have higher abundances than seagrass beds that are farther upstream.

Another important habitat factor is freshwater inflow. Freshwater inflow can be an important factor for many reasons. First, it can be a signal for juvenile or larval fish to recruit to the estuary from seaward spawning locations. Martin et al. (1992) found an increase in postlarval recruits in the St. Lucia estuary (South Africa) following an episodic flushing of the estuary. Grimes and Kingsford (1996) also suggested that river discharge plays an important role in larval recruitment. Freshwater inflow can also serve as a delivery system for nutrients that stimulate production and increase overall food availability, as described by Whitfield and Wooldridge (1994), resulting in an increase in zooplankton abundance (Mouny and Dauvin, 2002). Conversely, freshwater inflow can also physically flush communities out of estuaries. Telesh (1995) demonstrated that, in the Neva estuary (Russia), zooplankton densities had a negative relationship with water-current velocity. Current velocity can also have an impact on fish communities such as in the Elbe estuary (Germany), where Thiel et al. (1995) found that current velocity, along with salinity, were the principal predictors of fish species richness. The effect of freshwater inflow can change according to the morphology of the estuary. Marais (1982) found that river floods corresponded to an increase of mugilid fishes in the broad Swartkops estuary (South Africa) but, in the channel-like Sundays estuary (South Africa), mugilid abundance decreased after floods. Marais (1982) suggested that in the Swartkops estuary, floods deposited organic-rich sediments, which served as food for the mugilids but, in the Sundays estuary, the
floods instead washed away the organic-rich epibenthic layer. There are also estuaries where freshwater inflow seems to have little effect on estuarine community structure, such as the Cape Fear River estuary (USA, Weinstein et al., 1980).

In general, most studies that examine the relationship between habitat conditions and zooplankton or fish community structure in estuaries identify the salinity gradient as having the greatest effect on spatial variation in species abundance (e.g., Mouny and Dauvin, 2002; Thiel et al., 1995; Weinstein et al., 1980; Lopes, 1994; Telesh, 2004; Modéran et al., 2010). However, some authors note that this may not be entirely due to the direct effects of salinity, and that other factors that covary with salinity may be playing an equal or even greater role (Modéran et al., 2010; Shallengberg and Burns, 2003). In fact, Blaber and Blaber suggest that, when it came to juvenile fish selecting habitat, salinity and temperature were not very important at all, and that calm, shallow water, prey abundance, predators, and, most of all, turbidity were the most important factors (Blaber and Blaber, 1980). Turbidity can have a large effect either as a signal for recruitment (Blaber, 1987), as a limiting factor for benthic vegetation (Day et al., 1981), or as a refuge from predation (Cyrus and Blaber, 1987). Whitfield (1998) found that over 60 species of estuarine fish could survive in water with salinity of 1‰, and both Bok (1984) and Pooley (1975) found estuarine species in fresh water many kilometers from the sea, which suggests physiological constraints are not the primary reason for the frequent selection of salinity as an important factor.

There are two previous studies that performed inter-river comparisons on many of the same estuaries as the present study. The first is Burghart et al. (2013), which focused on the zooplankton community in these estuaries. Their study compared the water-quality characteristics of four spring-fed estuaries (Crystal, Homosassa, Chassahowitzka, and Weki
Wachee) and four surface-fed estuaries (Alafia, Anclote, Hillsborough, and Myakka) to data gathered from one year of monthly oblique plankton tows. First, indicator species for the spring-fed and surface-fed estuaries were determined using the indicator value method. The significance of these indicator species was tested using non-parametric multivariate analysis of variance (NP-MANOVA). NP-MANOVA was also used to test whether there was a difference in zooplankton community among the estuaries. Finally, CAP analysis was used to create an ordination of the zooplankton communities, and this was compared to Kruskal-Wallis tests on the median water-quality values for each estuary. Overall, the spring-fed estuaries were associated with lower turbidity, chlorophyll $a$, and color and higher secchi disk depth, which is indicative of a more oligotrophic state relative to the surface-fed estuaries. In their CAP analysis, the first axis represented 21.17% of the between-group variation and was interpreted to represent an increasing eutrophication gradient from the spring-fed estuaries to the surface-fed estuaries. The second axis represented 19.06% of the between-group variation, and was interpreted to represent the salinity gradient. The confusion matrix indicated samples from spring-fed sites were rarely misclassified into surface-fed estuaries and vice versa. In general, indicator values were higher for spring-fed estuaries than for surface-fed estuaries. Ten out of the 13 surface-fed indicator species were considered plankton-oriented. Conversely, out of the 20 indicator species for spring-fed estuaries, 17 were considered hyper-benthic. These indicator species also matched up with the gradient on the first CAP axis, with spring-fed indicator vectors pointing left and surface-fed indicator vectors pointing right. These differences were attributed to difference in basal-resource availability. In the spring-fed estuaries, higher water clarity led to increased light penetration, which allowed the growth of benthic microalgae and submerged aquatic vegetation.
(SAV). These provided a benthic basal resource for these estuaries. Conversely, the surface-fed estuaries primarily relied on phytoplankton as a basal resource.

The Burghart et al. (2013) results were consistent with the results of a later study by MacDonald et al. (2015). MacDonald et al. expanded on the scope of the Burghart et al. study, including data from monthly seine hauls and otter trawl deployments from 18 estuaries along the central west-Florida coast. The data from the plankton net tows were also subdivided into ichthyoplankton and invertebrates. Four types of community data (plankton-net ichthyoplankton, plankton-net invertebrates, seine catch, trawl catch) were compared with 41 habitat factors. First, Spearman rank correlations were performed to identify redundant habitat factors, which were removed. PCA was then performed on the normalized habitat factor data to create an ordination of the sites from all estuaries based on their habitat characteristics. This was compared to a distance-based redundancy analyses (db-RDA) of the biotic abundance data based on Bray-Curtis dissimilarity. The two types of ordination had very similar patterns, and it was determined that the first db-RDA axis, which explained from 22.8% (Trawl) to 31.9% (Seine) of the total variation, corresponded to the estuarine salinity gradient, and the second axis, which explained an additional 12.9% (ichthyoplankton) to 18% (invertebrates) of the total variation, corresponded to the division between spring-fed and surface-fed estuaries. The loading vectors from the environmental PCA ordination indicated light-associated factors were correlated with PCA axis 2, in agreement with Brughart et al. (2013). MacDonald et al. also created seriated heat maps representing cluster analysis of the sample areas based on the four community types. Each heat map indicated a transition from freshwater fauna to marine fauna and often, three distinct groups were evident (freshwater, upper estuary, and marine). MacDonald et al. emphasized the importance of freshwater inflow to maintain the salinity gradient depicted in those plots and
along the first db-RDA axis so the upper estuary community (which often contained
economically important species such as Red Drum, Snook, and Sand Seatrout) would be
maintained. Both the Burghart et al. (2013) and the Macdonald et al. (2015) studies relied on a
qualitative comparison of the community and habitat data. In contrast, the purpose of the present
study was to quantitatively relate the biotic data to habitat factors.

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Chapter 2 - The Influence of Habitat Metrics on Community and Abundance

Introduction:

Estuarine habitats are highly variable due to the interactions of hydrodynamics, biology, climate, sedimentation, geomorphology and land use (i.e., water quality). It is generally believed that the effect of these interactions is more likely to be captured if a multitude of species are considered, studies of habitat-factor effects often take a community-structure-based perspective. Estuarine communities include the juveniles of many economically important species such as red drum and snook, as well as prey items for these species such as copepods, mysids, and amphipods (Peebles, 2005). One way of looking at community structure is to consider beta diversity, which indicates how communities change from one location to another. By considering multiple species over many different estuaries with varying levels of different habitat factors, a space-for-time substitution can be used to predict how different communities might change if one or more factors change.

The process of habitat-factor analysis focuses on finding process-based explanations and models to explain community structure using an understanding of how different habitat characteristics affect vital rates (growth, mortality, and reproduction) both directly and indirectly. Habitat analysis is not to be confused with habitat suitability modeling or the development of habitat suitability indices. Habitat suitability modeling and habitat suitability indices are, more often than not, based purely on statistical correlations between species and habitat factors. Barry and Elith (2006) describe how missing covariates and sampling biases are a common source of errors in these types of models that lead to faulty predictions; examples are provided by Beck et
Beck et al. (2001) defined the value of a nursery ground as the number of new recruits contributed to the adult population per unit area. Dahlgren et al. (2006) amended this idea by pointing out that areas that may have a low per-unit-area density of juveniles but a large overall area, thus being equally or more important in terms of sustaining the adult population. Finally, Sheaves et al. (2006) suggested that not only the number of recruits, but also the quality of recruits, should be considered. They also pointed out that this approach to habitat qualification does not account for the effects of scale or importance of habitat complexity and connectivity (i.e., to account for ontogenetic shifts in prey or habitat).

Many analyses of habitat factors focus on the total number of species in a sample or alpha diversity (e.g., Worm et al., 2002; Gray, 2000, 1997; Bianchi, 2000) and it should not be suggested that the use of alpha diversity was inappropriate in these studies. However, in an estuary where, by definition, the environment is changing considerably over relatively short distances, beta diversity is a better measure of ecosystem function. For example, if managers were trying to only maximize alpha diversity in every site, they could simply cut off the freshwater supply and allow the more diverse marine taxa to invade as far upstream as possible. However, this higher diversity would not correspond to higher overall ecological value (Whitfield, 2005). Beta diversity was defined by Whittaker (1960, 1973) as the variation in species abundance and composition between sites in a given region. The study of beta diversity can address many important ecological and conservation-related questions. For example; if beta diversity responds to different habitat gradients (as often appears to be the case), then managers may seek to maintain not only the abundance of key species, but habitat characteristics as well. One of the more obvious benefits of high beta diversity is that ecosystems with high overall
diversity have been shown to be more resilient (Chapin et al., 2000). Thus, even if an invasion of diverse marine taxa were to maximize diversity at a given spot, higher beta diversity would help preserve the total diversity of the entire ecosystem. High beta diversity is also beneficial for larval and juvenile fish because, as the fish grow and their mouth gape increases, their preferred prey is likely to change as well. This is likely one of the primary causes of fish moving to different areas of an estuary as they age and grow, and maintaining these different prey fields is important for the growth and abundance of these species (Peebles, 2002).

Most studies that examine the relationship between environmental conditions and zooplankton or fish community structure in estuaries find that the salinity gradient has the largest effect on spatial variation in species abundance (Mouny and Dauvin, 2002; Thiel et al., 1995; Weinstein et al., 1980; Lopes, 1994; Telesh, 2004; Modéran et al., 2010). However, some authors note that this may not be entirely due to the direct effects of salinity, and that factors that covary with salinity may be playing an equal or even greater role (Modéran et al., 2010; Shallengberg and Burns, 2003). In fact, Blaber and Blaber (1980) suggest that, when it comes to juvenile fish selecting habitat, the availability of calm, shallow, waters with high prey abundance and low predation risk may be more important than salinity and temperature. In particular, they emphasized the role of turbidity as protection from visual predators, a position also held by Cyrus and Blaber (1987). Other factors that have been found to be important influences on estuarine community structure include the presence and location of vegetation (Whitfield, 1983, Whitfield, 1986, Bell et al., 1988, Connolly, 1994) and the input of fresh water and associated nutrients (Grimes and Kingsford, 1996; Whitfield and Wooldridge, 1994; Telesh, 1995; Thiel et al., 1995; Marais, 1982). One of the goals of the present study was to consider how habitat-factor covariation and sampling bias may inflate the importance of individual habitat factors.
In comparison to other studies, the present study uses a very large a suite of habitat factors as explanatory variables. Most studies that use multivariate approaches to describe changes in community structure focus on one geographic area and on a limited number of habitat factors related to sediment quality (Thrush et al., 2003; Ellingsen, 2002), pollution (Dauer, 1993; Warwick et al., 1990; Olsgard and Gray, 1995; Somerfield et al., 1994), or habitat complexity (Attrill et al., 2000; Connolly, 1994; Ohman and Rajasuriya, 1998; Chemello and Milazzo, 2002). In contrast, the present study considers a suite of 29 diverse factors and focuses specifically on ones that can be directly manipulated by management entities. The present study also included a wide variety of fauna from four distinct community types (plankton-net ichthyoplankton, plankton-net invertebrates, seine catch, trawl catch). Similar studies typically concentrate on one community, most often fish or macrobenthos (Brown, 2000; Ysebaert et al., 2003; Gaston et al., 1998; Warwick et al., 1991; Whitfield, 1999; Blaber and Blaber, 1980). This approach ignores the potential effects of conservation actions on other communities in the same geographic area that were not studied. The present study considered more than 400 taxa, ranging from fish to plankton and hyperbenthic invertebrates, most with vastly different life-history traits.

**Materials and Methods:**

**Study area:**

Personnel from the University of South Florida (USF) and Florida Fish and Wildlife Conservations Commission (FWC) sampled 18 tidal-river estuaries between 1988 and 2014 (Figure 1). From south to north, the sampled estuaries are: Peace River, Shell Creek, Myakka River, Myakkahatchee Creek, Shakett Creek/Cowpen Slough, Braden River, Manatee River,
Little Manatee River, Alafia River, Hillsborough River, Palm River/McKay Bay, Anclote River, Weeki Wachee River, Mud River, Homosassa River, Halls River, Chassahowitzka River, and Crystal River. The total distance along the West Florida coast covered by the present study was over 230 km.

The sample area covered a transition from temperate, saltmarsh grass estuaries in the north to subtropical mangrove estuaries in the south. Besides shoreline vegetation, these estuaries’ habitat characteristics varied in many ways. The Mud River estuary had the shortest tidal reach of 2.4 km, in contrast to the Myakka and Manatee estuaries that had tidal reaches of over 30 km. The Palm, Hillsborough, Braden, Shakett Creek/Cowpen Slough, Myakkahatchee, Manatee, and Shell Creek estuaries each contain some form of water-control structure, whereas the rest are unobstructed. Finally, the estuaries to the north are primarily spring-fed estuaries (Crystal, Homosassa, Halls, Weeki Wachee and Mud), whereas those to the south are primarily surface-fed (Peace, Shell, Myakka, Myakkahatchee, Shakett Creek/Cowpen Slough, Braden, Manatee, Little Manatee, Alafia, Hillsborough, Palm/McKay Bay, and Anclote). Due to lack of habitat data, the Little Manatee, Crystal, Halls, and Myakkahatchee estuaries were omitted from the analysis.
Figure 1
Map of the estuaries sampled (from MacDonald et al., 2015). The large embayment in the middle of the figure is Tampa Bay. The estuaries depicted in red are primarily surface-fed estuaries, and the estuaries depicted in blue are primarily spring-fed estuaries. The two-letter designations in parentheses are the abbreviations used in the results.
Data collection:

Each of the estuaries was subdivided into 4 to 7 zones covering the available salinity gradient. Zone 1 was where the tidal river met its receiving basin (GOM, Tampa Bay, or Charlotte Harbor) and the highest-number zone was where the estuary transitioned into fresh water upstream. At two stations in each of these zones, the USF conducted plankton tows in the channel and the FWC deployed seines at the shoreline. In most zones, the FWC also deployed an otter trawl at one location in the channel. Sampling by both USF and FWC was conducted monthly. The plankton tows were conducted with a 5m diameter 500 μm mesh conical plankton net equipped with a three-point nylon bridle, a calibrated flow meter (General Oceanics model 2030R or SeaGear model MF315), a 1 liter plastic cod-end jar, and a 9-kg (20-lb.) weight. These three-step oblique tows (bottom-midwater-surface) were conducted once per month for five minutes total tow duration during nighttime flood tides. The typical amount filtered during a tow was 70-80 cubic meters. The samples were preserved in 6-10% formalin. After each plankton tow, salinity, temperature, pH and dissolved oxygen were measured at one-meter intervals from surface to bottom.

Back at the lab, the plankton were separated into two size fractions using stacked sieves with mesh openings of 4 mm and 250 μm. These fractions were then identified and counted separately using microscopes with magnification as high as 90x, as necessary. For species that were particularly abundant or difficult to enumerate, an aliquot of 12-50% of the total sample was used. The immature ichthyoplankton were further sorted into preflexion, flexion, postflexion, metamorph, and juvenile stages (Peebles et al. 1991). Decapod larvae were classified as zoea, megalopa or mysis stages. Shrimps were classified as mysis, post-larval, or juvenile.
The seine collections were conducted using a 21.3 m center-bag seine with 3.2 mm mesh and leads spaced every 150 mm. The seine was deployed with the help of a boat, which dropped off one end of the seine on the shoreline, drove out in an arc away from the shore, and then dropped off the other end such that the crews at either end could walk towards each other along the shore. Each seine deployment covered roughly 68 square meters of bottom area. Otter trawl collections were made with a 6.1 m net with 38 mm stretched mesh, a 3.2 mm mesh liner, and tickler chain. It was towed for 5 minutes, which typically resulted in a coverage of around 720 square meters of bottom area. Both the otter trawls and seines were deployed under variable tidal conditions. The catch was identified, counted, and measured in the field using standard length for fish, total length for seahorses, disk width for rays, post-orbital head length for pink shrimp, and carapace width for crabs. With each deployment, data were collected for salinity, temperature, pH and dissolved oxygen in a similar manner to the plankton tows. The seine hauls generally caught shallow-water (<1.5 m depth) organisms, whereas trawls caught deeper-water (1.5 to 6 m depth) organisms.

Data for freshwater inflow were obtained from SWFWMD, Tampa Bay Water, and the United States Geological Survey. Data for static habitat factors such as depth, shoreline type, and bottom type were provided by FWC and were collected at the time of seine and trawl deployment. Water quality data (color, chlorophyll $a$, and turbidity) were obtained from the U.S. Environmental Protection Agency STORET database. Due to lack of data, these three water-quality factors were averaged over entire estuaries rather than being specific to zone. Flashiness, which is the daily variability of freshwater inflows, was calculated from freshwater inflow data using the method of Baker et al. (2004). Flushing time is the amount of time required for
freshwater inflow to equal the amount of water originally present in the river zone in the sense of Sheldon and Alber (2002).

Types of data analysis

Three types of multivariate data analysis were conducted: (1) community analysis with spring-fed and surface-fed estuaries separated, (2) species abundance analysis with spring-fed and surface-fed estuaries separated, and (3) an exercise that investigated the effects of data resolution on community analysis, with spring-fed and surface-fed estuaries combined.

Community analysis

The first part of the analysis consisted of a series of distance-based linear modeling (DistLM) procedures (PRIMER 7 software, PRIMER-E Ltd. [UK]; Clarke and Gorley 2006). The goal of this procedure was to identify the subset of habitat factors that best explains the variation in biological community structure. The BEST procedure (also contained in the PRIMER software package) was considered for this purpose but, based on observations made by Legendre et al. (2015), was determined to be inappropriate for the present study. DistLM, which is contained in the PERMANOV A+ addition to PRIMER 7, is homologous with distance-based redundancy analysis (Legendre and Anderson, 1999, McArdle and Anderson, 2001). Distance-based redundancy analysis (dB RDA) is a form of multivariate multiple regression that uses principle component analysis (PCoA) to create a Euclidean embedding of non-metric or semi-metric dissimilarity measures (such as Bray-Curtis dissimilarity). Since the PCoA embedding only includes the Euclidean portion of the data, the dissimilarity matrix can be corrected to account for the non-Euclidean portion using the method of Gower and Legendre (1986). This
Euclidean embedding is then be regressed against habitat factors in to uncover linear relationships. The best subset of habitat factors for each community is chosen with forward selection and the AICc selection criterion. This AICc criterion was selected because it includes a penalty for extra factors beyond the penalty included in the AIC criterion. The AICc is more appropriate for data sets with many possible explanatory factors because it decreases the chances of including too many factors in the final model (i.e., overfitting; Burnham and Anderson, 2002).

In the next step of the analysis, the habitat factors were divided into subsets representing different management entities (Table 1). Each subset contained all the habitat factors that could be modified by that management entity. The dbRDA was repeated, this time with the Fathom Toolbox for MATLAB (Jones, 2016), which allowed the inclusion of a covariate in both the AIC procedure and the dbRDA (partial dbRDA). The distance from each estuarine zone to the Gulf of Mexico (Distance-to-GOM) was used as a covariate for these analyses so that the variation in community structure due to dispersal distance and larval availability was removed. This analysis was performed for the two different types of estuaries (surface- and spring-fed), the four community types (plankton-ichthyoplankton, plankton-net invertebrates, seine catch, trawl catch), and with the complete suite of habitat factors, as well as the three habitat-factor subsets in Table 1, resulting in a total of 32 analyses.

*Rationale for using distance-to-GOM as a covariate*

Distance-to-GOM was related to the recruitment of marine-derived species into estuaries in the sense that individual estuarine zones may be closer or farther from spawning grounds located in the GOM, thereby affecting the likelihood of young animals successfully reaching the zone for use as habitat. Many of the abundant species in each of the studied
communities are marine migrants or are larval or juvenile stages that originate from the GOM, and thus distance-to-GOM had a potentially large effect on community composition. The effect of distance has been observed in two different Australian estuaries (Young and Carpenter, 1977; Hannan and Williams, 1996) as well as a North Carolina estuary (Etherington and Eggleston, 2000). In the present study (Figure 2), distance-to-GOM was found to be overly prominent in the dbRDA results. Much like salinity, distance-to-GOM covaries with many other factors (Appendix 3). Thus, distance-to-GOM was treated as a covariate to improve the evaluation of other habitat factors. Moreover, distance-to-GOM is not a habitat factor that can be manipulated by resource managers.

Table 1
A list of variables included in each management sector subset. These are the subsets seen in the partial dbRDA and multiple regression analysis.

<table>
<thead>
<tr>
<th>Water Management</th>
<th>Restoration</th>
<th>Water Quality</th>
</tr>
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<tbody>
<tr>
<td>flushing time</td>
<td>Depth</td>
<td>Chlorophyll</td>
</tr>
<tr>
<td>Flashiness</td>
<td>Slope</td>
<td>Color</td>
</tr>
<tr>
<td>Head Spring in Zone</td>
<td>Bottom Mud</td>
<td>Turbidity</td>
</tr>
<tr>
<td>Head Spring Sampled</td>
<td>Bottom Sand</td>
<td>Dissolved Oxygen</td>
</tr>
<tr>
<td>H2O Structure in Zone</td>
<td>Bottom Manmade</td>
<td></td>
</tr>
<tr>
<td>H2O Structure</td>
<td>Bottom Oysters</td>
<td></td>
</tr>
<tr>
<td>Tidal H2O Structure</td>
<td>SAV</td>
<td></td>
</tr>
<tr>
<td>Average Daily Flow</td>
<td>Algae Present</td>
<td></td>
</tr>
<tr>
<td>Salinity</td>
<td>Shoreline Mangroves</td>
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</tr>
<tr>
<td></td>
<td>Shoreline Lawns</td>
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<tr>
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<tr>
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<td>Shoreline Oyster</td>
<td></td>
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<tr>
<td></td>
<td>Shoreline Trees</td>
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</tr>
</tbody>
</table>

Rationale for separating spring-fed and surface-fed estuaries

Burghart et al. (2013) and MacDonald et al. (2015) both found that these two types of estuaries had very different ecological characteristics and community structures. The surface-fed estuaries tend to be more eutrophic, with lower water clarity and subsequently less benthic
primary production; most indicator species have associations with plankton. In contrast, the spring-fed estuaries tend to be more oligotrophic, with higher water clarity and more benthic primary production; most indicator species are benthically associated. Because of these differences, the communities in spring-fed estuaries are thought to be primarily supported by benthic basal resources, while surface-fed estuaries are thought to be primarily supported by planktonic basal resources. Spring-fed and surface-fed estuaries were analyzed separately in the community and species abundance analyses, but were combined to investigate the effects of data resolution on community analysis.

Species abundance analysis

In order to obtain information at the species level, analyses were performed on the same suite of habitat factors in regard to the abundance of indicator species with ecological (prey groups) or economic importance (finfish and shellfish). The prey groups that were considered were copepods, mysids, shrimp, polychaetes, gammaridean amphipods, and *Anchoa mitchilli* juveniles. The study by Peebles et al. (1991) found that all of these groups were important prey species in the Little Manatee River, which falls in the middle of the overall study area. The economically important species included fishes that have commercial or recreational value such as menhaden (*Brevoortia* spp.), sand seatrout (*Cynoscion arenarius*), sheepshead (*Archosargus probatocephalus*), spotted seatrout (*Cynoscion nebulosus*), channel catfish (*Ictalurus punctatus*), gray snapper (*Lutjanus griseus*), lane snapper (*Lutjanus synagris*), southern kingfish (*Menticirrhus americanus*), mullet (*Mugil cephalus, M. trichodon, and M. curema*), Atlantic croaker (*Micropogonias undulatus*), common snook (*Centropomus undecimalis*), spot (*Leiostomus xanthurus*), largemouth bass (*Micropterus salmoides*), Gulf flounder (*Paralichthys...
*albigutta*, and red drum (*Sciaenops ocellatus*). The economically important species also included blue crab (*Callinectes sapidus*) and pink shrimp (*Farfantepenaeus duorarum*). By analyzing all of these species separately, the habitat characteristics that affect different species can be assessed along with identification of species that might be “winners” or “losers” under different scenarios.

The first step of this analysis was to divide each habitat factor into five groups that ranged from zones (river segments) containing low levels of the factor to zones containing high levels of the factor. Then, canonical analysis of principal coordinates (CAP; Anderson and Willis, 2003) was used to identify significant difference in community structure between Group-1 zones (lowest level of habitat factor) and Group-5 zones (highest level of habitat factor) for each habitat factor and each of the four community types (plankton-net ichthyoplankton, plankton-net invertebrates, seine catch, trawl catch). CAP analysis first conducts a principal coordinates analysis (PCoA) on a dissimilarity matrix of the abundance data (i.e., Bray-Curtis dissimilarity), and then an optimal number of principal coordinate axes ($m$) are chosen by minimizing the misclassification error (i.e., how often a new data point was assigned to the wrong group), using the leave-one-out approach (Lachenbruch and Mickey, 1968). In this approach, one sample was left out of the dataset and CAP analysis was performed on the remainder of the data. The left-out data point was then placed back into canonical space and classified into one of the groups. This process was repeated for each data point to determine the overall misclassification rate. Next, the misclassification rate was calculated for each potential value of $m$ to determine which $m$ was ideal for the CAP analysis. The optimal $m$ should include as much of the between-group variation as possible (minimizing the misclassification) while leaving out the within-group variation (“noise”). After $m$ was selected, canonical discriminant
analysis (James and Wilkinson, 1971) was performed on the PCoA eigenvectors to obtain an ordination and to determine the percentage of variation in the abundance dissimilarity matrix that was explained by the grouping (i.e., how much of the variation was between-group variation). The significance of this percentage was determined by shuffling the group membership of the zones and recalculating the trace statistic (sum of canonical eigenvalues) for a given number of iterations (i.e., 1000) in order to derive a $p$-value (Anderson, 2001).

If the CAP analysis identified a significant difference in community structure between zones with high and low levels for a given factor, then indicator value (IndVal) analysis (Dufrene and Legendre, 1997) was conducted on the zones to determine which species were most responsible for the difference between the two habitat-factor groups (high level and low level). Similarity percentage analysis (SIMPER) (Clarke, 1993) was also considered for this purpose but, SIMPER often identifies species that have the most variation rather than the ones that contribute most to between-group variation (Warton et al., 2012). In contrast, IndVal uses a species’ relative abundance combined with its relative frequency of occurrence in different groups of samples to provide a value that is independent of the relative abundance of other species. This value is at its maximum (100) when every zone in a group contains the species and the species is not found in any other group. The significance was tested by shuffling the group membership of the zones and recalculating the IndVal for a given species to create a null distribution and corresponding $p$-value. Only species with at least one significant IndVal were considered for the analysis of species abundance. These species were subsequently divided into important prey species and economically important species (Table 2).
Table 2
A list of all the individual species featured in the IndVal and multiple regression analysis. Species that have an asterisk (*) were split into multiple size classes. Not all of the size classes had significant indicator values so not all species have all size classes included in the analyses.

<table>
<thead>
<tr>
<th>Prey Species</th>
<th>Economically Important Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>Anchoa juveniles</td>
<td>Fish</td>
</tr>
<tr>
<td>Polychaetes</td>
<td>Archosargus probatocephalus *</td>
</tr>
<tr>
<td>Gammarid amphipods</td>
<td>Archosargus probatocephalus postflexion</td>
</tr>
<tr>
<td>Copepods</td>
<td>Brevoortia spp.</td>
</tr>
<tr>
<td>Acatia tonsa</td>
<td>Brevoortia spp. Postflexion</td>
</tr>
<tr>
<td>Labidocera aestiva</td>
<td>Brevoortia spp. Metamorphs</td>
</tr>
<tr>
<td>Pseudodiaptomus coronatus</td>
<td>Brevoortia smithi juveniles</td>
</tr>
<tr>
<td>Paracalanids</td>
<td>Brevoortia patronus juveniles</td>
</tr>
<tr>
<td>Diaptomus spp.</td>
<td>Cynoscion arenarius*</td>
</tr>
<tr>
<td>Oithona spp.</td>
<td>Cynoscion arenarius flexion</td>
</tr>
<tr>
<td>Siphonostomatids</td>
<td>Cynoscion arenarius postflexion</td>
</tr>
<tr>
<td>Centropages velificatus</td>
<td>Cynoscion arenarius juveniles</td>
</tr>
<tr>
<td>Centropages hamatus</td>
<td>Cynoscion nebulosus</td>
</tr>
<tr>
<td>unidentified calanoids</td>
<td>Cynoscion nebulosus preflexion</td>
</tr>
<tr>
<td>Calanopia americana</td>
<td>Cynoscion nebulosus flexion</td>
</tr>
<tr>
<td>Temora turbinata</td>
<td>Cynoscion nebulosus postflexion</td>
</tr>
<tr>
<td>Mesocyclops edax</td>
<td>Centropomus undecimalis</td>
</tr>
<tr>
<td>Macrocyclops albidus</td>
<td>Ictalurus punctatus</td>
</tr>
<tr>
<td>Orthocyclops modestus</td>
<td>Lutjanus griseus</td>
</tr>
<tr>
<td>unidentified harpacticoids</td>
<td>Lutjanus synagris</td>
</tr>
<tr>
<td>Cyclops spp.</td>
<td>Leiostomus xanthurus*</td>
</tr>
<tr>
<td>Monstrilla sp</td>
<td>Leiostomus xanthurus juveniles</td>
</tr>
<tr>
<td>Mysids</td>
<td>Menticirrhus americanus*</td>
</tr>
<tr>
<td>unidentified Americamysis juveniles</td>
<td>Mugil cephalus*</td>
</tr>
<tr>
<td>Americamysis almyra</td>
<td>Mugil cephalus juveniles</td>
</tr>
<tr>
<td>Americamysis bahia</td>
<td>Mugil curema</td>
</tr>
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</table>
Table 2 (Continued)

<table>
<thead>
<tr>
<th>Prey Species</th>
<th>Economically Important Species</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Americamysis stucki</em></td>
<td><em>Micropterus salmoides</em></td>
</tr>
<tr>
<td><em>Bowmaniella dissimilis</em></td>
<td><em>Morone saxatilis</em></td>
</tr>
<tr>
<td><em>Taphromysis bowmani</em></td>
<td><em>Mugil trichodon</em></td>
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<tr>
<td><strong>Shrimp</strong></td>
<td><strong>Micropogonias undulates</strong></td>
</tr>
<tr>
<td><em>Palaemonetes pugio adults</em></td>
<td><em>Orthopristis chrysoptera</em></td>
</tr>
<tr>
<td><em>Hippolyte zostericola postlarvae</em></td>
<td><em>Paralichthys albigutta</em></td>
</tr>
<tr>
<td><em>Hippolyte zostericola juveniles</em></td>
<td><strong>Sciaenops ocellatus</strong>*</td>
</tr>
<tr>
<td><em>Tozeuma carolinense postlarvae</em></td>
<td><em>Sciaenops ocellatus</em> postflexion</td>
</tr>
<tr>
<td><em>Ambidexter symmetricus postlarvae</em></td>
<td><strong>Crabs</strong></td>
</tr>
<tr>
<td><em>Ambidexter symmetricus juveniles</em></td>
<td><em>Callinectes sapidus</em>**</td>
</tr>
<tr>
<td>alphaeid postlarvae</td>
<td><em>Callinectes sapidus juveniles</em></td>
</tr>
<tr>
<td><em>Lucifer faxoni juveniles and adults</em></td>
<td><strong>Shrimp</strong></td>
</tr>
<tr>
<td>penaeid metamorphs</td>
<td><em>Farfantepenaeus duorarum</em>**</td>
</tr>
<tr>
<td><em>Farfantepenaeus duorarum juveniles</em></td>
<td></td>
</tr>
<tr>
<td>Palaemonetes spp. Postlarvae</td>
<td></td>
</tr>
<tr>
<td><em>Periclimenes longicaudatus juveniles</em></td>
<td></td>
</tr>
<tr>
<td>Upogebia spp. postlarvae</td>
<td></td>
</tr>
</tbody>
</table>

For the last part of the species abundance analysis, special consideration was given to the utility of the models for estuary managers. Therefore, distance-to-GOM was again held as a covariate both for the AIC selection and multiple regression. The habitat factors were divided into three groups based on management sector (Table 1). AIC selection was performed for each species using the full suite of habitat factors, as well as each of the three subsets of habitat factors to determine which habitat factors substantially contributed to variation in abundance. Then, multiple-regression analysis (Pearson, 1938) was performed on each of the important
species using the subset of factors chosen by AIC. When combined, these two procedures resulted in a regression equation for each species in each type of estuary (spring-fed and surface-fed) for each management sector. Because the habitat factors were standardized to z-scores, the coefficients in these equations indicate the relative contribution of each selected habitat factor as well as whether that habitat factor had a positive or negative effect on the abundance of that species.

Reduction in spatial resolution

Because some habitat factors were only available at a lower spatial resolution, the spatial resolution of all of the factors was reduced to this scale to investigate the effect of data resolution on the results of the community analyses. Inconsistent data resolution over space and time is a common problem that arises in habitat-factor analysis. For example, a factor that costs more to measure may be measured at a lower temporal or spatial frequency. Other factors are inherently limited in dimensionality, such as freshwater inflow rate and flashiness, where a single time-averaged value (e.g., daily freshwater inflow, annual flashiness) for these factors must be applied to all zones within a given estuary (in cases where multiple point sources of inflow are not being considered independently).

In order to evaluate the effect of data resolution on the results of the habitat-factor analyses, both the biological and habitat data were averaged over entire estuaries. A number of factors in the initial analysis could only be resolved to the level of the river inflow variables (inflow, flashiness), which created a bias against the inflow variables as explanatory factors. By averaging other, higher resolution factors, this bias was removed. The dbRDA and partial dbRDA analyses were repeated under these conditions to investigate the effect of disparate
resolutions. Because only three spring-fed estuaries were included in the present study, none of the results from the spring-fed analysis at lower resolution were significant. In order to include some influence from the spring-fed estuaries, the lower resolution analysis was repeated with the spring-fed and surface-fed estuaries combined.

**Results:**

*dbRDA*

The coefficient of multiple determination between the subset of habitat factors and the biological data ranged from 0.27 (spring-fed ichthyoplankton) to 0.76 (surface-fed invertebrates) (Table 3). Salinity explained the most variation in every community except surface-fed ichthyoplankton, with an average percent explained variation of over 30%. Color explained the most variation in the surface-fed ichthyoplankton community but the amount of variation it explained ($R^2 = 0.089$) was much lower than the amount typically explained by salinity. With the exception of the spring-fed trawl community, which did not have any significant habitat factors, salinity was the only factor selected for the communities in spring-fed estuaries (Figure 2). Other than salinity, the factor that explained the most variation was distance-to-GOM for surface-fed invertebrates ($R^2 = 0.11$). Ordinations for each analysis are presented in Appendix 1.
Table 3
The results from the dbRDA for four community types in two different types of estuaries. dbRDA uses the AICc selection criterion to determine which factor explained the most variation in abundance between zones for a given community, and then if any other factors explained a substantial amount of additional variation. The third column identifies the overall $R^2$ for model. The fourth column identifies the factors selected by AICc. These factors are in order of importance with the amount of variation explained (partial $R^2$) in parentheses to the right.

<table>
<thead>
<tr>
<th>Community</th>
<th>System</th>
<th>R2</th>
<th>Variable Ranks</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ichthyoplankton</td>
<td>Spring-fed</td>
<td>0.27</td>
<td>Salinity (0.27)</td>
</tr>
<tr>
<td>Ichthyoplankton</td>
<td>Surface-fed</td>
<td>0.45</td>
<td>1. Color (0.089) 2. Temperature (0.079) 3. Flashiness (0.064) 4. Flow (0.055) 5. Dissolved Oxygen (0.049) 6. H2O Control Structure (0.046) 7. Bottom Sand (0.034) 8. Distance to the Gulf (0.032)</td>
</tr>
<tr>
<td>Invertebrates</td>
<td>Spring-fed</td>
<td>0.43</td>
<td>Salinity (0.43)</td>
</tr>
<tr>
<td>Invertebrates</td>
<td>Surface-fed</td>
<td>0.76</td>
<td>1. Salinity (0.31) 2. Distance to the Gulf (0.11) 3. Depth (0.092) 4. Temperature (0.075) 5. Flashiness (0.058) 6. Flow (0.045) 7. H2O Control Structure (0.040) 8. Chlorophyll (0.035)</td>
</tr>
<tr>
<td>Seine</td>
<td>Spring-fed</td>
<td>0.37</td>
<td>Salinity (0.37)</td>
</tr>
</tbody>
</table>
Table 3 (Continued)

<table>
<thead>
<tr>
<th>Community</th>
<th>System</th>
<th>R2</th>
<th>Variable Ranks</th>
</tr>
</thead>
</table>
| Seine     | Surface-fed | 0.70 | 1. Salinity (0.31)  
2. Depth (0.062)  
3. Distance to the Gulf (0.057)  
4. Bottom Mud (0.052)  
5. SAV (0.033)  
6. Flow (0.032)  
7. Bottom Manmade (0.029)  
8. Flashiness (0.027)  
9. Chlorophyll (0.021)  
10. Bottom Sand (0.018)  
11. Temperature (0.017)  
12. Turbidity (0.015)  
13. Dissolved Oxygen (0.014)  
14. Shoreline Terrestrial (0.015) |
| Trawl     | Spring-fed | Not Significant |                                                                                     |
| Trawl     | Surface-fed | 0.47 | 1. Salinity (0.19)  
2. Flow (0.079)  
3. Dissolved Oxygen (0.058)  
4. Bottom Mud (0.044)  
5. Distance to the Gulf (0.040)  
6. Flashiness (0.034)  
7. Bottom Manmade (0.034) |
Figure 2
How often each factor was selected by AICc from the dbRDA for spring-fed and surface-fed estuaries. The factor that explained the most variation in the abundance of a given community was selected first and subsequent factors were only included in the model if they explained substantial additional variation. Spring-fed estuaries are in blue and surface-fed are in orange. The factor that was selected most frequently has the potential to alter the most communities.

Flashiness was selected as having a significant impact in all four surface-fed estuaries even though this impact was usually minor ($R^2$ of 0.027 to 0.064). Average daily inflow and distance-to-GOM were also selected in all four surface-fed estuaries with $R^2$ values ranging from 0.032 (seine) to 0.079 (trawl) and 0.032 (ichthyoplankton) to 0.11 (invertebrates) respectively. Temperature and dissolved oxygen were selected for three out of the four surface-fed communities. Temperature had a larger $R^2$ (>0.07) for invertebrates and ichthyoplankton and a very small $R^2$ for seine (<0.02). Dissolved oxygen was more important for trawl ($R^2 = 0.058$), less so for ichthyoplankton ($R^2 = 0.049$), and not very important for seine ($R^2 = 0.014$). Finally,
even though depth was only selected twice, it ranked high and had a comparatively large $R^2$ for the seine and invertebrates.

**Partial dbRDA**

The partial dbRDA analyses using the full suite of habitat factors unsurprisingly had the highest $R^2$ values since the AIC was able to select the optimal subset of factors. These $R^2$ values ranged from 0.15 (surface-fed ichthyoplankton) to 0.43 (surface-fed invertebrates) (Table 4). Ordinations for all of the partial dbRDA analyses can be found in Appendix 2. The $R^2$ of the covariate (distance-to-GOM) ranged from 0.085 (surface-fed ichthyoplankton) to 0.32 (spring-fed seine). Water management was the most influential management area in four out of the eight communities. Restoration was the most influential in two out of the eight and water quality was most influential in one out of the eight (Figure 3). Water management was also most influential in spring-fed trawl, but the AIC value for the water management model, as well as for the model with all the factors, was not more than 2 greater than the null model, suggesting that both of these models were not substantially better than a model with no factors.
The results of partial dbRDA analyses with distance-to-GOM as a covariate for three management sectors in four community types in two different types of estuaries. The AIC selection criterion was used with distance-to-GOM as a covariate to select the factor that explained the most variation in abundance for a given community and subsequent factors were only included in the model if they explained a substantial amount of additional variation. The third column represents which subset of habitat factors were used (WM = water management, Res = restoration, WQ = Water Quality) (see Table 1). A single asterisk (*) denotes the most influential management sector and two asterisks (**) denotes that the p-value for the model was not significant (p > 0.05). The fourth column identifies the factors selected by AIC with distance as a covariate. These factors are in order of importance with the amount of variation explained (partial $R^2$) in parentheses to the right.

<table>
<thead>
<tr>
<th>Community</th>
<th>System</th>
<th>Env Variables</th>
<th>R2</th>
<th>Selected variables</th>
<th>R2 of covariate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ichthyo...</td>
<td>Spring-fed</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>All</td>
<td>0.24</td>
<td>Salinity (0.24)</td>
<td>0.17</td>
</tr>
<tr>
<td></td>
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<td>WM*</td>
<td>0.24</td>
<td>Salinity (0.24)</td>
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</tr>
<tr>
<td></td>
<td></td>
<td>Res</td>
<td>0.14</td>
<td>Shoreline Manmade (0.14)</td>
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<tr>
<td></td>
<td></td>
<td>WQ</td>
<td>0.21</td>
<td>Chlorophyll (0.21)</td>
<td>0.17</td>
</tr>
<tr>
<td></td>
<td></td>
<td>All</td>
<td>0.15</td>
<td>Color (0.078)</td>
<td>0.085</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Flashiness (0.069)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>WM</td>
<td>0.069</td>
<td>Flashiness (0.069)</td>
<td>0.085</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Res</td>
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<td>Shoreline Oysters (0.060)</td>
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<td></td>
<td></td>
<td>WQ*</td>
<td>0.078</td>
<td>Color (0.078)</td>
<td>0.085</td>
</tr>
<tr>
<td>Invertebrates</td>
<td>Spring</td>
<td></td>
<td></td>
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<tr>
<td></td>
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<td>All</td>
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<td>Salinity (0.21)</td>
<td>0.31</td>
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<td>WM*</td>
<td>0.22</td>
<td>Salinity (0.21)</td>
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<tr>
<td></td>
<td></td>
<td>Res</td>
<td>0.15</td>
<td>SAV (0.15)</td>
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<td></td>
<td></td>
<td>WQ</td>
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<td>Chlorophyll (0.19)</td>
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<tr>
<td></td>
<td></td>
<td>All</td>
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<td></td>
<td></td>
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<td>Depth (0.092)</td>
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<td>Temperature (0.074)</td>
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<td>WM*</td>
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<td>H2O Structure (0.084)</td>
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<td>Flashiness (0.070)</td>
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<tr>
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<td></td>
<td>Res</td>
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<td>Shoreline Emergent (0.12)</td>
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<td>WQ</td>
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<td>Color (0.070)</td>
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<tr>
<td></td>
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<td>WQ**</td>
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<td>Bottom DO (0.082)</td>
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<td>Depth (0.14) Shoreline Emergent (0.066)</td>
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The $R^2$ values for each management area subset as calculated by partial dbRDA for each of the four community types from spring-fed (a) and surface-fed (b) estuaries. The sector with the highest $R^2$ value has the model that explained the most variation in community structure and that sector therefore has the greatest potential to change that community by changing the value of one or more of the factors included in the model. Water management is in blue, restoration is in orange, and water quality is in gray.
Only salinity and chlorophyll were significantly influential for both spring-fed and surface-fed estuaries (Figure 4). Salinity almost always explained at least 10% of the variation (with the exception of surface-fed trawl), and often over 20% (spring-fed ichthyoplankton, spring-fed and surface-fed invertebrates, and spring-fed trawl). Chlorophyll was not as important in the surface-fed estuaries ($R^2 \approx 0.05$) as it was in the spring-fed estuaries ($R^2 \approx 0.2$). For surface-fed estuaries, depth and emergent vegetation on the shoreline were both selected. In each case, depth had the higher $R^2$ and emergent vegetation on the shoreline had the second highest. Flashiness and color were both selected twice in surface-fed estuaries, but neither of these factors explained more than 10% of the variation.

![Figure 4](image)

**Figure 4**
How often each factor was selected by AIC with distance-to-GOM as a covariate in the partial dbRDA for the four community types. The factor that explained the most variation in the abundance of a given community was selected first and subsequent factors were only included in the model if they explained substantial additional variation. Spring-fed estuaries are in blue and surface-fed are in orange. Only models using the water management, restoration, and water quality factor subsets (see Table 1) were included (models with all factors as options for selection were omitted). The factor that was selected most frequently has the potential to alter the most communities.
**Indicator values:**

None of the CAP analyses for spring-fed estuaries showed a significant difference between the groups with high and low levels of each factor; the following results are only for surface-fed estuaries. A table of all significant indicator values as well as more detailed results are presented in Appendix 4. For prey species, the significant indicator values ranged from 57.4 (Anchoa mitchilli juveniles for the low group of bottom DO) to 100 (multiple species) (Indicator values for each species not presented here. See Appendix 4 for averages.). The factors that had the most species with significant indicator values for high or low levels were salinity (22 species), pH (21 species), H2O Structure in zone (19 species), shoreline terrestrial (18 species), and emergent vegetation on the shoreline (17 species) (Figure 5). Salinity and pH had more species associated with high levels and H2O Structure in zone, emergent vegetation on the shoreline and shoreline terrestrial had more species associated with low levels. Other important factors included flushing time (15 species) and distance-to-GOM (15 species). Overall long flushing time was favorable to more species and low distance-to-GOM was more favorable to more species.
Figure 5
Number of prey species with a significant indicator value for either high (blue) or low (orange) levels of each factor. Indicator values were calculated by determining whether a species was at a higher abundance in zones with high or low levels of a given factor. Indicator values were at their maximum value (100) when a species is present in all zones in the high or low group and absent in all other zones. The total number of prey species was 38.

For economically important species, the significant indicator values ranged from 39.17 (Sciaenops ocellatus size 60-69mm for high levels of tidal H2O structure) to 100 (multiple species) (Indicator values for each species not presented here. See Appendix 4 for averages.).

Three factors (pH, depth, and flushing time) had significant indicator values for the most species groups (44 species groups, 42 species groups, and 36 species groups respectively) (Figure 6).

These numbers were based on different species size classes and developmental stages being counted separately so that ontogenetic shifts in habitat preference were captured. Overall, more species were associated with low depth, high pH, and high flushing time (Figure 6).
**Figure 6**
Number of economically important species that had a significant indicator value for either high (blue) or low (orange) levels of each factor. Indicator values were calculated by determining whether a species was at a higher abundance in zones with high or low levels of a given factor. Indicator values were at their maximum value (100) when a species was present in all zones in the high or low group and was absent in all other zones. The total number of economically important species groups was 76.
Partial multiple regression:

The $R^2$ values for the significant multiple regressions of prey species ranged from 0.28 ($Oithona$ spp. regression with all factors) to >0.99 (alphaeid postlarvae regression with all factors) for spring-fed estuaries and from 0.11 ($Acartia tonsa$ regression with water management factors) to 0.96 ($Labidocera aestiva$ regression with all factors) for surface-fed estuaries (Appendix 5, Table 8). The $R^2$ values for the covariate (distance-to-GOM) ranged from 0.001 ($Americamysis almyra$) to 0.79 (alphaeid postlarvae) for spring-fed estuaries and from 0.001 ($Americamysis almyra$) to 0.85 ($Bowmaniella dissimilis$) for surface-fed estuaries. The average $R^2$ for the covariate was higher in spring-fed estuaries than in surface-fed estuaries. A full list of all significant regression equations and more detailed results are presented in Appendix 5. In both spring-fed and surface-fed estuaries, the restoration management sector regressions had the highest $R^2$ for the most species when compared to the other two management sectors (Figure 7).

Flushing time was included in the most equations for spring-fed estuaries, with all but one of the coefficients being positive (Figure 8). SAV, pH, and salinity were also featured frequently in the regression equations for spring-fed sites, though not nearly as frequently as flushing time. All of the pH coefficients were negative while the salinity and SAV coefficients were more or less half positive and half negative. For surface-fed estuaries, pH explained a significant amount of variation in the abundance in the most species (12 species) (Figure 9). While most of the coefficients on pH were positive, it was not an overwhelming majority. Bottom oysters, emergent vegetation on the shoreline, and flushing time all explained significant variation for eight species. All of the coefficients for bottom oysters were positive and most of the coefficients for flushing time were positive as well. Emergent vegetation on the shoreline, on the other hand, had mostly negative coefficients.
The number of important prey species for which each management sector had the largest $R^2$ value, as calculated by multiple regression with distance as a covariate, out of the three management sectors. If a sector has the highest $R^2$ for a given species, that means it explained the most variation in abundance for that species and has the greatest potential increase or decrease the abundance of that species by changing the value or one or more factors included in the model. Only significant multiple regression analyses were included.

The $R^2$ values for the significant multiple regressions of economically important species ranged from 0.31 (Micropterus salmoides regression with water quality factors) to 1 (multiple species) for spring-fed estuaries and from 0.063 (Sciaenops ocellatus postflexion regression with water quality factors) to 0.73 (Brevoortia spp. postflexion regression with all factors) for surface-fed estuaries (Table 6). The $R^2$ values for the covariate (distance-to-GOM) ranged from 0.002 (multiple species) to 0.85 (Paralichthys albigutta) for spring-fed estuaries and from zero (multiple species) to 0.51 (Callinectes sapidus juveniles) for surface-fed estuaries (Appendix 4, Table 7). The average $R^2$ for the covariate was higher in spring-fed estuaries than in surface-fed estuaries though both of these averages were lower than those observed for prey species. As with prey species, both spring-fed and surface-fed estuaries, the restoration management sector regressions had the highest $R^2$ for the most species when compared to the
other two management sectors though there were more exceptions than with prey species (Figure 10).

**Figure 8**
The number of prey species that included each factor in their regression equations from the full suite of factors for spring-fed estuaries. Factors were selected using the AIC selection criterion with distance-to-GOM as a covariate. The factor that explained the most variation in the abundance of a given species was selected first and subsequent factors were only included in the model if they explained substantial additional variation. Blue represents multiple regression equations where the factor had a positive coefficient and orange represents equations where the factor had a negative coefficient. Only significant regressions are included.
Figure 9
The number of prey species that included each factor in their regression equations from the full suite of factors for surface-fed estuaries. Factors were selected using the AIC selection criterion with distance-to-GOM as a covariate. The factor that explained the most variation in the abundance of a given species was selected first and subsequent factors were only included in the model if they explained substantial additional variation. Blue represents multiple regression equations where the factor had a positive coefficient and orange represents equations where the factor had a negative coefficient. Only significant regressions are included.

In spring-fed estuaries, bottom sand (13 species groups), depth (10 species groups), and flushing time (9 species groups) were included in the regression equations for the most economically important species groups (Figure 11). Bottom sand had more positive coefficients than negative but not many more. Depth had half positive coefficients and half negative coefficients. Flushing time had mostly positive coefficients. For surface-fed estuaries, depth explained a significant amount of information for the most species groups (23 species groups) followed by flashiness (22 species groups), SAV (18 species groups), and inflow (18 species groups) (Figure 12). Depth has negative coefficients for all but one of the regression equations. Flashiness had positive coefficients for all but two of the equations.
Figure 10
The number of economically important species groups for which each management sector had the largest R² value, as calculated by multiple regression with distance as a covariate, out of the three management sectors. If a sector has the highest R² for a given species group, that means it explained the most variation in abundance for that species group and has the greatest potential increase or decrease the abundance of that species group by changing the value or one or more factors included in the model. Only significant multiple regression analyses were included.
The number of economically important species groups that included each factor in their regression equations from the full suite of factors for spring-fed estuaries. Factors were selected using the AIC selection criterion with distance-to-GOM as a covariate. The factor that explained the most variation in the abundance of a given species group was selected first and subsequent factors were only included in the model if they explained substantial additional variation. Blue represents multiple regression equations where the factor had a positive coefficient and orange represents equations where the factor had a negative coefficient. Only significant regressions are included.
Figure 12
The number of economically important species groups that included each factor in their regression equations from the full suite of factors for surface-fed estuaries. Factors were selected using the AIC selection criterion with distance-to-GOM as a covariate. The factor that explained the most variation in the abundance of a given species group was selected first and subsequent factors were only included in the model if they explained substantial additional variation. Blue represents multiple regression equations where the factor had a positive coefficient and orange represents equations where the factor had a negative coefficient. Only significant regressions are included.

Reduction in Spatial Resolution:
There were only three spring-fed estuaries for the present study, and thus independent analysis of the spring-fed estuaries was not feasible. Instead, analyses with (1) variable factor resolutions and (2) homogenous factor resolutions were compared for surface-fed estuaries and for all of the estuaries combined. The dRDA $R^2$ values ranged from 0.216 (ichthyoplankton) to 0.327 (invertebrates) for surface-fed estuaries and from 0.229 (ichthyoplankton) to 0.336 (trawl) for all estuaries. Overall, the $R^2$ values were lower than those seen in the factor resolution
analyses and fewer factors were selected as explaining substantial amounts of variation. Distance-to-GOM was the only factor selected for invertebrates, seine, and trawl, and emergent vegetation on the shoreline was the only factor selected for ichthyoplankton in surface-fed sites (Figure 13). For all of the sites combined, the homogenous variation analysis selected distance-to-GOM for seine and trawl, dissolved oxygen for invertebrates, and algae for ichthyoplankton. For the partial dbRDA, the significant $R^2$ values ranged from 0.151 (seine water quality) to 0.210 (ichthyoplankton all factors) for the surface-fed sites and from 0.105 (trawl water quality) to 0.200 (invertebrates all factors and restoration). As seen in the dbRDA, far fewer factors were selected as explaining a substantial amount of variation in the homogenous resolution analysis than in the analysis with factor resolution. In fact, for invertebrates in surface-fed estuaries, after the variation from distance-to-GOM was removed, no other factors explained a substantial amount of variation. In the analysis with all of the estuaries combined, invertebrates selected algae as the only factor to explain a substantial amount of variation. When all of the factors were an option, ichthyoplankton and seine selected emergent vegetation on the shoreline (Figure 14). Ichthyoplankton also selected emergent vegetation on the shoreline when all estuaries were combined, yet seine selected algae instead. Trawl selected bottom oysters in both surface-fed estuaries and all estuaries combined. The restoration management sector had the largest $R^2$ value for all of the communities for both surface-fed estuaries and all estuaries combined (Figure 15).
The number of communities that selected each factor in the original dbRDA (in orange) for surface-fed estuaries (a) and all estuaries combined (b) as well as the results from the dbRDA where all data were averaged over entire estuaries to force all factors to be at the same resolution (in blue). The factors were selected using AICc selection criterion where the factor that explained the most variation in abundance for a given community was selected first and subsequent factors were only included in the model if they explained a substantial amount of additional variation.
Figure 14
The number of communities that selected each factor in the original partial dbRDA (in orange) for surface-fed estuaries (a) and all estuaries combined (b) as well as the results from the partial dbRDA where all data were averaged over entire estuaries to force all factors to be at the same resolution (in blue). The factors were selected using AIC selection criterion with distance-to-GOM as a covariate where the factor that explained the most variation in abundance for a given community was selected first and subsequent factors were only included in the model if they explained a substantial amount of additional variation.
A comparison between the $R^2$ values of different management sectors when data has either factor or homogenous resolution. The top graph (a) depicts the $R^2$ from the partial dbRDA values for each management area subset for each of the three communities for surface-fed estuaries (invertebrates were excluded because no factors explained a substantial amount of variation). The sector with the highest $R^2$ value has model that explained the most variation in abundance for a given community and that sector therefore has the greatest potential to change that community by changing the value of one or more of the factors included in the model. Water management is in blue, restoration is in orange, and water quality is in gray. The lower graph (b) identifies how many communities each sector had the largest $R^2$ value when all estuaries were combined for both factor (orange) and homogenous (blue) resolutions.
Discussion:

Community analysis:

The ichthyoplankton community had the lowest $R^2$ in both types of estuaries in the dbRDA. This suggests there was a source of variation that was missing from the analysis. The most likely explanation is that the supply of ichthyoplankton was highly seasonal (i.e., Houde and Lovda, 1984, Peebles et al. 1991) whereas the abundance data were averaged over an entire year. Nonetheless, water color was determined to be the most important factor for ichthyoplankton in surface-fed estuaries (Table 3). The main effect of water color is through light attenuation. This has a direct effect on communities by decreasing water clarity and indirect effects by limiting benthic growth of algae and plants (Malkin, 2010; Radabaugh and Peebles 2012). However, since turbidity has a stronger negative correlation with SAV than color ($r = -0.17$ and $-0.27$ respectively, neither significant), and neither turbidity nor SAV were selected as significantly influential, it would seem that the influence of water color for ichthyoplankton was not related to benthic plant growth. It is more likely a simple indicator of freshwater inflow in surface-fed estuaries, which tend to be highly colored (Peebles and Flannery 1992). Larval fish were most abundant at the seaward ends of the estuarine transects, and moved out of the estuaries during periods of high freshwater inflow, which were also periods of high color (Peebles and Flannery 1992, Peebles 2005).

Blaber (1987) suggested that postlarvae in the marine environment may follow turbidity gradients in order to find ideal estuarine habitat. Other studies have suggested that turbid waters can provide an advantage to young fish because of the protection from visual predators (Cyrus and Blaber, 1987a, 1987b). All of these studies focus on South African estuaries where turbidity levels are often very high. Comparatively, southwest Florida estuaries have low turbidity
(highest value in the present study was 8.3 NTU in Braden River; see also Peebles and Flannery 1992), yet water color and phytoplankton levels are often high enough to provide significant light attenuation (McPhearson and Miller, 1987, Chen et al., 2007). In Florida estuaries, color may provide the same function as turbidity does in South African estuaries. However, it should be noted that, due to lack of data, both color and turbidity levels were averaged over entire estuaries, and thus it is possible that local areas of high turbidity (e.g., convergent zones where benthic particles are re-suspended) would not be evident in the data.

Temperature was identified as an influential factor in all four communities in the dbRDA, most likely due to its covariation with the estuarine gradient. Habitat factors, including temperature, were analyzed as annual averages so seasonality could not have influenced this result. Instead, it is likely that average water temperature is a proxy for how much cool rainwater was entering the estuary during the summer when the water temperatures in receiving basins were relatively high (29-32°C in Tampa Bay, according to NOAA’s Tampa Bay Operational Forecast System). This relationship was evident in a study by Peebles et al. (1991) where, in a plot of water temperatures in different estuary zones of Little Manatee River over the course of a year, the upstream-most estuarine zones had lower summer water temperatures than the zones that were closer to Tampa Bay. In the present study, there was also a significant negative correlation between the average temperature of estuary zones and distance-to-GOM for surface-fed estuaries ($r = -0.31, p = 0.020$). Thus, water temperature is another covariate of the overall estuarine gradient. It is possible there is a separate effect of more or less summer rainfall on communities in surface-fed estuaries. Other studies have documented organisms moving out of the estuaries during periods of high freshwater inflow, which were also periods of reduced upstream water temperature (Peebles and Flannery 1992, Peebles 2005).
Flashiness and average daily inflow were both selected as significantly important for all four community types in surface-fed estuaries (Figure 2) but were not significant for any community type in spring-fed systems. Burghart et al. (2013) suggested that freshwater inflow was less impactful for the spring-fed estuaries because these estuaries are shorter along their principle axes, and have much smaller watersheds than their surface-fed counterparts. This leads to less overall variation in inflow among spring-fed estuaries. While the $R^2$ values were all under 0.1 in surface-fed estuaries, these two inflow-related factors were still clearly having an effect on the communities in surface-fed estuaries (Table 3). Freshwater inflow can be important to estuarine estuaries for many reasons that are not mutually exclusive. First, freshwater inflows deliver nutrients that stimulate primary and secondary production. Grange et al. (2000) compared the low-inflow Kariega estuary and the high-inflow Great Fish estuaries (both in South Africa) and found that the Kariega estuary had lower overall chlorophyll, zooplankton concentrations, and larval and juvenile fish densities. For, the present study, while chlorophyll was weakly correlated with average daily inflow ($r = 0.18$), the correlation was not significant ($p = 0.20$), which suggests other factors were also involved. However, it should be mentioned that the chlorophyll data were non-synoptic and at a lower spatial resolution which may account for the non-significant correlation. Freshwater inflows also have a direct effect on current speed and flushing time. The balance between fresh water delivering nutrients for phytoplankton blooms and also providing the force to flush them downstream is where the influence of flashiness comes in. Streams with higher variability in freshwater inflows (higher flashiness) will also have higher variability in the durations and locations of phytoplankton blooms. Freshwater inflows also deliver olfactory cues that encourage the recruitment of young fish to estuaries. For example, Martin et al. (1992) found a marked increase in the densities of postlarval marine
species in the St. Lucia estuary (South Africa) after an episodic flushing event. This also suggests that freshwater inflows may be more influential at certain times of the year due to the seasonality of ichthyoplankton supply. Therefore, since the data in the present study were averaged over an entire year, the full influence of freshwater inflow may have been underestimated.

Finally, the overall estuarine gradient is maintained by a balance of freshwater inflow and tidal intrusion. Salinity was overwhelmingly selected as the most influential factor on community composition in both spring-fed and surface-fed estuaries (Table 3 and Table 4). In fact, salinity was selected as the only substantially influential factor for all of the spring-fed estuary communities and explained the most variation in three out of the four surface-fed communities in the dbRDA. This agrees with the findings of similar studies (Mouny and Dauvin, 2002; Thiel et al., 1995; Weinstein et al., 1980; Lopes, 1994; Telesh, 2004; Modéran et al., 2010). However, a possible reason for the dominance of salinity in this analysis is its covariation with distance-to-GOM. As with average freshwater inflows and freshwater inflow variability, distance-to-GOM was selected as significantly important in all four community types for surface-fed estuaries. This could be because the surface-fed estuaries had more variation in distance-to-GOM, as opposed to spring-fed estuaries. All of the spring-fed estuaries ended at the GOM and were relatively short in length, whereas most of the surface-fed estuaries entered Tampa Bay or Charlotte Harbor and were more variable in length (Figure 1). This meant that salinity and distance-to-GOM were more strongly covaried in spring-fed estuaries (Appendix 3) and, because salinity was selected in every spring-fed estuary, distance-to-GOM did not explain a substantial amount of additional variation. Since estuarine zones that were closer to the GOM were presumably easier for fish and invertebrate larvae to get to, these zones are likely to have
communities with higher abundances of migrating life stages. Zones closer to the GOM will also have higher salinities than zones farther from the GOM, which is why these two factors covary. Thus, a zone that has high salinity may differ in community from a zone with lower salinity, yet this may have little to do with the salinity directly. In order to remove this effect, distance-to-GOM was used as a covariate for the remainder of the community analysis.

Effect of covariate

Overall, each community had a lower $R^2$ value when variation in distance-to-GOM was removed than when that variation was included in the total variation. This was an expected result because at least some of the factors selected for each community covaried with distance-to-GOM (Appendix 3). The covariate explained more information in the spring-fed estuaries than in the surface-fed estuaries for every community (Figure 16). This may be because all of the spring-fed estuaries connect directly to the GOM, whereas only one surface-fed estuary (Anclote) had the GOM as its receiving basin (Figure 1). Therefore, spring-fed estuaries are easier to access for marine transients, and species that are more heavily affected by distance-to-GOM may have more computational weight in these estuaries. Or, distance-to-GOM may explain more information because, since spring-fed estuaries enter the GOM directly, distance-to-GOM lines up more closely to the overall estuarine gradient in spring-fed estuaries than in surface-fed estuaries. The largest difference in $R^2$ before and after variation explained by distance-to-GOM was removed was observed for the surface-fed seine community (Figure 16). Salinity lost almost half of its explanatory power and most of the other previously selected factors (SAV, flashiness, inflow etc.) shared enough variation with distance-to-GOM that they no longer explained a substantial amount of variation on their own. The two exceptions were
average depth and the percent bottom cover by mud (Table 4). Neither of these factors had a significant correlation with distance-to-GOM (Appendix 3), which is likely why they were retained.

Interestingly, the community where distance-to-GOM had the lowest $R^2 (0.085)$ was the surface-fed ichthyoplankton community, and yet there was still a fairly large difference between the $R^2$ values of the dbRDA and the partial dbRDA (Figure 16). Of the original eight factors selected, only water color and freshwater inflow variability (flashiness) were retained. Both of these factors had a significant correlation with distance-to-GOM (Appendix 3), but presumably, the variation explained by these two factors did not overlap very much with the small amount of variation explained by distance-to-GOM. On the other hand, water temperature was originally the second-most influential factor, but was not selected at all by the partial dbRDA. This could mean that much of the variation explained by temperature was also explained by distance-to-GOM. This would make sense because temperature and distance-to-GOM were significantly correlated. It follows, at least for ichthyoplankton, that the influence of water temperature in the dbRDA was likely due to its covariation with the overall estuarine gradient.
Figure 16
The $R^2$ values for the dbRDA, the covariate (distance-to-GOM), and the partial dbRDA for each community in each type of estuary. This dbRDA determines how much community abundance variation was explained by an optimal subset of factors (selected with AIC). The covariate $R^2$ is the amount of variation explained by distance-to-GOM for each community. The partial dbRDA $R^2$ is how much variation is explained after the variation explained by distance-to-GOM has been removed. Spring-fed trawl is missing for dbRDA because it did not have a significant result. The dbRDA $R^2$ is in blue, the partial dbRDA $R^2$ is in orange, and the $R^2$ of the covariate is in gray.
Figure 17
A comparison between the factors selected by dbRDA and by partial dbRDA with distance-to-GOM as a covariate for spring-fed (a) and surface-fed (b) estuaries. Both these analyses select the factor that explained the most community abundance variation first and will only select additional factors if they explained a substantial amount of additional variation. However, partial dbRDA uses distance-to-GOM as a covariate so the variation explained by distance-to-GOM was removed before the selection of factors occurred. Only the partial dbRDA models using all of the habitat factors were included (management sector models omitted). dbRDA is in blue and partial dbRDA is in orange.
As expected, salinity lost much of its explanatory power after the variation explained by distance-to-GOM had been removed. In each case, salinity by itself explained less variation in the partial dbRDA than the dbRDA. In the dbRDA, salinity was the only factor selected for every spring-fed estuary. This was also true in the partial dbRDA excepting the spring-fed seine community which selected presence of a head spring in the zone instead (Figure 17). The selection of this binary factor (head-spring presence) suggests there was a specific community associated with the head springs, most likely related to fresh, clear water. *Lucania goodei* was the species most associated with head springs, whereas *Leiostomus xanthurus* and *Lucania parva* were less common near head springs in comparison with other zones. Another pattern that emerged was smaller size classes of *Gambusia holbrooki* were associated with deep, low-salinity waters and a high percent of mud bottoms (Appendix 2, Figure A2 (u)).

*Species analysis*

For the indicator-value analysis of both important prey species and economically important species, average salinity and pH were selected most often, with most species being associated with higher levels of both factors (Figures 5 and 6). As with salinity, pH also changes gradually along the estuarine gradient and covaries with distance-to-GOM (Appendix 3). However, the overall impact of pH was further complicated by its relationship with water temperature, respiration rates, and photosynthesis. Jarvie et al. (2000) found that the diurnal variation in pH in the Tweed estuary could be explained by the diurnal patterns of phytoplankton photosynthesis and respiration, because pH can be modified by dissolved CO\(_2\) concentrations and photosynthesis consumes CO\(_2\) while respiration produces CO\(_2\). Thus, while pH in surface waters is initially controlled by acidic rainfall and the buffering capacity of associated surface
geology (karst and carbonate-based sediments), the interplay between primary and secondary production in the estuary can modify it (Howland et al., 2000). Water temperature can also play a role because it affects the partial pressure of dissolved CO$_2$, which in turn affects the speciation of inorganic carbon. Other things being equal, water at a higher temperature will be able to contain less dissolved CO$_2$, which will then result in a higher pH. This was verified in the present database, where temperature and pH had a significant positive correlation ($r = 0.33, p = 0.016$). Therefore, an organism that was associated with high pH (as most of them were) could be associating with the marine end of the estuary, with higher water temperature, or with higher rates of photosynthesis.

Unlike the indicator value analysis, the multiple regression analysis did not consider the factors independently, which reduced (but by no means eliminated) the problem of covariation. In the multiple regression analysis, pH was still important for many surface-fed prey species, yet salinity no longer stood out as an explanatory factor, which suggests pH has influence beyond its covariation with the estuarine gradient. The same is somewhat true for surface-fed economically important species, though pH was not even within the top five most selected factors. The potential effect of pH may have varied with species. For example, *Callinectes sapidus* (blue crab) juveniles had their largest indicator value for high levels of salinity and a fairly substantial indicator value for pH as well. Distance-to-GOM had a large R$^2$ value for *Callinectes sapidus* juveniles (0.51). Once the variation from distance-to-GOM was removed, however, neither pH nor salinity was selected as explaining a significant amount of variation, suggesting that the influence from these two factors in the indicator-value analysis was from covariation with distance-to-GOM. Conversely, *Orthocyclops modestus*, a freshwater copepod, had a very high indicator value for salinity and a very low R$^2$ with distance-to-GOM (0.080). Once the variation
from distance-to-GOM was removed, salinity was still selected and it had the largest coefficient. Many species also fell between these two extremes, with pH and salinity explaining some, but not as much, of the variation after the variation from distance-to-GOM had been removed.

Besides pH and salinity, many prey species had significant indicator values for the presence of a water-control structure in the zone, percent cover of shoreline lawns or shoreline trees (shoreline terrestrial), and percent cover of emergent shoreline vegetation (emergent vegetation on the shoreline). The amount of shoreline lawns or shoreline trees had a significant correlation with distance-to-GOM ($r = 0.39 \ p = 0.006$) and, once the variation from distance-to-GOM was removed in the multiple regression analysis, it was only selected as explaining a significant amount of variation twice. This suggests that, for most species, the amount of shoreline lawns or shoreline trees was only selected because of its covariation with the overall estuarine gradient. This is supported by the fact that the few species that were associated with high percent cover of shoreline lawns or shoreline trees were freshwater species. Whether there was a water-control structure within the zone was only selected twice in the multiple regression analysis and it did not have a significant correlation with distance-to-GOM ($r = 0.059 \ p = 0.673$). This suggests that the presence of a water-control structure within a zone covaried with some other factor that explained more variation for most species. Thus, when the factors were no longer considered independently, the presence or absence of a water control structure within a zone was no longer very influential.

Other than pH and salinity, the factors that appeared to be most important for prey species in the multiple regression analysis were flushing time, freshwater inflows, and percent bottom cover by oysters for surface-fed estuaries, and flushing time, submerged vegetation, and percent shoreline cover by mangroves for spring-fed estuaries. Flushing time was correlated with
salinity in surface-fed sites \((r = 0.48, p = 0.001)\) and with distance-to-GOM in spring-fed sites \((r = -0.50, p = 0.04)\), so there may be a component of the variation explained by flushing time that was due to the overall estuarine gradient. In many cases for both spring and surface-fed sites, flushing time was selected along with salinity or pH, suggesting that flushing time had an influence outside of covariation. It is possible that most species had a positive correlation with flushing time because the majority are planktonic and are not able to remain in areas where the flushing time was too short and currents were fast (Sterner et al., 1996).

Although pH was selected for many species in spring-fed and surface-fed estuaries, the regression coefficients for pH were all negative in spring-fed estuaries while surface-fed estuaries had more of a mixture of positive and negative coefficients. This might be because all of the spring-fed estuaries enter the GOM directly while all but one of the surface-fed estuaries enter Tampa Bay or Charlotte Harbor (Figure 1). Therefore, in spring-fed estuaries, using distance-to-GOM as a covariate removes a lot more of the variation from the overall estuarine gradient. Consequently, the main explanatory power of pH in spring-fed estuaries was not due to the estuarine gradient (which has mostly been removed), but instead to the balance of respiration and photosynthesis discussed earlier. Thus, the negative coefficient for pH for spring-fed estuaries may reflect the possibility that these prey groups occurred in areas with high ratios of respiration to photosynthesis.

Percent bottom cover by oysters, submerged vegetation, and percent shoreline cover by mangroves each relate to different forms of shelter and structure in the estuarine environment. The findings of the present study are in agreement with studies such as that by Shervette et al. (2011), which found that species of crabs and shrimp preferred vegetated habitat and oyster reefs to non-structured habitat. Some species seemed to prefer only one kind of structure, while others
had a positive correlation with several types of structure. For example, alphaeid postlarvae (snapping shrimps) had a positive realationship with submerged vegetation in spring-fed estuaries and no relationship with any of the other structure-related factors, whereas Hippolyte zostericola postlarvae (shrimp) had the highest regression coefficient for percent bottom cover by oysters, but also had positive relationships with submerged vegetation and the percent of the bottom that was manmade. In the case of submerged vegetation, the positive and negative coefficients associated with habitat factors may be partially due to its relationship with water clarity and also position along the estuarine gradient, as submerged vegetation is restricted to downstream (low-color) zones in the surface-fed estuaries. The species that seemed to avoid submerged vegetation (Pseudodiaptomus coronatus and unidentified harpacticoids) may be associating with low water clarity conditions instead; both are bottom-associated copepods.

Among economically important species, the habitat factors that had significant indicator values for the most species were pH, depth, and flushing time. All three of these factors had a significant correlation with salinity, which suggests a fair amount of the species that were associated with these factors may have reflected covariation with other factors along the estuarine gradient. This is supported by the fact that the only species associated with high water depth and low flushing time (Micropterus salmoides, largemouth bass) is also a freshwater species. In the multiple regressions, where variation from distance-to-GOM was removed and the factors were no longer considered independently, water depth was still important, but flushing time and pH were no longer among the top factors. Thus, while pH and flushing time still explained a significant amount of variation for a few species, notably Paralichthys albigutta (Gulf flounder), which had the largest regression coefficient for pH for both seine and trawl gear types, and Mugil trichodon (fantail mullet), which had its largest coefficient for flushing time,
most economically important species were not associated with these factors. The potential reasons for these few species having significant variation explained by pH and flushing time are discussed above, but since most of the economically important species groups are not planktonic, it is possible that these species’ associations with long flushing times exist because they were targeting planktonic prey rather than being directly affected by flushing time.

As with prey species, surface-fed estuaries had more economically important species groups with freshwater inflow as an explanatory factor than did spring-fed estuaries. The reasons for the importance of freshwater inflow are the same as those discussed for prey species. However, for economically important species, freshwater inflow variability (flashiness) also appeared to play an important role for many species, which was not the case for the prey groups. The mechanisms behind the flashiness relationship may be the same as those discussed in the community analysis.

Water depth was also very important for economically important species in both surface-fed and spring-fed estuaries. This agrees with some of the results of Marshall and Elliott (1998), who found that several estuarine species had a significant relationship with water depth, and those of Blaber and Blaber (1980), who found juvenile fish preferred shallow waters. Depth explained a significant amount of variation for the most species groups in surface-fed estuaries and the second-most species groups in spring-fed estuaries. In spring-fed estuaries, there appeared to be a weak pattern of smaller members of a species being associated with shallow waters (negative coefficient for depth) and larger members with deeper water (positive coefficient for depth), whereas in surface-fed estuaries, all but one species (*Micropterus salmoides*) had negative coefficients for depth. Possible effects of depth occur through shallower waters having slower currents and more refuges from aquatic predators.
Submerged vegetation was the final important factor for surface-fed economically important species, particularly *Sciaenops ocellatus* (red drum). This agrees with the findings of Petry et al. (2003), who found that macrobenthic growth explained a significant amount of variation in fish assemblages, and also with those of Tonn and Magnuson (1982), who found that fish species richness was significantly related to vegetation diversity. Submerged vegetation can provide habitat complexity and critical refuge from predation. It can also provide a source of food either directly or indirectly as a substrate for epiphytic growth. A study by Moncreiff and Sullivan (2001) found that epiphytic and benthic microalgal growth was the most important source of primary productivity (i.e., basal resource) for fish in a subtropical seagrass habitat. However, only one species (*Leiostomus xanthurus* <20mm) had a positive coefficient for submerged vegetation. Thus, for the other 16 species, these positive effects are not the source of the importance of submerged vegetation. Instead, it is likely that the availability of submerged vegetation is related to position along the estuarine gradient within the surface-fed estuaries, where it is largely restricted to downstream (low-color) zones where these species are less abundant.

Percent bottom cover by sand was featured frequently in spring-fed estuaries and somewhat frequently in surface-fed estuaries. This agrees with the work of Jenkins and Wheatley (1998) and Guidetti (2000), both of which reported that a few species of fish preferred unvegetated sand habitat while most others preferred habitats with more structure. While the coefficients for surface-fed estuaries were mostly negative [exceptions being *Paralichthys albigutta*, *Micropterus salmoides*, and *Mugil curema* (white mullet)], the spring-fed coefficients were nearly evenly divided between positive and negative. *Micropterus salmoides* also had a positive coefficient in the spring-fed estuaries and several size classes of *Sciaenops ocellatus* had
large negative coefficients in both spring-fed and surface-fed estuaries. However, different size classes of *Callinectes sapidus* had positive coefficients in spring-fed estuaries and negative coefficients in surface-fed estuaries. This may be evidence of an ontogenetic shift in habitat preference since the positive coefficients were associated with smaller size classes and the negative coefficients were associated with larger size classes.

*Three management sectors*

Based on the R² values in the community analysis, water management was most often the management sector with the greatest potential for changing beta diversity in spring-fed and surface-fed estuaries (Figure 3). The exceptions to water management being selected as most influential were the two seine communities, which selected restoration, and surface-fed ichthyoplankton, which selected water quality. Within water management, salinity was selected as most influential habitat factor seven out of eight times and was often the only factor selected (Appendix 5). While this may be partially due to covariation, it is likely that water management entities can still go a long way towards maintaining beta diversity by ensuring there is enough fresh water entering these estuaries to maintain the salinity gradient. It is also evident that, at least for surface-fed ichthyoplankton, flashiness is a major factor in determining community structure. Both of these habitat factors can be managed through selection of the timing and volume of freshwater withdrawals and discharges over water-control structures. As the agricultural, industrial, and municipal demands for fresh water continue to grow, consideration of these effects needs to be included in water-management plans. The percent-of-flow approach proposed by Flannery et al. (2002) seems to be a reasonable means of achieving elevated inflow levels and inflow variability.
For both prey species and economically important species, the restoration management sector had the highest $R^2$ for the most species in both spring-fed and surface-fed estuaries, followed by water management and then water quality (Figures 7 and 10). Thus, while the water-management sector can have the greatest influence on overall community structure, the restoration sector can have the largest influence on selected species. However, considering the water-management sector was often selected because of salinity having a high $R^2$ value, there may be further complications to these findings.

Other issues with salinity

Many studies on estuary habitat find that salinity was highly influential for both communities and species (Mouny and Dauvin, 2002; Thiel et al., 1995; Weinstein et al., 1980; Lopes, 1994; Telesh, 2004; Modéran et al., 2010). It is often assumed that the reason for this may be that different species were associated with different salinities because of physiological limitations and the energetic costs of osmoregulation. A number of studies have reported that different species have different salinities that are associated with an optimum growth rate (Peterson et al., 1996; Watanabe et al., 1989; Imsland et al., 2001), yet most of these studies are based on controlled experiments, whereas in the field, the mosaic of food density and shelters from predation make the process of improving growth rate and survival more complex. Older studies that based their energy-consumption measurements on oxygen consumption found that osmoregulation could account for 20-50% of the total energy budget for fish (Rao, 1968; Nordlie and Lefler, 1975), but newer studies that make direct measurements of ionic fluxes and/or urea synthesis find the energy cost to be closer to 10% of the total energy budget (Boeuf and Payan, 2001; Kidder and Petersen, 2006). This latter estimated cost would be much easier to offset with
increased food availability or decreased predation risk. A review by Whitfield (1999) supports the idea that salinity is not usually physiologically limiting by citing instances of estuarine fish being found many tens of kilometers upstream. Another paper featuring many of the same estuaries from the present study found that, while different stages of bay anchovy tended to follow a similar pattern of ontogenetic habitat shift, there was no central tendency in the salinity at which each stage was caught, with a high level of variability existing among tidal rivers (Peebles et al., 2007). Thus, while the effect of salinity in terms of osmoregulatory energetic costs may be a factor in its selection and high $R^2$ values, salinity is not likely to be the only influential habitat factor.

Salinity changes gradually over the estuarine gradient as do many other habitat factors. Thus, many habitat factors covary naturally. In particular, salinity is likely to covary with most of the influential habitat factors considered here, as discussed individually above. Covariation with larval supply was addressed by using distance-to-GOM as a covariate, which decreased the explanatory power of salinity; the amount of variation explained by salinity decreased for every community after variation explained by distance-to-GOM had been removed in the partial dbRDA. The indicator-value analysis did not use a covariate, and salinity was a significant habitat factor for the most prey species and for 32 of the economically important species. In the multiple regression analysis, which did hold distance-to-GOM as a covariate, salinity was not in the top four most frequently selected factors for either the prey groups or the economically important species. However, salinity was still selected first for most partial dbRDAs and often had the highest coefficient in the multiple regression analysis, and thus it would appear that covariation with distance-to-GOM was not the only reason for its apparent importance.
Primary productivity maxima are usually located near the mouths or middle reaches of the tidal rivers in the study area. This is due to interactions between nutrient input (usually from freshwater inflows but also from sediment resuspension and remineralization), downstream dilution of light-attenuating materials (notably color), and flushing time, which increases as the tidal river initially widens towards the mouth. Many spawning adults and migrant larval and juvenile fish are likely to target these areas of high productivity, as observed in the study by Peebles (2002). Water clarity is usually at a minimum at the edge of the intruding tidal salt wedge (Roman, 2001) and increases with distance upstream, with particularly clear water being found at head springs. Turbidity levels are relatively low (in comparison with estuaries elsewhere), yet turbidity may be locally important because it can contribute to the predation-refuge effect and because of its effect on shading benthic primary-producer growth (Radabaugh and Peebles, 2012); certain species appear to associate with turbidity, as reported by Roman (2001) and Cyrus and Blaber (1987a,b). In the case of water clarity and phytoplankton biomass, the related data were averaged over entire estuaries, and thus such finer-scale patterns were not captured. It is likely that one of the main reasons that salinity had such high $R^2$ values and was selected so often was that the salinity data were a better representation of these effects than the low-resolution chlorophyll and turbidity data.

Data resolution and bias

Because the data taken from the EPA STORET database were not available for every estuary zone, these water-quality factors (color, chlorophyll and, turbidity) could only be resolved at the estuary level rather than the zone level. These data were also of an overall lower quality because the annual averages were based on fewer samples. There were also factors such
as inflow and flashiness that, by their natures, could only be resolved at the estuary level. Then, there were factors that were, by their natures, binary (presence/absence of a water-control structure, presence/absence of a tidal-river water-control structure, and whether the head spring was sampled). All of this means that there was a potential bias in the analysis towards more nuanced, higher resolution factors (such as factors measured in direct association with every biological collection).

When conducting habitat-factor analyses, multiparameter-sonde-based data may explain most of the variation in abundance data for several reasons. Sonde-based data are easy to collect. Most sonde equipment comes with sensors for measuring temperature, salinity, and dissolved oxygen, and as a result, many estuarine biotic-environmental databases include these factors at the same spatial and temporal resolutions as the biotic data. Other factors such as turbidity, pH, chlorophyll $a$, and even bottom and shoreline types may be missing or may exist at much lower spatial and temporal resolutions, especially in databases from older data-collection efforts. Local minima and maxima in some factors can be very influential (Roman, 2001, Islam et al., 2005) and averaged values will not capture these process-based patterns.

**Repeated analysis with homogenous resolution**

In the dbRDA, there was a stark contrast between the original results and the results with all of the data averaged over entire estuaries. In the original data, salinity was selected as explaining the most variation in three out of the four community types in surface-fed estuaries and in two out of four when all estuaries were combined. For the data with homogenized resolution, the same three surface-fed communities selected distance-to-GOM instead, and when all estuaries were combined, seine and trawl communities selected distance-to-GOM as well.
While the original dbRDA revealed the importance of distance-to-GOM, the lower resolution effort identified the importance of this factor even more clearly. Surface-fed invertebrates were an extreme case where, after the variation explained by distance-to-GOM was removed, no other factor explained a substantial amount of the remaining variation. For the other three surface-fed communities, percent shoreline cover by emergent vegetation was selected twice and percent bottom cover by oysters was selected once in the partial dbRDA when all factors were an option. Both of these factors were also selected when all estuaries were combined. The amount of emergent vegetation is a reasonably good proxy for how developed a particular estuary is, with more natural, undeveloped estuaries having more emergent vegetation. However, in the surface-fed estuaries, the presence of emergent shoreline vegetation increases in the middle and upper reaches of the estuary. Oysters also represent a more natural bottom type and also provide structural habitat for estuarine organisms, but tend to be most abundant in the downstream reaches of both types of estuaries. While returning estuaries to a state with more vegetation and oysters is likely to have a positive effect, these two habitat factors also have strong distributional trends along the estuarine gradient.

Problems with data-resolution bias can change the results of habitat-factor analyses. In the future, care could be taken to make sure all factors are measured at the same resolution and without bias. In particular, the present study would have benefitted from higher resolution data, particularly water quality data, so that local maxima and minima could be included in the models and other multivariate analyses. This emphasizes the need for monitoring programs to consider not only the necessary temporal frequency of sampling, but also the most effective spatial resolution.
The estuarine gradient and covariation

Besides problems with data-resolution bias, there are also issues related to covariation in our data. Most of the habitat factors that were determined to be influential (salinity, pH, emergent vegetation, mangrove, and lawn-and-trees shoreline types, oyster bottom type, SAV, color, temperature, and flushing time) follow the pattern of the estuarine gradient where values are higher at one end of the estuary and gradually (or abruptly in the case of SAV in surface-fed estuaries) shift to lower values at the other end of the estuary. Since many of the analyzed species follow this same pattern, any of these variables are capable of explaining the variation in both communities and individual species abundance. This was discussed in previous sections, but it presents a problem when using this sort of linear regression-based analysis for habitat analysis. Instead of determining influential habitat factors, this analysis may simply be describing the qualities of the freshwater end and marine end of these estuaries without determining which of these qualities are directly responsible for biotic distributions. This is likely a limitation in many similar habitat analyses on estuaries as well as a reason why studies often find that salinity or other estuarine-gradient-related factors (e.g. sediment grain size) explain the most variation in abundance or community. In the future, estuary habitat analyses should take this effect into consideration and contemplate the removal of the gradient either through use of a covariate (e.g. salinity) or removing trends with spatial analysis.

Depth, sandy bottom type, and flashiness were exceptions to this gradient trend. In particular, flashiness, which had the same value for every zone within an estuary, was incapable of following the estuarine gradient. Despite being at a lower spatial resolution, flashiness explained a significant amount of variation for many economically important species which suggests it has an important role in estuaries that has not been thoroughly investigated in the
literature. Flashiness is also not a factor considered in most water management plans for estuaries which our data suggests is an oversight. Further research is needed to see how flashiness affects estuarine species and how it should be managed.

Conclusions:

(1) Distance to a source of marine migrants can have a strong effect on estuarine communities.

We saw this effect mostly in surface-fed estuaries. In the dbRDA, distance-to-GOM was selected by the AICc in all four community types in surface-fed estuaries. Even though it was not selected in the spring-fed dbRDA, when it was included as a covariate in the partial dbRDA, it explained around 30% of the variation in three out of the four community types. Distance-to-GOM also commonly explained large proportions of variation for species (Table 8 and 10). When all of the data were averaged over entire estuaries, distance-to-GOM was the only factor selected in three out of the four community types in the dbRDA. Since the distance to a receiving basin can covary with many other factors (Appendix 3), it should be held as a covariate or otherwise accounted for so that the importance of covarying factors is not overestimated.

(2) Issues with bias and factor resolution can overinflate the influence of higher resolution factors.

Even though much of the initial analysis frequently selected salinity as an important factor and many other studies have found similar results, other literature suggests that it is not the process directly influencing these species. Our results from the analysis
with all data averaged over entire estuaries seems to support findings that suggest salinity does not have a strong, direct influence at the estuary level. In the partial dbRDA, salinity was selected frequently when resolutions were variable for both surface-fed estuaries and for all estuaries combined. When all the factors were forced to the same resolution, salinity was not selected at all. The consequence of these effects could be seen when comparing management sectors as well. With factor resolutions, water management was often selected as the most influential sector (mostly due to salinity having a high $R^2$ value) but, when all the resolutions were homogenous, the restoration sector had the largest $R^2$ values every time. The same type of biases encountered here is somewhat common in other habitat-factor studies, especially those conducted in estuaries. Our results emphasize the importance that future studies take care to measure all factors at the same spatial and temporal resolution and recognize that higher resolution factors will likely have the strongest relationship with abundance patterns and estuarine community structure. If habitat factors are measured at different resolutions, and are being compared to one another, the lowest resolution can be applied to all factors or, depending up on data quality, the lower resolution factors might be excluded from the analysis to avoid this bias.

(3) Covariation along the estuarine gradient obscures the results of habitat analysis. Many of the analyzed estuarine species and habitat factors follow the same estuarine gradient pattern so, numerous analyzed habitat factors are capable of explaining the estuarine gradient abundance variation regardless of any process-based role. This is true of many similar studies on estuaries and is likely a substantial limitation for this type of analysis on estuarine species and communities. A clear exception is flashiness
which was selected despite its lower spatial resolution and lack of estuarine gradient pattern. Further research is needed to determine the process by which flashiness affects estuarine species and how it should be included in water management plans.

(4) Restoration of natural habitat types has the largest overall potential to positively impact estuarine species.

Factors related to physical habitat and state of urbanization were selected with some frequency at every stage of the analysis. How much emergent vegetation there was on the shoreline explained significant amounts of variation in three out of the four surface-fed communities in the partial dbRDA and was also frequently selected for the multiple regression of surface-fed prey species. The presence of submerged aquatic vegetation was selected often for spring-fed prey species and for surface-fed economically important species along with bottom sand. Many of these factors had both positive and negative coefficients which demonstrates the need for heterogeneous habitats to allow for both higher diversity and ontogenetic habitat shifts. Whether there were oysters as a substrate was important for many surface-fed prey species. Access to shallow areas was important for more surface-fed economically important species than any other factor. This could be of particular concern if development results in rip/rap or seawalls that eliminate these shallow areas. When the resolution of all the factors was homogenized, eliminating both the resolution bias and the effect of the estuarine gradient, the partial dbRDA results included only restoration sector factors, most often emergent vegetation on the shoreline. Tidal rivers that have undergone less urban development usually have more emergent vegetation, and so this factor is a good proxy for how well a natural
environment has been preserved in a given estuary. The analysis of economically important species and prey species and the analysis with factors at homogenous low resolutions both found that the restoration management sector factors resulted in models with the most variation explained. Therefore, it would seem that even though factors related to freshwater inflow or water quality may be important, the most positive change can happen by restoring the natural state of these estuaries and maintaining a variety of structure and bottom types.

References:


Appendix 1 - dbRDA Ordinations

Figure A1 (Continued on next page)
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The ordinations from dbRDA with AICc selection criterion on four community types (ichthyoplankton, invertebrates, seine, and trawl) from spring-fed and surface-fed estuaries (a-g). The dbRDA creates a Euclidean embedding of the Bray Curtis dissimilarity matrix of the estuary zones and then performs multivariate multiple regression using an optimal subset of factors selected by AICc. The ordinations depict all of the estuary zones as blue squares. Their ordination is based on the Bray Curtis dissimilarities. (Zones closer together were more similar in terms of community and those farther apart) The vector plot labeled with the selected factors identifies how influential each factor is on each axis. If a zone is farther along that vector, it has a higher level of that factor. If there is no vector plot, it is because only one factor was selected so the data are only depicted on one axis (and a jittered axis). The spring-fed trawl community is absent because it did not have a significant result.
Appendix 2 - Partial dbRDA Ordinations

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Figure A2
The ordinations from partial dbRDA with AIC selection criterion and distance-to-GOM as a covariate on four community types (ichthyoplankton, invertebrates, seine, and trawl) from spring-fed and surface-fed estuaries (a–af). The partial dbRDA creates a Euclidean embedding of the Bray Curtis dissimilarity matrix of the estuary zones and then performs multivariate multiple regression using an optimal subset of factors selected by AIC after the variation explained by distance-to-GOM is removed. Each analysis was performed with all the factors as options and with each of the management sector subsets (see Table 1). The ordinations depict all of the
estuaries in blue. Their ordination is based on the Bray Curtis dissimilarities. (Zones closer together were more similar in terms of community and those farther apart) Each axis is labeled with how much of the total variation is depicted on that axis. The red vector plot labeled with the selected factors identifies how influential each factor is on each axis. If a zone is farther along that vector, it has a higher level of that factor. The green vector plot depicts the same information for the five species that were most responsible for the difference between samples.
Appendix 3 - Correlation Table for Distance-to-GOM

Table 5
The Pearson correlation between distance-to-GOM with all other factors and the corresponding p-value. The R^2 value is the proportion of total variation in a given factor that is explained by distance-to-GOM. The highlighted cells represent significant correlations. Different columns represent different subsets of estuary zones that were used for each sampling procedure.

<table>
<thead>
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<th>Factor</th>
<th>Ichthyoplankton, Invertebrate, and Seine Spring-fed</th>
<th>Trawl Spring-fed</th>
<th>Ichthyoplankton and Seine Surface-fed</th>
<th>Invertebrate Surface-fed</th>
<th>Trawl Surface-fed</th>
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<td>0.81</td>
<td>0.034</td>
<td>0.037</td>
</tr>
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<td>0.855</td>
<td>-0.59</td>
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<td>-0.19</td>
</tr>
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<td>-0.036</td>
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Table 5 (Continued)

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<th>Trawl Spring-fed</th>
<th>Ichthyoplankton and Seine Surface-fed</th>
<th>Invertebrate Surface-fed</th>
<th>Trawl Surface-fed</th>
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<td>R²</td>
<td>p</td>
<td>R²</td>
<td>p</td>
<td>R²</td>
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<td>0</td>
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<td>0.059</td>
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<tr>
<td>Chlorophyll</td>
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<td>0.196</td>
<td>0.62</td>
<td>0.133</td>
<td>0.35</td>
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</table>
Appendix 4 - Indicator Value Analysis

Prey Species:

When considering the indicator values for groups of species (for groups see Table 2), pH and salinity were still important for both mysids (though the average indicator value for pH is only based on one species having a strong association with high pH) and shrimp but not for copepods. This is because, while some copepods were strongly associated with high pH, *Mesocyclops edax, Macrocyclops albidus,* and *Orthocyclops modestus* were associated with low pH which leads to a low average indicator value. A similar, but less extreme pattern is seen in shoreline terrestrial and distance-to-GOM. The mysids *Bowmaniella dissimilis* and *Taphromysis bowmani* have strong associations with low levels of water control structures leading to a high average indicator for mysids overall. The most consistent pattern for mysids was that three out of the six species were associated with low levels of shoreline oysters. Nine out of the 14 shrimp species were associated with low levels of emergent vegetation on the shoreline and eight had an association with low levels of H2O structure in zone though there were only two species that had any kind of association with H2O structure or tidal H2O structure. Both shrimp and polychaetes had a somewhat weak but significant association with high levels of flashiness and, even though the average indicator value for flashiness for copepods was low, it had the highest indicator value for Monstrilla spp.

Four different species of copepods had a significant indicator value for low levels of emergent vegetation on the shoreline and five different species selected emergent vegetation on the shoreline with a negative coefficient in the multiple regression analysis. *Centropages*
velificatus and Calanopia americana had their largest coefficients in front of emergent vegetation on the shoreline and Acatia tonsa and Labidocera aestiva had an indicator value over 80. Many shrimp species also had significant indicator values for low levels of emergent vegetation on the shoreline but this appears to be a result of the overall estuarine gradient. Most of these shrimp species also have large indicator values for high levels of salinity and pH and low levels for distance-to-GOM. Once the variation from distance-to-GOM is removed in the multiple regression, only two species of shrimp selected emergent vegetation on the shoreline as explaining a significant amount of variation. While emergent vegetation on the shoreline is not significantly correlated with distance-to-GOM (r = 0.24 p = 0.095) it is correlated with salinity (r = -0.65 p = 0.001) and pH (r = -0.45 p = 0.002). Thus, it would appear that for many of the species that had significant indicator values for emergent vegetation on the shoreline, once the factors were not considered independently, emergent vegetation on the shoreline did not explain a significant amount of variation on top of salinity or pH and most of these species did select pH or salinity, often with the highest coefficient. There were 8 species that were exceptions to. In each of these cases, emergent vegetation on the shoreline appears to be selected instead of pH or salinity (which were not selected); thus, some of that explained variation is probably due to covariation. However, since emergent vegetation on the shoreline presumably explained more variation than either pH or salinity (since it was the preferred factor) there must be some independent effect of emergent vegetation on the shoreline for these species. It could be due to local color levels (since color is averaged over whole estuaries and emergent vegetation on the shoreline is not, it may be a better indicator) and associated water clarity. It could also be that the leaf litter from shoreline trees provides a food source for some species either directly or indirectly as a nitrogen source. Odum and Heald (1972) found that vascular plant detritus made
up 30% of the gut contents of two different mysids and the only one of the eight species that selected emergent vegetation on the shoreline with a positive coefficient was a mysid (*Bowmaniella dissimilis*).

While flushing time only had a significant influence on 15 species, it had the highest overall indicator value for eight out of those 15 (Table 6). pH also had the highest indicator value for eight species. In particular, flushing time had an indicator value of over 90 for *Acatia tonsa* *Labidocera aestiva*, and *Lucifer faxoni* juveniles and adults and an indicator value of 100 for alpheaid postlarvae. pH had an indicator value of 100 for *Hippolyte zostericola* postlarvae, *Ambidexter symmetricus* postlarvae, *Farfantepenaeus duorarum* juveniles, *Americamysis stucki*, and *Temora turbinata*. *Temora turbinata* also had an indicator value of 100 for distance-to-GOM and *Farfantepenaeus duorarum* juveniles also had an indicator value of 100 for both distance-to-GOM and salinity. Tidal H2O structure, H2O structure, and distance-to-GOM all had the highest indicator values for six species. It is of note that Tidal H2O structure and H2O structure had identical sets of zones selected for the high and low group subsets, so their results were identical as well (i.e., they have the highest indicator values for the same species).
Table 6
The results of the indicator value analysis for the important prey species. Indicator values were calculated by determining whether a species is present exclusively in zones with high or low levels of a given factor. Indicator values are at their maximum value (100) when a species was present in all zones in the high or low group and was absent in all other zones. Only significant indicator values are depicted in these results. Indicator values for low levels of the factor were represented as negative numbers and the averages were calculated from these numbers. See Table 2 for species within groups. Gammaridean amphipods and polychaetes contain multiple species but all of these were enumerated together so there was only one calculation for each of these groups. The highest indicator value column refers to how often each factor had the highest indicator value (or one of the highest if multiple factors had the same indicator value) for a given species.

<table>
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<th>Indicator Value Results</th>
<th>Highest IndVal</th>
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<td>Low</td>
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</tr>
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<td>5</td>
<td>7</td>
</tr>
<tr>
<td>Average Slope</td>
<td>2</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>Bottom Mud</td>
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<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Bottom Sand</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Bottom Manmade</td>
<td>2</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>Bottom Oysters</td>
<td>5</td>
<td>1</td>
<td>6</td>
</tr>
<tr>
<td>SAV Present</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Algae Present</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Shoreline Mangroves</td>
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</tr>
<tr>
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<tr>
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<td>Flushing Time</td>
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</tr>
<tr>
<td>Flashiness</td>
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<td>6</td>
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</tbody>
</table>
Economically Important Species:

Many of the economically important species were divided into different size classes (for a list, see Table 2). If the indicator values are averaged across all size classes (with developmental stages being kept separate), pH still had the most significant indicator values (21 species) but it is followed by salinity and distance-to-GOM (17 species each) and then depth (15 species). The average indicator values for each factor were also less extreme (Table 7) because the values were not inflated by many size classes all having large indicator values for a given factor. However, since the overall effects of each factor (with the exception of bottom mud and bottom manmade, neither of which were very important in either scenario) were the same in both analyses, the version with separate size classes will be used for the remainder of the analysis because of the potential importance of ontogenetic shifts in habitat preference.

Overall, more species were associated with low depth, high pH, and high flushing time. The exception for depth was Micropterus salmoides which was also one of the exceptions for pH and flushing time. In general, the significant indicator values associated with pH were for the group of sites associated with high pH. The other species that were exceptions to this rule were Ictalurus punctatus (though it only had an indicator value of 50) and Callinectes sapidus larger than 69mm (only for the seine samples). Most of the significant indicator values for flushing time were for the group of sites associated with high flushing time with Micropterus salmoides being the only exception.
Table 7
The results of the indicator value analysis for economically important species. Indicator values were calculated by determining whether a species is present exclusively in zones with high or low levels of a given factor. Indicator values are at their maximum value (100) when a species was present in all zones in the high or low group and was absent in all other zones. Only significant indicator values are depicted in these results. Average indicator values for low levels of the factor are represented as negative and all averages were calculated only from the significant indicator values. The highest indicator value column refers to how often each factor had the highest indicator value (or one of the highest if multiple factors had the same indicator value) for a given species. The first section of the table includes the results when all of the size classes were treated separately and these are the results that will be used for the discussion. The second section includes the results when the size classes were averaged for each species. The first section has 76 groups total and the second section has 36 groups total.

<table>
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Table 7 (Continued)

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</table>

Though pH had the most species groups with significant indicator values, flushing time had the most indicator values that were the largest overall for that species group (Table 4). This is mostly due to it having the highest indicator value for eight out of the 9 groups for *Menticirrhus americanus* though it was still very important for several other species. pH did have the most indicator values that were the largest overall for that species group after flushing time (9 species groups) and it was followed by flashiness and salinity (7 species groups each).

When all of the indicator values were averaged across all species groups, flushing time had the highest value associated with high levels of the factor. It was followed by depth (for low level) and slope (for low level).
Appendix 5 - Multiple Regression on Species Abundance

In both spring-fed and surface-fed estuaries, the restoration management sector regressions had the highest $R^2$ for the most species when compared to the other two management sectors (Figure 7 and 10). The exceptions in spring-fed estuaries were *Palaemonetes pugio* adults, *Hippolyte zostericola* juveniles, and *Anchoa mitchilli* juveniles which all had the largest $R^2$ in the water management sector. The exceptions for surface-fed estuaries were *Farfantepenaeus duorarum* juveniles, Gammaridean amphipods, *Mesocyclops edax*, *Calanopia americana*, Siphonostomatids, and Paracalanids which all had the largest $R^2$ in the water management sector and unidentified Americamysis juveniles which had the largest $R^2$ in the water quality sector.

Flushing time was the factor that was featured in the most equations for spring-fed estuaries with all but one of the coefficients being positive (Figure 8). The species with the negative coefficient was *Upogebia* spp. juveniles. Residence was also one of the two factors that most frequently had the highest coefficient in their respective equations (tied with shoreline mangroves) (Figure A3). pH, SAV, and salinity were also featured frequently in the regression equations for spring-fed sites though not nearly as frequently as flushing time. All of the pH coefficients were negative while the salinity and SAV coefficients were more or less half positive and half negative. While pH, bottom oysters, emergent vegetation on the shoreline, and flushing time had significant influence for the most species, salinity and inflow most often had the highest coefficient in their respective equations (explained the most variation for a given species). Flushing time had nearly
as many instances of having the highest coefficient but none of the other frequently included factors stood out from the others.

In spring-fed estuaries, bottom sand, depth, and flushing time were included in the regression equations for the most economically important species groups. Bottom sand was also had the highest coefficient in its given equation most frequently followed by head spring in zone and flushing time (Figure A4). In particular, head spring in zone had the highest coefficient for five of the smaller class sizes for *Callinectes sapidus*. For surface-fed estuaries, depth explained a significant amount of information for the most species groups followed by flashiness, SAV, and flow. Depth has negative coefficients for all of the regression equations except for *Micropterus salmoides*. Flashiness had positive coefficients for all equations except for *Sciaenops ocellatus* 60-69mm and *Lutjanus synagris*. Flashiness was featured in five out of the six Brevoortia spp. equations with four of those having the largest coefficient as well. Flashiness was also featured in three of the smaller size classes/stages of *Cynoscion arenarius* with all three instances having the highest coefficient. SAV had negative coefficients for all equations except *Leiostomus xanthurus* <20mm. SAV seemed particularly important for *Sciaenops ocellatus* where it was selected for five out of the ten species groups. Flow had positive coefficients for all equations except for three different size classes of *Leiostomus xanthurus*. Flow also seemed important for *Menticirrhus americanus* where it was selected for six out of the nine species groups and had the highest coefficient for four of them. Overall depth had the highest coefficient in their given equations most frequently followed by flashiness and inflow (Figure A4).
Table 8
The $R^2$ values from the multiple regression analysis on each of the important prey species with different subsets of habitat factors. (All = All factors, WM = Water Management Res = Restoration WQ = Water Quality) (See Table 1). The $R^2$ value is the proportion of total variation in a given species’ abundance that is explained by a given factor once the variation explained by distance-to-GOM is removed. Only $R^2$ values from significant regressions are shown, but the significance of the covariate $R^2$ values is not known.

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</table>
The number of prey species for which a given factor had the largest coefficient (explained the most variation) in the multiple regression analysis with distance-to-GOM as a covariate for spring-fed (a) and surface-fed (b) estuaries. The multiple regression analysis selects an optimal subset of factors using AIC where the factor explaining the most variation in a given species’ abundance is selected first and only factors that explained a substantial amount of additional variation will be added. Then, the multiple regression function optimizes the coefficients on each factor to minimize the squared differences between the model and the original data. Since the factors are normalized, the coefficients designate the relative weight of each factor in determining the given species’ abundance. Only significant regressions are included.
As with prey species, for both spring-fed and surface-fed estuaries, the restoration management sector regressions had the highest $R^2$ for the most economically important species groups though there were more exceptions than with prey species (Figure 10). Notably, three of the spring-fed regressions where water management had the largest $R^2$ were for different size classes of *Sciaenops ocellatus*, both *Leiostomus xanthurus* and *Menticirrhus americanus* had three size classes where water management had the largest $R^2$ for surface-fed estuaries, and three of the six surface-fed regressions where water quality had the largest $R^2$ were for different size classes of *Cynoscion arenarius*.

Table 9
The $R^2$ values from the multiple regression analysis on each of the economically important species on the left with different subsets of habitat factors. (All = All factors, WM = Water Management, and WQ = Water Quality). The second column identifies the different size classes (in mm) and life stages for each species. The letter in parentheses signifies which type of gear the group originated from. (P = plankton tow, S = seine net, and T = otter trawl). The covariate used for the AIC selection and multiple regression was distance-to-GOM. Only $R^2$ values from significant regressions are shown.

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<th>Surface</th>
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Table 10
The $R^2$ values from the initial regression between the economically important species abundance data and the covariate (distance-to-GOM). The size classes are in mm. The $R^2$ value denotes what proportion of the variation in abundance for a given species is explained by distance-to-GOM. Blank spaces (as opposed to zero values) signify that particular species or size class was absent from the abundance data for that estuary (i.e., *Cynoscion arenarius* was not found in spring-fed estuaries). The significance of these $R^2$ values is not known.

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<td><em>Lutjanus griseus</em></td>
<td>(S)</td>
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<td>(T)</td>
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<td><em>Lutjanus synagris</em></td>
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<td>(T)</td>
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<td>&lt;20 (S)</td>
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<td>&lt;20 (T)</td>
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<td>20 to 29 (S)</td>
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<td>20 to 29 (T)</td>
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<td>30 to 39 (S)</td>
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<td>40 to 49 (S)</td>
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<td>40 to 49 (T)</td>
<td>0.053</td>
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<td>&gt;49 (S)</td>
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<td>&gt;79 (T)</td>
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<td><em>Menticirrhus americanus</em></td>
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<td>50 to 59 (T)</td>
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<td>60 to 69 (T)</td>
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<td>&gt;79 (T)</td>
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<td>25 to 29 (S)</td>
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<td>40 to 44 (S)</td>
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<td><em>Micropterus salmoides</em></td>
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<td><em>Mugil trichodon</em></td>
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Table 10 (Continued)

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<tr>
<th>Species</th>
<th>Size Class</th>
<th>Spring</th>
<th>Surface</th>
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<tr>
<td><em>Micropogonias undulatus</em></td>
<td>(T)</td>
<td>0.12</td>
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<td><em>Orthopristis chrysoptera</em></td>
<td>(S)</td>
<td>0.72</td>
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<td><em>Paralichthys albigutta</em></td>
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<td>(T)</td>
<td>0.85</td>
<td>0.31</td>
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<td><em>Sciaenops ocellatus</em></td>
<td>postflexion (P)</td>
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<td>&lt;20 (S)</td>
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<td>50 to 59 (S)</td>
<td>0.023</td>
<td>0.19</td>
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<td>60 to 69 (S)</td>
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<td>&gt;69 (S)</td>
<td>0.36</td>
<td>0.052</td>
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<tr>
<td>Average</td>
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<td>0.21</td>
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</table>
The number of economically important species groups for which a given factor had the largest coefficient (explained the most variation) in the multiple regression analysis with distance-to-GOM as a covariate for spring-fed (a) and surface-fed (b) estuaries. The multiple regression analysis selects an optimal subset of factors using AIC where the factor explaining the most variation in a given species group’s abundance is selected first and only factors that explained a substantial amount of additional variation will be added. Then, the multiple regression function optimizes the coefficients on each factor to minimize the squared differences between the model and the original data. Since the factors were normalized, the coefficients designate the relative weight of each factor in determining the given species group’s abundance. Only significant regressions are included.

**Figure A4**

The number of economically important species groups for which a given factor had the largest coefficient (explained the most variation) in the multiple regression analysis with distance-to-GOM as a covariate for spring-fed (a) and surface-fed (b) estuaries. The multiple regression analysis selects an optimal subset of factors using AIC where the factor explaining the most variation in a given species group’s abundance is selected first and only factors that explained a substantial amount of additional variation will be added. Then, the multiple regression function optimizes the coefficients on each factor to minimize the squared differences between the model and the original data. Since the factors were normalized, the coefficients designate the relative weight of each factor in determining the given species group’s abundance. Only significant regressions are included.
Regression Equations:

This section contains all of the multiple regression equations from both prey species and economically important species. The factors are presented in the order of their AIC selection. The $R^2$ values for the equations are the percent of the remaining variation explained after the variation from the covariate (W) (distance-to-GOM) is removed. For each equation, $Y$ is fourth rooted abundance of the given species. If the equation with all factors only selects factors from one management sector, the equation from that sector is identical and is not included. Only significant models are shown.

**Polychaetes**

**Surface-fed** ($W \ R^2 = 0.014$)

All factors ($R^2 = 0.81$)

$Y = (0.127)\text{Bottom Manmade} - (0.236)\text{Depth} - (0.142)\text{pH} + (0.191)\text{H2O Structure} + (0.166)\text{Bottom Sand} + (0.121)\text{Flashiness}$

**Restoration** ($R^2 = 0.48$)

$Y = (0.209)\text{Bottom Manmade} - (0.120)\text{Depth}$

**Anchoa mitchilli juveniles**

**Spring-fed** ($W \ R^2 = 0.018$)

All factors ($R^2 = 0.57$)

$Y = (0.185)\text{Bottom Mud}$

**Water Management** ($R^2 = 0.59$)
Y = (0.040)Salinity + (0.214)H2O Structure

Surface-fed (W R^2 = 0.139)

All factors (R^2 = 0.20)

Y = (0.128)Flashiness

Water Management Flashiness model not significant

Restoration (R^2 = 0.18)

Y = (0.107)Bottom Mud + (0.088)Shoreline Manmade

COPEPODS

Acartia tonsa

Spring-fed (W R^2 = 0.020)

All factors (R^2 = 0.69)

Y = (0.290)Temperature + (0.228)Flow

Restoration (R^2 = 0.60)

Y = (0.285)Shoreline Manmade – (0.227)Algae

Surface-fed (W R^2 = 0.055)

All factors (R^2 = 0.84)

Y = (1.090)Salinity + (0.212)Shoreline Terrestrial

Water Management (R^2 = 0.11)

Y = (-0.235)Salinity

Restoration (R^2 = 0.74)

Y = (0.251)Shoreline Oysters + (0.305)Shoreline Mangroves – (0.257)Shoreline Emergent
**Labridocera aestiva**

*Spring-fed* (W $R^2 = 0.62$)

*All factors* ($R^2 = 0.61$)

\[ Y = (0.240)SAV + (0.140)\text{Shoreline Manmade} \]

*Surface-fed* (W $R^2 = 0.010$)

*All factors* ($R^2 = 0.96$)

\[ Y = (0.194)\text{Shoreline Oysters} + (0.376)\text{Salinity} + (0.175)\text{Bottom Oysters} - (0.094)\text{Bottom Mud} + (0.093)\text{Chlorophyll} \]

*Restoration* ($R^2 = 0.91$)

\[ Y = (0.278)\text{Shoreline Oysters} + (0.252)\text{Bottom Oysters} + (0.209)\text{Shoreline Mangroves} - (0.087)\text{Bottom Mud} \]

**Pseudodiaptomus coronatus**

*Spring-fed* (W $R^2 = 0.11$)

*All factors* ($R^2 = 0.97$)

\[ Y = (0.059)\text{Flashiness} - (0.095)pH - (0.090)SAV + (0.099)\text{Salinity} \]

*Water Management* ($R^2 = 0.42$)

\[ Y = (-0.152)\text{Flashiness} \]

*Restoration* ($R^2 = 0.87$)

\[ Y = (0.092)\text{Bottom Oysters} + (0.109)\text{Slope} - (0.085)\text{Bottom Sand} \]

*Water Quality* ($R^2 = 0.57$)

\[ Y = (-0.180)\text{Turbidity} + (0.109)DO \]
Surface-fed (W R² = 0.083)

All factors (R² = 0.71)

Y = (0.171)Salinity + (0.111)Flow – (0.055)Slope

Water Management (R² = 0.48)

Y = (-0.084)Salinity – (0.049)Flow + (0.056)Flushing time

Restoration (R² = 0.51)

Y = (-0.099)Slope + (0.086)Shoreline Mangroves

Water Quality (R² = 0.38)

Y = (-0.126)Chlorophyll

Paracalanids

Spring-fed (W R² = 0.39)

All factors (R² = 0.85)

Y = (-0.065)Shoreline Oysters + (0.064)Bottom Oysters

Surface-fed (W R² = 0.23)

All factors (R² = 0.29)

Y = (0.087)Flow

Restoration (R² = 0.13)

Y = (0.037)Shoreline Mangroves

Diaptomus spp.

Spring-fed (W R² = 0.11)

All factors (R² = 0.867)
\[ Y = (0.064)\text{Depth} - (0.154)\text{Salinity} + (0.065)\text{Temperature} \]

*Water Management* \((R^2 = 0.43)\)

\[ Y = (0.085)\text{Salinity} \]

*Restoration* \((R^2 = 0.67)\)

\[ Y = (0.105)\text{Depth} - (0.091)\text{Bottom Oysters} \]

*Surface-fed* \((W \, R^2 = 0.061)\)

*All factors* \((R^2 = 0.50)\)

\[ Y = (-0.087)\text{pH} + (0.102)\text{Flow} \]

*Restoration* \((R^2 = 0.46)\)

\[ Y = (-0.056)\text{Shoreline Oysters} - (0.050)\text{Bottom Sand} \]

*Water Quality* \((R^2 = 0.22)\)

\[ Y = (0.015)\text{Chlorophyll} - (0.045)\text{Turbidity} \]

**Oithona spp.**

*Spring-fed* \((W \, R^2 = 0.074)\)

*All factors* \((R^2 = 0.28)\)

\[ Y = (0.024)\text{Temperature} \]

*Surface-fed* \((W \, R^2 = 0.012)\)

*All factors* \((R^2 = 0.87)\)

\[ Y = (0.291)\text{Residence\_Time} \]

*Restoration* \((R^2 = 0.46)\)

\[ Y = (0.174)\text{Shoreline\_Mangroves} + (0.106)\text{Bottom\_Sand} \]
Siphonostomatids

Spring-fed (W R² = 0.39)

All factors (R² = 0.83)

\[ Y = (0.070)\text{Head Spring Sampled} + (0.039)\text{Slope} \]

Water Management (R² = 0.70)

\[ Y = (-0.025)\text{Flashiness} + (0.086)\text{Flushing time} \]

Restoration (R² = 0.82)

\[ Y = (0.086)\text{Bottom Oysters} + (0.062)\text{Shoreline Mangroves} \]

Water Quality (R² = 0.58)

\[ Y = (-0.083)\text{Turbidity} - (0.084)\text{Color} \]

Surface-fed (W R² = 0.019)

Water Management (R² = 0.423)

\[ Y = (-0.057)\text{Salinity} + (0.060)\text{Flushing time} + (0.039)\text{H2O Structure} + (0.090)\text{Flashiness} \]

Restoration (R² = 0.42)

\[ Y = (0.084)\text{Shoreline Oysters} + (0.081)\text{SAV} \]

Centropages velificatus

Surface-fed (W R² = 0.74)

All factors (R² = 0.48)

\[ Y = (-0.039)\text{Shoreline Emergent} + (0.025)\text{Shoreline Manmade} \]

Centropages hamatus

Surface-fed (W R² = 0.21)
All factors \( R^2 = 0.39 \)

\[ Y = (0.083)pH - (0.046)\text{Shoreline Mangroves} \]

**Unidentified calanoids**

Spring-fed \( W\ R^2 = 0.14 \)

All factors \( R^2 = 0.67 \)

\[ Y = (0.082)\text{Bottom Sand} + (0.053)\text{Head Spring Sampled} \]

Restoration \( R^2 = 0.66 \)

\[ Y = (0.070)\text{Bottom Sand} - (0.048)\text{SAV} \]

Water Quality \( R^2 = 0.43 \)

\[ Y = (0.053)\text{DO} \]

Surface-fed \( W\ R^2 = 0.13 \)

All factors \( R^2 = 0.67 \)

\[ Y = (0.030)\text{Shoreline Manmade} - (0.056)\text{Chlorophyll} + (0.035)\text{Shoreline Oysters} - (0.023)\text{Temperature} \]

Restoration \( R^2 = 0.42 \)

\[ Y = (0.047)\text{Shoreline Manmade} \]

**Calanopia Americana**

Spring-fed \( W\ R^2 = 0.48 \)

All factors \( R^2 = 0.73 \)

\[ Y = (0.161)\text{Shoreline Mangroves} \]

Surface-fed \( W\ R^2 = 0.74 \)
All factors \((R^2 = 0.36)\)

\[ Y = (-0.075)\text{Shoreline Emergent} - (0.059)\text{Flushing time} \]

\textit{Water Management} \((R^2 = 0.12)\)

\[ Y = (0.047)\text{Flushing time} \]

\textit{Temora turbinata}

\textit{Spring-fed} \((W \ R^2 = 0.69)\)

\[ Y = (-0.065)\text{pH} \]

\textit{Restoration} \((R^2 = 0.56)\)

\[ Y = (0.092)\text{Bottom Manmade} + (0.085)\text{Shoreline Emergent} \]

\textit{Surface-fed} \((W \ R^2 = 0.55)\)

\[ Y = (-0.052)\text{Shoreline Emergent} + (0.044)\text{SAV} \]

\textit{Mesocyclops edax}

\textit{Spring-fed} \((W \ R^2 = 0.012)\)

\[ Y = (-0.357)\text{Salinity} - (0.098)\text{pH} - (0.088)\text{Head Spring in Zone} \]

\textit{Surface-fed} \((W \ R^2 = 0.075)\)
All factors ($R^2 = 0.65$)

\[ Y = (0.191)\text{Depth} + (0.86)\text{H2O Structure in Zone} \]

Water Management ($R^2 = 0.66$)

\[ Y = (0.043)\text{H2O Structure in Zone} + (0.211)\text{Salinity} + (0.073)\text{H2O Structure} \]

Restoration ($R^2 = 0.65$)

\[ Y = (0.224)\text{Depth} + (0.074)\text{Bottom Mud} \]

**Macrocyclops albidus**

Surface-fed ($W \, R^2 = 0.032$)

All factors ($R^2 = 0.32$)

\[ Y = (0.026)\text{Shoreline Oysters} \]

**Orthocyclops modestus**

Surface-fed ($W \, R^2 = 0.080$)

All factors ($R^2 = 0.65$)

\[ Y = (-0.127)\text{Salinity} - (0.092)\text{Flashiness} + (0.050)\text{Depth} \]

Water Management ($R^2 = 0.21$)

\[ Y = (0.066)\text{Salinity} + (0.005)\text{Flashiness} \]

Restoration ($R^2 = 0.57$)

\[ Y = (0.022)\text{Shoreline Terrestrial} + (0.069)\text{Shoreline Emergent} - (0.060)\text{Bottom Mud} + (0.058)\text{Depth} \]

Unidentified harpacticoids
Spring-fed (W $R^2 = 0.39$

*All factors* ($R^2 = 0.50$

$Y = (-0.076)SAV$

*Water Management* ($R^2 = 0.50$

$Y = (-0.076)Flashiness$

Surface-fed (W $R^2 = 0.41$

*All factors* ($R^2 = 0.58$

$Y = (-0.071)Depth - (0.041)Temperature - (0.036)Shoreline Emergent$

*Water Management* ($R^2 = 0.43$

$Y = (0.031)H2O Structure in Zone - (0.080)Salinity$

*Restoration* ($R^2 = 0.55$

$Y = (-0.056)Depth + (0.051)SAV + (0.035)Bottom Oysters$

**Cyclops spp.**

Spring-fed (W $R^2 = 0.20$

*All factors* ($R^2 = 0.97$

$Y = (0.036)Flushing time + (0.007)Bottom Sand$

*Restoration* ($R^2 = 0.89$

$Y = (-0.027)Slope + (0.019)Depth - (0.015)Algae$

Surface-fed (W $R^2 = 0.16$

*All factors* ($R^2 = 0.36$

$Y = (0.095)Bottom Manmade$
Monstrilla spp.

Spring-fed (W $R^2 = 0.37$)

All factors ($R^2 = 0.995$)

\[ Y = (0.014)\text{Shoreline Emergent} - (0.092)\text{pH} + (0.114)\text{Flushing time} + (0.152)\text{Shoreline Mangroves} + (0.035)\text{Flow} \]

Restoration ($R^2 = 0.52$)

\[ Y = (-0.111)\text{Shoreline Emergent} \]

Surface-fed (W $R^2 = 0.21$)

All factors ($R^2 = 0.55$)

\[ Y = (0.036)\text{Shoreline Manmade} - (0.066)\text{Bottom Sand} - (0.055)\text{Shoreline Emergent} \]

Water Management ($R^2 = 0.37$)

\[ Y = (0.055)\text{H2O Structure} - (0.002)\text{Flow} + (0.082)\text{Flushing time} \]

Water Quality ($R^2 = 0.44$)

\[ Y = (-0.084)\text{Tubidity} - (0.095)\text{Chlorophyll} + (0.079)\text{DO} \]

Gammaridean amphipods

Spring-fed (W $R^2 = 0.11$)

All factors ($R^2 = 0.38$)

\[ Y = (-0.268)\text{Shoreline Terrestrial} \]

Surface-fed (W $R^2 = 0.30$)

All factors ($R^2 = 0.30$)

\[ Y = (-0.206)\text{H2O Structure} - (0.362)\text{Flow} \]
MYSIDS

**Unidentified Americamysis juveniles**

**Spring-fed** (W $R^2 = 0.040$)

**Restoration** ($R^2 = 0.91$)

$Y = (-0.542)SAV - (0.389)Algae + (0.312)Shoreline Terrestrial - (0.139)Bottom Sand$

**Water Quality** ($R^2 = 0.33$)

$Y = (-0.262)Turbidity$

**Surface-fed** (W $R^2 = 0.026$)

**All factors** ($R^2 = 0.81$)

$Y = (0.377)Bottom Mud + (0.164)Color + (0.237)Bottom Sand - (0.201)SAV - (0.087)Slope$

**Restoration** ($R^2 = 0.51$)

$Y = (0.242)Bottom Mud - (0.187)Bottom Manmade$

**Water Quality** ($R^2 = 0.52$)

$Y = (0.429)Color + (0.238)Turbidity + (0.154)DO - (0.202)Chlorophyll$

**Americamysis almyra**

**Spring-fed** (W $R^2 = 0.0010$)

**Restoration** ($R^2 = 0.73$)

$Y = (-0.317)SAV - (0.231) Bottom Sand$

**Water Quality** ($R^2 = 0.47$)

$Y = (-0.341)Turbidity$

**Surface-fed** (W $R^2 = 0.0010$)
All factors \( (R^2 = 0.80) \)

\[
Y = (0.395)\text{Bottom Mud} + (0.215)\text{Color} - (0.201)\text{SAV} + (0.208)\text{Bottom Sand}
\]

Restoration \( (R^2 = 0.62) \)

\[
Y = (0.406)\text{Bottom Mud} - (0.251)\text{SAV} + (0.262)\text{Bottom Sand}
\]

Water Quality \( (R^2 = 0.39) \)

\[
Y = (0.280)\text{Color}
\]

**Americamysis bahia**

Spring-fed \( (W \ R^2 = 0.64) \)

All factors \( (R^2 = 0.96) \)

\[
Y = (0.088)\text{Flushing time} + (0.052)\text{SAV} + (0.108)\text{Shoreline Mangroves} + (0.055)\text{DO}
\]

Water Management \( (R^2 = 0.20) \)

\[
Y = (-0.079)\text{Flushing time}
\]

Restoration \( (R^2 = 0.55) \)

\[
Y = (0.110)\text{SAV}
\]

Surface-fed \( (W \ R^2 = 0.038) \)

All factors \( (R^2 = 0.46) \)

\[
Y = (0.116)\text{Flushing time} + (0.073)\text{Turbidity}
\]

Restoration \( (R^2 = 0.43) \)

\[
Y = (-0.090)\text{Shoreline Emergent} - (0.094)\text{Depth} - (0.077)\text{SAV}
\]

**Americamysis stucki**

Spring-fed \( (W \ R^2 = 0.39) \)
All factors \((R^2 = 0.85)\)

\[ Y = (0.062) \text{Flushing time} - (0.030) \text{Shoreline Oysters} \]

Restoration \((R^2 = 0.90)\)

\[ Y = (-0.071) \text{Slope} + (0.044) \text{Depth} \]

Surface-fed \((W \ R^2 = 0.21)\)

All factors \((R^2 = 0.70)\)

\[ Y = (0.129) \text{Flushing time} + (0.087) \text{pH} \]

Restoration \((R^2 = 0.64)\)

\[ Y = (0.072) \text{Shoreline Mangroves} - (0.065) \text{Bottom Mud} - (0.075) \text{Slope} - (0.060) \text{Shoreline Emergent} \]

Water Quality \((R^2 = 0.24)\)

\[ Y = (-0.106) \text{Bottom DO} \]

*Bowmaniella dissimilis*

Spring-fed \((W \ R^2 = 0.48)\)

All factors \((R^2 = 0.77)\)

\[ Y = (0.427) \text{Shoreline Emergent} + (0.278) \text{Salinity} \]

Water Management \((R^2 = 0.60)\)

\[ Y = (0.355) \text{H2O Structure} - (0.079) \text{Tidal H2O Structure} \]

Restoration \((R^2 = 0.64)\)

\[ Y = (0.0418) \text{Shoreline Emergent} \]

Water Quality \((R^2 = 0.58)\)

\[ Y = (0.407) \text{Color} \]
Surface-fed (W R² = 0.32)

All factors (R² = 0.85)

Y = (0.145)Color + (0.196)Shoreline Emergent + (0.195)Shoreline Mangroves –
(0.107)Chlorophyll – (0.080)H2O Structure in Zone

Restoration (R² = 0.69)

Y = (0.253)Shoreline Emergent – (0.269)Slope + (0.148)Shoreline Mangroves + (0.183)Depth

Taphromysis bowmani

Spring-fed (W R² = 0.16)

All factors (R² = 0.61)

Y = (-0.228)Bottom Manmade

Water Quality (R² = 0.34)

Y = (-0.168)Chlorophyll

Surface-fed (W R² = 0.009)

All factors (R² = 0.68)

Y = (0.203)Color + (0.143)Slope – (0.154)H2O Structure – (0.0143)pH

Restoration (R² = 0.49)

Y = (-0.287)Shoreline Manmade – (0.217)Shoreline Mangroves

SHRIMPS

Palaemonetes pugio adults

Spring-fed (W R² = 0.14)
All factors ($R^2 = 0.91$)

\[ Y = (-0.163)\text{Shoreline Manmade} + (0.106)\text{Turbidity} + (0.064)\text{Head Spring in Zone} + (0.052)\text{Flushing time} \]

Water Management ($R^2 = 0.55$)

\[ Y = (-0.120)\text{Flow} + (0.117)\text{Flushing time} \]

Restoration ($R^2 = 0.48$)

\[ Y = (-0.104)\text{Shoreline Manmade} \]

**Hippolyte zostericola postlarvae**

Spring-fed ($W R^2 = 0.63$)

All factors ($R^2 = 0.79$)

\[ Y = (-0.120)\text{pH} + (0.084)\text{DO} + (0.078)\text{Shoreline Terrestrial} \]

Restoration ($R^2 = 0.32$)

\[ Y = (-0.088)\text{Bottom Mud} \]

Water Quality ($R^2 = 0.32$)

\[ Y = (-0.088)\text{Color} \]

Surface-fed ($W R^2 = 0.36$)

All factors ($R^2 = 0.89$)

\[ Y = (0.105)\text{pH} + (0.122)\text{SAV} + (0.170)\text{Bottom Oysters} - (0.140)\text{H2O\_Structure} + (0.092)\text{Bottom Manmade} \]

Water Management ($R^2 = 0.42$)

\[ Y = (-0.119)\text{Salinity} - (0.108)\text{H2O\_Structure} \]

Restoration ($R^2 = 0.77$)
Y = (0.199)SAV + (0.137)Bottom Oysters – (0.076)Depth

Water Quality \( R^2 = 0.25 \)

Y = (-0.132)Chlorophyll

\textbf{Hippolyte zostericola juveniles}

Spring-fed \( W R^2 = 0.42 \)

\textit{All factors} \( R^2 = 0.73 \)

Y = (-0.069)Flow + (0.072)Flushing time

Surface-fed \( W R^2 = 0.31 \)

\textit{All factors} \( R^2 = 0.49 \)

Y = (0.131)pH – (0.061)Shoreline Mangroves

Water Management \( R^2 = 0.16 \)

Y = (-0.048)Salinity

Restoration \( R^2 = 0.45 \)

Y = (0.071)SAV – (0.040)Shoreline Emergent

Water Quality \( R^2 = 0.16 \)

Y = (-0.048)DO

\textbf{Tozeuma crolinense postlarvae}

Surface-fed \( W R^2 = 0.073 \)

\textit{All factors} \( R^2 = 0.41 \)

Y = (0.051)Bottom Oysters
Ambidexter symmetricus postlarvae

Spring-fed ($R^2 = 0.20$)

All factors ($R^2 = 0.97$)

$Y = (0.100)\text{Flushing time} + (0.020)\text{Bottom Sand}$

Water Management ($R^2 = 0.54$)

$Y = (-0.068)\text{Flow}$

(Flushed time selected but coefficient = 0)

Restoration ($R^2 = 0.89$)

$Y = (-0.075)\text{Slope} + (0.051)\text{Depth} - (0.042)\text{Algae}$

Surface-fed ($R^2 = 0.30$)

All factors ($R^2 = 0.72$)

$Y = (0.088)\text{Flushing time} + (0.079)\text{pH}$

Restoration ($R^2 = 0.53$)

$Y = (-0.083)\text{Shoreline Emergent} - (0.077)\text{Depth}$

Water Quality ($R^2 = 0.26$)

$Y = (-0.082)\text{Bottom DO}$

Ambidexter symmetricus juveniles

Surface-fed ($R^2 = 0.30$)

All factors ($R^2 = 0.27$)

$Y = (0.064)\text{pH}$

Restoration ($R^2 = 0.19$)

$Y = (-0.045)\text{Shoreline Emergent}$
**Alphaeid postlarvae**

Spring-fed ($W^2 = 0.79$)

All factors ($R^2 = 0.996$)

\[ Y = (0.054)\text{Turbidity} - (0.058)\text{Depth} + (0.109)\text{Slope} + (0.046)\text{SAV} + (0.044)\text{Flushing time} + (0.038)\text{Flashiness} \]

Restoration ($R^2 = 0.53$)

\[ Y = (0.132)\text{Shoreline Mangroves} \]

Surface-fed ($W^2 = 0.16$)

All factors ($R^2 = 0.77$)

\[ Y = (0.111)\text{Salinity} + (0.081)\text{Flushing time} + (0.111)\text{Bottom Oysters} + (0.067)\text{Bottom DO} \]

Water Management ($R^2 = 0.58$)

\[ Y = (-0.102)\text{Salinity} + (0.146)\text{Flushing time} \]

Restoration ($R^2 = 0.71$)

\[ Y = (-0.087)\text{Shoreline Emergent} - (0.107)\text{Slope} + (0.076)\text{Bottom Oysters} \]

Water Quality ($R^2 = 0.323$)

\[ Y = (-0.128)\text{Chlorophyll} \]

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**Lucifer faxoni juveniles and adults**

Spring-fed ($W^2 = 0.53$)

All factors ($R^2 = 0.65$)

\[ Y = (0.073)\text{Shoreline Manmade} \]

Surface-fed ($W^2 = 0.34$)
All factors ($R^2 = 0.57$)

$Y = (0.252)\text{Bottom Oysters} + (0.145)\text{SAV}$

Water Management ($R^2 = 0.064$) (p = 0.05)

$Y = (-0.086)\text{Salinity}$

Penaeid metamorphs

Spring-fed ($W R^2 = 0.40$)

All factors ($R^2 = 0.93$)

$Y = (-0.180)\text{pH} + (0.094)\text{Flushing time} + (0.070)\text{DO}$

Restoration ($R^2 = 0.59$)

$Y = (-0.130)\text{Algae} + (0.117)\text{Shoreline Terrestrial}$

Surface-fed ($W R^2 = 0.65$)

All factors ($R^2 = 0.73$)

$Y = (-0.014)\text{Shoreline Emergent} + (0.111)\text{Flow} + (0.049)\text{Bottom Oysters} + (0.044)\text{Bottom Manmade}$

Restoration ($R^2 = 0.65$)

$Y = (-0.068)\text{Shoreline Emergent}$

Farfantepenaeus dourarum juveniles

Spring-fed ($W R^2 = 0.59$)

All factors ($R^2 = 0.87$)

$Y = (-0.135)\text{Bottom Manmade} + (0.066)\text{Slope} + (0.033)\text{Bottom Sand}$

Surface-fed ($W R^2 = 0.52$)
All factors \( (R^2 = 0.77) \)
\[ Y = (0.086)\text{Flow} - (0.002)\text{Flashiness} + (0.042)\text{pH} + (0.032)\text{Temperature} \]

Water Management \( (R^2 = 0.31) \)
\[ Y = (-0.026)\text{Flow} - (0.015)\text{Flashiness} - (0.029)\text{Salinity} \]

Restoration \( (R^2 = 0.26) \)
\[ Y = (-0.045)\text{Slope} \]

Palaemonetes spp. Postlarvae

Spring-fed \( (W \ R^2 = 0.39) \)
All factors \( (R^2 = 0.84) \)
\[ Y = (0.186)\text{Temperature} - (0.176)\text{Salinity} + (0.068)\text{Shoreline Oysters} \]

Restoration \( (R^2 = 0.60) \)
\[ Y = (-0.152)\text{SAV} + (0.084)\text{Bottom Sand} \]

Surface-fed \( (W \ R^2 = 0.021) \)
All factors \( (R^2 = 0.71) \)
\[ Y = (0.198)\text{Salinity} + (0.138)\text{Bottom Mud} + (0.081)\text{Bottom Oysters} \]

Restoration \( (R^2 = 0.59) \)
\[ Y = (0.145)\text{Bottom Oysters} + (0.134)\text{Bottom Mud} + (0.084)\text{Shoreline Mangroves} \]

Periclimenes longicaudatus juveniles

Spring-fed \( (W \ R^2 = 0.27) \)

Restoration \( (R^2 = 0.51) \)
\[ Y = (0.066)\text{Shoreline Oysters} \]
Surface-fed ($R^2 = 0.74$)

All factors ($R^2 = 0.70$)

$$Y = (-0.032)\text{Shoreline Emergent} \ – \ (0.016)\text{Flushing time} \ + \ (0.036)\text{SAV} \ – \ (0.028)\text{Bottom Sand} \ + \ (0.018)\text{Color}$$

Restoration ($R^2 = 0.66$)

$$Y = (-0.024)\text{Shoreline Emergent} \ – \ (0.037)\text{Bottom Sand} \ + \ (0.040)\text{SAV} \ + \ (0.017)\text{Shoreline Terrestrial}$$

Water Quality ($R^2 = 0.12$)

$$Y = (-0.020)\text{Turbidity}$$

Upogebia spp. Postlarvae

Spring-fed ($R^2 = 0.26$)

All factors ($R^2 = 0.53$)

$$Y = (0.192)\text{Shoreline Mangroves}$$

Surface-fed ($R^2 = 0.081$)

All factors $R^2 = 0.69$

$$Y = (0.074)\text{Shoreline Oysters} \ + \ (0.058)\text{pH}$$

Water Management ($R^2 = 0.18$)

$$Y = (-0.055)\text{Salinity}$$

Restoration ($R^2 = 0.64$)

$$Y = (0.089)\text{Shoreline Oysters} \ – \ (0.033)\text{Depth}$$

Upogebia spp juveniles
Spring-fed ($R^2 = 0.24$)

All factors ($R^2 = 0.93$)

$Y = (0.157)\text{Bottom Oysters} - (0.052)\text{Flushing time} - (0.034)\text{Bottom Manmade Water Management}$

Water Management ($R^2 = 0.51$)

$Y = (-0.097)\text{Flashiness}$

Restoration ($R^2 = 0.83$)

$Y = (0.146)\text{Bottom Oysters}$

Surface-fed ($R^2 = 0.33$)

All factors ($R^2 = 0.66$)

$Y = (-0.094)\text{Flow} - (0.025)\text{H2O Structure} + (0.046)\text{pH} - (0.022)\text{Shoreline Oysters}$

Restoration ($R^2 = 0.37$)

$Y = (0.046)\text{SAV} + (0.026)\text{Shoreline Emergent}$

Water Quality ($R^2 = 0.092$)

$Y = (0.021)\text{Turbidity}$

ECONOMICALLY IMPORTANT SPECIES

*Callinectes sapidus juveniles*

Spring-fed ($R^2 = 0.24$)

Restoration ($R^2 = 0.70$)

$Y = (0.069)\text{Bottom Mud} - (0.054)\text{Algae}$

Surface ($R^2 = 0.51$)

All factors ($R^2 = 0.20$)

$Y = (-0.040)\text{Depth}$
**Brevoortia patronus juveniles**

Surface-fed \( (W R^2 = 0.059) \)

All factors \( (R^2 = 0.42) \)

\[ Y = (0.034)\text{Flashiness} + (0.018)\text{pH} \]

**Brevoortia smithi juveniles**

Spring-fed \( (W R^2 = 0.096) \)

All factors \( (R^2 = 0.38) \)

\[ Y = (0.037)\text{Temperature} \]

Restoration \( (R^2 = 0.62) \)

\[ Y = (0.057)\text{Shoreline Manmade} + (0.053)\text{Bottom Mud} \]

Surface-fed \( (W R^2 = 0.026) \)

All factors \( (R^2 = 0.38) \)

\[ Y = (0.090)\text{Flashiness} \]

**Brevoortia spp. Postflexion larvae**

Spring-fed \( (W R^2 = 0.079) \)

All factors \( (R^2 = 0.69) \)

\[ Y = (-0.098)\text{Bottom Sand} \]

Surface-fed \( (W R^2 = 0.023) \)

All factors \( (R^2 = 0.73) \)
\[ Y = (0.041)\text{Flashiness} - (0.425)\text{H2O Structure} + (0.284)\text{Tidal H2O Structure} - (0.089)\text{Turbidity} - (0.046)\text{Bottom DO} - (0.041)\text{Bottom Sand} - (0.029)\text{Slope} \]

**Brevoortia spp. Metamorphs**

*Spring-fed* (\( W R^2 = 0.056 \))

*All factors* (\( R^2 = 0.47 \))

\[ Y = (-0.064)\text{Bottom Sand} \]

*Surface-fed* (\( W R^2 = 0.037 \))

*All factors* (\( R^2 = 0.34 \))

\[ Y = (0.141)\text{Flashiness} \]

Water management model not significant

**Ictalurus punctatus juveniles** (not included in table)

*Surface-fed* (\( W R^2 = 0.012 \))

*All factors* (\( R^2 = 0.058 \))

\[ Y = (-0.011)\text{Tidal H2O Structure} \]

Water management model not significant

**Mugil cephalus juveniles**

*Surface-fed* (\( W R^2 = 0.063 \))

*All factors* (\( R^2 = 0.38 \))

\[ Y = (0.052)\text{Flashiness} - (0.030)\text{Chlorophyll} \]
Archosargus probatocephalus postflexion larvae

Surface-fed \( (W R^2 = 0.054) \)

All factors \( (R^2 = 0.31) \)

\[ Y = (0.045)\text{Turbidity} \]

Water Quality model not significant

Cynoscion arenarius flexion larvae

Surface-fed \( (W R^2 = 0.003) \)

All factors \( (R^2 = 0.60) \)

\[ Y = (0.103)\text{Shoreline Oysters} + (0.047)\text{Flashiness} - (0.043)\text{Tidal H2O Structure} - (0.046)\text{SAV} \]

Water Management \( (R^2 = 0.20) \)

\[ Y = (-0.057)\text{Salinity} - (0.055)\text{Flashiness} \]

Restoration \( (R^2 = 0.57) \)

\[ Y = (0.081)\text{Shoreline Oysters} - (0.053)\text{SAV} - (0.092)\text{Depth} + (0.064)\text{Slope} \]

Cynoscion arenarius postflexion larvae

Surface-fed \( (W R^2 = 0.008) \)

All factors \( (R^2 = 0.51) \)

\[ Y = (0.085)\text{Shoreline Oysters} + (0.039)\text{Flashiness} + (0.035)\text{Flow} - (0.033)\text{SAV} \]

Water Management \( (R^2 = 0.16) \)

\[ Y = (-0.045)\text{Salinity} - (0.046)\text{Flashiness} \]

Restoration \( (R^2 = 0.44) \)

\[ Y = (0.074)\text{Shoreline Oysters} - (0.054)\text{SAV} + (0.035)\text{Bottom Sand} \]
**Cynoscion arenarius juveniles**

Surface-fed (W $R^2 = 0.021$)

All factors ($R^2 = 0.29$)

$Y = (-0.053)\text{Depth} - (0.038)\text{Bottom Mud}$

**Cynoscion nebulosus preflexion larvae**

Spring-fed (W $R^2 = 0.20$)

All factors ($R^2 = 0.97$)

$Y = (0.051)\text{Flushing time} + (0.010)\text{Bottom Sand}$

Water Management ($R^2 = 0.54$)

$Y = (-0.035)\text{Flow}$  (Flushing time was selected but the coefficient was 0)

Restoration ($R^2 = 0.89$)

$Y = (-0.038)\text{Slope} + (0.026)\text{Depth} - (0.021)\text{Algae}$

Surface-fed (W $R^2 = 0.11$)

All factors ($R^2 = 0.18$)

$Y = (0.037)\text{Flushing time}$

**Cynoscion nebulosus flexion larvae**

Surface-fed (W $R^2 = 0.060$)

All factors ($R^2 = 0.24$)

$Y = (0.036)\text{Flashiness} - (0.031)\text{SAV}$

Water Management ($R^2 = 0.11$)
\[ Y = (-0.035)\text{Flashiness} \]

*Restoration* \((R^2 = 0.11)\)

\[ Y = (-0.035)\text{SAV} \]

**Cynoscion nebulosus postflexion larvae**

*Surface-fed* \((W R^2 = 0.10)\)

*All factors* \((R^2 = 0.35)\)

\[ Y = (0.026)\text{Flashiness} + (0.021)\text{Bottom Oysters} - (0.019)\text{SAV} \]

*Water Management* \((R^2 = 0.13)\)

\[ Y = (-0.027)\text{Flashiness} \]

*Restoration* \((R^2 = 0.21)\)

\[ Y = (-0.022)\text{SAV} + (0.020)\text{Bottom Oysters} \]

**Leiostomus xanthurus juveniles**

*Surface-fed* \((W R^2 = 0.10)\)

*All factors* \((R^2 = 0.35)\)

\[ Y = (0.026)\text{Flashiness} + (0.021)\text{Bottom Oysters} - (0.019)\text{SAV} \]

*Water Management* \((R^2 = 0.13)\)

\[ Y = (-0.027)\text{Flashiness} \]

*Restoration* \((R^2 = 0.21)\)

\[ Y = (-0.022)\text{SAV} + (0.020)\text{Bottom Oysters} \]

**Sciaenops ocellatus postflexion larvae**
Surface-fed (W $R^2 = 0.24$)

All factors ($R^2 = 0.19$) (Algae was selected first and then removed for regression)

\[ Y = (-0.034)\text{SAV} + (0.021)\text{Shoreline Terrestrial} \]

Water Quality ($R^2 = 0.063$)

\[ Y = (-0.022)\text{Turbidity} \]

**Archosargus probatocephalus**

Spring-fed (W $R^2 = 0.044$)

All factors ($R^2 = 0.58$)

\[ Y = (-0.219)\text{Head Spring in Zone} + (0.141)\text{Depth} \]

Surface-fed (W $R^2 = 0.000$)

All factors ($R^2 = 0.38$)

\[ Y = (-0.166)\text{Depth} - (0.097)\text{Color} - (0.099)\text{Bottom Sand} \]

Restoration ($R^2 = 0.34$)

\[ Y = (-0.234)\text{Depth} - (0.152)\text{Bottom Sand} + (0.106)\text{Shoreline Terrestrial} \]

**Brevoortia spp.**

Spring-fed (W $R^2 = 0.029$)

All factors ($R^2 = 0.51$)

\[ Y = (0.589)\text{Salinity} - (0.290)\text{Color} \]

Surface-fed (W $R^2 = 0.003$)

All factors ($R^2 = 0.27$)

\[ Y = (0.376)\text{Flashiness} - (0.308)\text{Slope} \]
Cynoscion arenarius

Surface-fed ($W R^2 = 0.16$)

All factors ($R^2 = 0.26$) (Algae selected in AIC but excluded from regression)

$Y = (-0.283)\text{Shoreline Terrestrial}$

Cynoscion nebulosus

Spring-fed ($W R^2 = 0.002$)

All factors ($R^2 = 0.95$)

$Y = (-0.158)\text{Bottom Sand} + (0.188)\text{Flushing time} - (0.284)\text{SAV} - (0.185)\text{Slope}$

Restoration ($R^2 = 0.48$)

$Y = (-0.226)\text{Bottom Sand}$

Water Quality ($R^2 = 0.41$)

$Y = (0.235)\text{Color}$

Surface-fed ($W R^2 = 0.004$)

All factors ($R^2 = 0.58$)

$Y = (-0.202)\text{Depth} + (0.184)\text{Flashiness} + (0.142)\text{Shoreline Mangroves}$

Water Management ($R^2 = 0.42$)

$Y = (-0.008)\text{Flashiness} - (0.291)\text{Salinity} + (0.034)\text{H2O Structure}$

Restoration ($R^2 = 0.37$)

$Y = (-0.265)\text{Depth}$

Callinectes sapidus 10 to 19mm
Spring-fed (W $R^2 = 0.038$)

All factors ($R^2 = 0.93$)

$Y = (-0.487)\text{Head Spring in Zone} + (0.366)\text{Salinity} + (0.167)\text{Bottom Sand}$

Restoration ($R^2 = 0.42$)

$Y = (-0.258)\text{Bottom Sand}$

Surface-fed (W $R^2 = 0.096$)

All factors ($R^2 = 0.84$)

$Y = (0.351)\text{Salinity} - (0.240)\text{Depth} - (0.286)\text{pH} + (0.073)\text{Turbidity} + (0.086)\text{Bottom Mud} - (0.061)\text{Color}$

Water Management ($R^2 = 0.38$)

$Y = (-0.202)\text{Salinity} - (0.048)\text{H2O Structure}$

Restoration ($R^2 = 0.47$)

$Y = (-0.193)\text{Slope} + (0.114)\text{Shoreline Oysters}$

Water Quality ($R^2 = 0.36$)

$Y = (-0.210)\text{Bottom DO}$

*Callinectes sapidus* 20 to 29mm

Spring-fed (W $R^2 = 0.002$)

All factors ($R^2 = 0.89$)

$Y = (-0.208)\text{Head Spring in Zone} - (0.118)\text{pH} + (0.085)\text{Temperature}$

Restoration ($R^2 = 0.41$)

$Y = (-0.172)\text{Bottom Sand}$

Surface-fed (W $R^2 = 0.10$)
All factors ($R^2 = 0.49$)

$Y = (-0.155)\text{Depth} - (0.090)\text{Bottom DO}$

Water Management ($R^2 = 0.37$)

$Y = (-0.148)\text{Salinity}$

Restoration ($R^2 = 0.37$)

$Y = (-0.148)\text{Depth}$

Water Quality ($R^2 = 0.37$)

$Y = (-0.148)\text{Bottom DO}$

Callinectes sapidus 30 to 39mm

Spring-fed (W $R^2 = 0.013$)

All factors ($R^2 = 0.87$)

$Y = (-0.317)\text{Head Spring in Zone} - (0.124)\text{Depth}$

Restoration ($R^2 = 0.42$)

$Y = (-0.236)\text{Depth}$

Surface-fed (W $R^2 = 0.00020$)

All factors ($R^2 = 0.26$)

$Y = (0.111)\text{Chlorophyll} - (0.104)\text{Depth}$

Water Management ($R^2 = 0.16$)

$Y = (-0.131)\text{Salinity}$

Restoration ($R^2 = 0.16$)

$Y = (-0.131)\text{Depth}$
**Callinectes sapidus 40 to 49mm**

Spring-fed ($W^2 = 0.0030$)

All factors ($R^2 = 0.94$)

\[ Y = (-0.357)\text{Head Spring in Zone} - (0.156)\text{Depth} - (0.127)\text{Bottom Mud} \]

Surface-fed ($W^2 = 0.0030$)

All factors ($R^2 = 0.23$)

\[ Y = (-0.135)\text{Do} - (0.128)\text{Bottom Oysters} \]

Restoration ($R^2 = 0.15$)

\[ Y = (-0.144)\text{Bottom Oysters} + (0.103)\text{Shoreline Oysters} \]

**Callinectes sapidus 50 to 59mm**

Surface-fed ($W^2 = 0.037$)

All factors ($R^2 = 0.13$)

\[ Y = (0.123)\text{Salinity} \]

Water Management model not significant

Restoration ($R^2 = 0.088$)

\[ Y = (0.075)\text{Shoreline Oysters} \]

**Callinectes sapidus 60 to 69mm**

Spring-fed ($W^2 = 0.039$)

All factors ($R^2 = 0.78$)

\[ Y = (-0.364)\text{Bottom Oysters} - (0.258)\text{SAV} \]

Surface-fed ($W^2 = 0.050$)
All factors ($R^2 = 0.12$)

$Y = (0.085)\text{Shoreline Oysters}$

**Callinectes sapidus <10mm**

Spring-fed ($W R^2 = 0.017$)

All factors ($R^2 = 0.73$)

$Y = (-0.240)\text{Head Spring in Zone} - (0.121)pH$

Restoration ($R^2 = 0.44$)

$Y = (-0.187)\text{Bottom Sand}$

Surface-fed ($W R^2 = 0.093$)

All factors ($R^2 = 0.29$)

$Y = (0.264)\text{Salinity} - (0.127)pH$

Restoration ($R^2 = 0.12$)

$Y = (-0.113)\text{Slope}$

**Callinectes sapidus >69mm**

Spring-fed ($W R^2 = 0.23$)

All factors ($R^2 = 0.87$)

$Y = (-0.424)\text{Bottom Manmade} - (0.215)\text{Flushing time} + (0.137)\text{Shoreline Manmade}$

Restoration ($R^2 = 0.554$)

$Y = (-0.215)\text{Bottom Manmade}$

Surface-fed ($W R^2 = 0.031$)

All factors ($R^2 = 0.14$)
\[ Y = (-0.118)\text{Bottom DO} \]

**Centropomus undecimalis**

*Spring-fed* (\( W^2 = 0.096 \))

*All factors* (\( R^2 = 0.38 \))

\[ Y = (0.101)\text{Temperature} \]

*Surface-fed* (\( W^2 = 0.094 \))

*All factors* (\( R^2 = 0.59 \))

\[ Y = (0.264)\text{Turbidity} - (0.079)\text{Bottom Sand} + (0.108)\text{Temperature} - (0.167)\text{DO} - (0.126)\text{Chlorophyll} \]

*Water Management* (\( R^2 = 0.25 \))

\[ Y = (-0.102)\text{Flashiness} - (0.003)\text{Tidal H2O Structure} + (0.121)\text{H2O Structure} \]

*Restoration* (\( R^2 = 0.29 \))

\[ Y = (0.172)\text{Bottom Mud} + (0.121)\text{Bottom Oysters} \]

**Farfantepenaeus duorarum**

*Surface-fed* (\( W^2 = 0.31 \))

*Water Management* (\( R^2 = 0.31 \))

\[ Y = (0.124)\text{Flushing time} - (0.326)\text{Salinity} + (0.109)\text{Flow} - (0.044)\text{Flashiness} \]

*Restoration* (\( R^2 = 0.49 \))

\[ Y = (0.277)\text{Shoreline Mangroves} - (0.122)\text{Depth} \]

*Water Quality* (\( R^2 = 0.13 \))

\[ Y = (-0.167)\text{Chlorophyll} \]
**Ictalurus punctatus**

None in Spring-fed. Surface-fed all not significant

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**Lutjanus griseus**

*Spring-fed* (W R² = 0.031)

*All factors* (R² = 0.44)

\[ Y = (0.103)\text{Bottom Sand} \]

*Water Management* (R² = 0.39)

\[ Y = (0.097)\text{Salinity} \]

*Surface-fed* (W R² = 0.28)

*All factors* (R² = 0.14)

\[ Y = (0.103)\text{Shoreline Mangroves} \]

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**Lutjanus synagris**

None in Spring-fed estuaries.

*Surface-fed* (W R² = 0.27)

*All factors* (R² = 0.069)

\[ Y = (0.030)\text{H2O Structure} \]

---

**Leiostomus xanthurus 20 to 29mm**

*Spring-fed* (W R² = 0.056)

*All factors* (R² = 0.52)
\[ Y = (0.539)\text{Salinity} \]

Water Management model not significant

\textit{Restoration} \( (R^2 = 0.78) \)

\[ Y = (-0.334)\text{Bottom Sand} - (0.305)\text{Algae} + (0.202)\text{Shoreline Manmade} \]

Water Quality \( (R^2 = 0.36) \)

\[ Y = (-0.284)\text{Turbidity} \]

Surface-fed \( (W \ R^2 = 0.29) \)

All factors \( (R^2 = 0.47) \)

\[ Y = (-0.421)\text{Slope} - (0.384)\text{Flow} - (-0.321)\text{Tidal H2O Structure} \]

Water Management \( (R^2 = 0.32) \)

\[ Y = (0.176)\text{Salinity} + (0.159)\text{Tidal H2O Structure} - (0.600)\text{Flow} \]

\textit{Restoration} \( (R^2 = 0.30) \)

\[ Y = (-0.501)\text{Slope} \]

\textit{Leiostomus xanthurus 30 to 39mm}

\textit{Spring-fed} \( (W \ R^2 = 0.014) \)

All factors \( (R^2 = 0.49) \)

\[ Y = (-0.347)\text{pH} \]

\textit{Restoration} \( (R^2 = 0.44) \)

\[ Y = (0.305)\text{Slope} \]

Water Quality \( (R^2 = 0.44) \)

\[ Y = (0.305)\text{Chlorophyll} \]

Surface-fed \( (W \ R^2 = 0.33) \)
All factors ($R^2 = 0.33$)

\[ Y = (-0.377)\text{Slope} \]

Water Management ($R^2 = 0.35$)

\[ Y = (0.103)\text{Tidal H2O Structure} + (0.074)\text{Salinity} - (0.410)\text{Flow} \]

Water Quality ($R^2 = 0.073$)

\[ Y = (0.177)\text{Turbidity} \]

Leiostomus xanthurus 40 to 49mm

Spring-fed ($W \ R^2 = 0.014$)

\[ Y = (0.302)\text{Shoreline Manmade} - (0.211)\text{Bottom Sand} \]

Water Quality ($R^2 = 0.35$)

\[ Y = (0.232)\text{Chlorophyll} \]

Surface-fed ($W \ R^2 = 0.29$)

All factors ($R^2 = 0.27$)

\[ Y = (-0.294)\text{Slope} \]

Water Management ($R^2 = 0.32$)

\[ Y = (0.070)\text{Tidal H2O Structure} - (0.294)\text{Flow} - (0.087)\text{Flushing time} \]

Water Quality ($R^2 = 0.29$)

\[ Y = (-0.122)\text{Color} - (0.262)\text{Bottom DO} \]

Leiostomus xanthurus <20mm

Spring-fed ($W \ R^2 = 0.20$)
All factors ($R^2 = 0.68$)

\[ Y = (-0.273) \text{Bottom Sand} - (0.173) \text{Algae} \]

Surface-fed ($R^2 = 0.32$)

All factors ($R^2 = 0.38$)

\[ Y = (-0.310) \text{Slope} + (0.260) \text{SAV} \]

Water Management ($R^2 = 0.30$)

\[ Y = (-0.235) \text{Salinity} - (0.255) \text{H2O Structure} \]

Water Quality ($R^2 = 0.10$)

\[ Y = (0.219) \text{Turbidity} \]

**Leiostomus xanthurus >49mm**

Spring-fed ($R^2 = 0.030$)

Restoration ($R^2 = 0.81$)

\[ Y = (-0.437) \text{Bottom Sand} + (0.264) \text{Shoreline Manmade} - (0.251) \text{Bottom Oysters} \]

Water Quality ($R^2 = 0.46$)

\[ Y = (-0.299) \text{Turbidity} \]

Surface-fed ($R^2 = 0.17$)

All factors ($R^2 = 0.41$)

\[ Y = (-0.372) \text{Flow} - (0.264) \text{Depth} - (0.336) \text{Salinity} + (0.185) \text{Flushing time} \]

Restoration ($R^2 = 0.094$)

\[ Y = (-0.172) \text{Slope} \]

**Menticirrhus americanus**
None in Spring-fed

Surface-fed \((W \, R^2 = 0.018)\)

All factors \((R^2 = 0.54)\)

\[
Y = (0.128)\text{Shoreline Mangroves} + (0.110)\text{Flow} - (0.120)\text{Depth} - (0.114)\text{SAV} - (0.099)\text{Shoreline Emergent}
\]

Restoration \((R^2 = 0.36)\)

\[
Y = (0.153)\text{Shoreline Mangroves} - (0.132)\text{Depth}
\]

Water Quality \((R^2 = 0.16)\)

\[
Y = (-0.151)\text{Chlorophyll}
\]

**Mugil cephalus 25 to 29mm**

Spring-fed \((W \, R^2 = 0.079)\)

All factors \((R^2 = 0.90)\)

\[
Y = (0.260)\text{Color} - (0.277)\text{Shoreline Terrestrial} + (0.117)\text{Shoreline Manmade}
\]

Restoration \((R^2 = 0.77)\)

\[
Y = (-0.124)\text{Bottom Sand} - (0.314)\text{Shoreline Terrestrial} + (0.222)\text{Shoreline Mangroves}
\]

Surface-fed \((W \, R^2 = 0.086)\)

All factors \((R^2 = 0.19)\)

\[
Y = (-0.227)\text{Chlorophyll} + (0.207)\text{Flashiness}
\]

**Mugil cephalus 30 to 34mm** (not included in table)

Surface-fed \((W \, R^2 = 0.024)\)

All factors \((R^2 = 0.089)\)
Y = (-0.159)Shoreline Mangroves

**Mugil cephalus 35 to 39mm** (not included in table)

*Surface-fed* (W $R^2 = 0.00$)

*All factors* ($R^2 = 0.17$)

Y = (-0.200)Salinity + (0.150)Botom Sand

**Mugil cephalus 40 to 44mm**

*Surface-fed* (W $R^2 = 0.0040$)

*All factors* ($R^2 = 0.091$)

Y = (-0.130)Bottom Oysters

**Mugil cephalus <25mm**

*Spring-fed* (W $R^2 = 0.032$)

*All factors* ($R^2 = 0.55$)

Y = (-0.259)Bottom Sand

*Surface-fed* (W $R^2 = 0.12$)

*All factors* ($R^2 = 0.15$)

Y = (0.224)Color

*Restoration* ($R^2 = 0.16$)

Y = (-0.210)Bottom Oysters – (0.169)Shoreline Terrestrial

**Mugil cephalus >44mm** (not included in table)
Surface-fed \( (W R^2 = 0.014) \)

*All factors* \( (R^2 = 0.078) \)

\[ Y = (-0.128) \text{Shoreline Oysters} \]

**Mugil curema**

Surface-fed \( (W R^2 = 0.058) \)

*All factors* \( (R^2 = 0.11) \)

\[ Y = (0.113) \text{Bottom Sand} \]

*Water Quality* \( (R^2 = 0.073) \)

\[ Y = (-0.092) \text{Bottom DO} \]

**Micropterus salmoides**

Spring-fed \( (W R^2 = 0.61) \)

*All factors* \( (R^2 = 0.52) \)

\[ Y = (0.289) \text{Bottom Sand} \]

*Water Management* \( (R^2 = 0.42) \)

\[ Y = (0.235) \text{Salinity} + (0.206) \text{Flashiness} \]

*Water Quality* \( (R^2 = 0.31) \)

\[ Y = (-0.251) \text{Color} \]

Surface-fed \( (W R^2 = 0.27) \)

*All factors* \( (R^2 = 0.63) \)

\[ Y = (0.184) \text{Depth} - (0.136) \text{Temperature} + (0.010) \text{Shoreline Emergent} + (0.070) \text{Bottom Sand} \]

*Water Management* \( (R^2 = 0.41) \)
Y = (0.104)Salinity + (0.100)Flow

Restoration (R^2 = 0.50)

Y = (0.138)Depth – (0.128)Shoreline Mangroves

**Mugil trichodon**

Surface-fed (W R^2 = 0.18)

All factors (R^2 = 0.54)

Y = (0.280)Flushing time + (0.154)Shoreline Manmade + (0.167)Flow

Water Management (R^2 = 0.21)

Y = (-0.065)Flushing time – (0.080)Flow – (0.172)Salinity

Restoration (R^2 = 0.52)

Y = (-0.312)Shoreline Emergent - (0.208)Bottom Oysters - (0.204)Shoreline Terrestrial + (0.138)Bottom Sand

Water Quality (R^2 = 0.097)

Y = (-0.161)Color

**Orthopristis chrysoptera**

Spring-fed (W R^2 = 0.72)

All factors (R^2 = 0.81)

Y = (0.101)pH + (0.168)Shoreline Mangroves – (0.050)Shoreline Oysters

Restoration (R^2 = 0.49)

Y = (-0.139)Shoreline Emergent – (0.106)Shoreline Manmade

Surface-fed (W R^2 = 0.24)
All factors \((R^2 = 0.34)\)

\[ Y = (0.169)\text{pH} - (0.081)\text{Bottom Mud} - (0.098)\text{Shoreline Mangroves} \]

Restoration \((R^2 = 0.13)\)

\[ Y = (0.098)\text{SAV} \]

Water Quality \((R^2 = 0.096)\)

\[ Y = (-0.076)\text{Color} \]

**Paralichthys albigutta**

Spring-fed \((W \ R^2 = 0.62)\)

All factors \((R^2 = 0.55)\)

\[ Y = (-0.165)\text{Algae} \]

Surface-fed \((W \ R^2 = 0.22)\)

All factors \((R^2 = 0.38)\)

\[ Y = (0.126)\text{pH} + (0.062)\text{Bottom Sand} \]

Water Management \((R^2 = 0.23)\)

\[ Y = (-0.019)\text{Flushing time} + (0.073)\text{Flashiness} - (0.062)\text{Salinity} \]

Restoration \((R^2 = 0.18)\)

\[ Y = (0.093)\text{Bottom Sand} \]

Water Quality \((R^2 = 0.13)\)

\[ Y = (-0.079)\text{Bottom DO} \]

**Sciaenops ocellatus 20 to 29mm**

Spring-fed \((W \ R^2 = 0.045)\)
All factors ($R^2 = 0.51$)

$Y = (0.220)\text{Shoreline Emergent}$

Surface-fed ($W \ R^2 = 0.028$)

All factors ($R^2 = 0.60$)

$Y = (-0.234)\text{Depth} - (0.157)\text{SAV} + (136)\text{Flashiness} + (0.133)\text{Shoreline Oysters} - (0.125)\text{Bottom Manmade}$

Restoration ($R^2 = 0.53$)

$Y = (-0.250)\text{Depth} - (0.176)\text{SAV} - (0.128)\text{Bottom Manmade} + (0.114)\text{Shoreline Oysters}$

Water Quality ($R^2 = 0.12$)

$Y = (-0.164)\text{Chlorophyll}$

Sciaenops ocellatus 30 to 39mm

Spring-fed ($W \ R^2 = 0.098$)

All factors ($R^2 = 0.60$)

$Y = (-0.178)\text{Bottom Sand} - (0.173)\text{Bottom Oysters}$

Water Management ($R^2 = 0.86$)

$Y = (0.060)\text{Flow} - (0.535)\text{H2O Structure} - (0.363)\text{Tidal H2O Structure} - (0.500)\text{H2O Structure in Zone} - (0.024)\text{Flashiness}$

Surface-fed ($W \ R^2 = 0.066$)

All factors ($R^2 = 0.47$)

$Y = (-0.269)\text{Depth} - (0.189)\text{SAV} + (0.124)\text{H2O Structure} + (0.128)\text{Chlorophyll}$

Water Management ($R^2 = 0.35$)

$Y = (-0.212)\text{Flashiness} - (0.260)\text{Salinity}$
Restoration \((R^2 = 0.35)\)

\[Y = (-0.260)\text{Depth} - (212)\text{SAV}\]

Water Quality \((R^2 = 0.083)\)

\[Y = (-0.135)\text{Chlorophyll}\]

**Sciaenops ocellatus 40 to 49mm**

Spring-fed \((W \ R^2 = 0.095)\)

All factor \((R^2 = 0.63)\)

\[Y = (-0.165)\text{Bottom Sand} - (0.162)\text{Bottom Oysters}\]

Water Management \((R^2 = 0.85)\)

\[Y = (0.079)\text{Flow} - (-0.480)\text{H2O Structure} - (0.331)\text{Tidal H2O Structure} - (0.467)\text{H2O Structure in Zone} - (0.009)\text{Flashiness}\]

Surface-fed \((W \ R^2 = 0.13)\)

All factor \((R^2 = 0.68)\)

\[Y = (-0.275)\text{Depth} + (0.138)\text{H2O Structure} - (0.105)\text{SAV} - (0.224)\text{Bottom Manmade} - (0.088)\text{Color} + (0.112)\text{H2O Structure in Zone} + (0.106)\text{Shoreline Manmade}\]

Water Management \((R^2 = 0.39)\)

\[Y = (-0.168)\text{Flashiness} - (0.228)\text{Salinity}\]

Restoration \((R^2 = 0.54)\)

\[Y = (-0.0219)\text{Depth} - (0.132)\text{SAV} + (0.173)\text{Bottom Mud} - (0.132)\text{Shoreline Emergent}\]

**Sciaenops ocellatus 50 to 59mm**

Spring-fed \((W \ R^2 = 0.023)\)
Restoration ($R^2 = 0.36$)

$Y = (-0.153)\text{Shoreline Terrestrial}$

Surface-fed ($W \ R^2 = 0.19$)

All factors ($R^2 = 0.49$)

$Y = (-0.205)\text{Slope} - (0.113)\text{Bottom Sand} + (0.107)\text{Chlorophyll}$

Water Management ($R^2 = 0.22$)

$Y = (-0.154)\text{Salinity} - (0.015)H2O \text{ Structure in Zone}$

Restoration ($R^2 = 0.44$)

$Y = (-0.161)\text{Slope} - (0.095)\text{Bottom Sand} + (0.083)\text{Shoreline Mangroves}$

Water Quality ($R^2 = 0.30$)

$Y = (-0.167)\text{Chlorophyll}$

*Sciaenops ocellatus 60 to 69mm*

Spring had none

Surface-fed ($W \ R^2 = 0.13$)

All factors ($R^2 = 0.63$)

$Y = (-0.155)\text{Slope} - (0.137)\text{Bottom DO} + (-0.098)\text{Flashiness} + (0.131)\text{Shoreline Manmade} - (0.086)\text{Bottom Manmade}$

Water Management ($R^2 = 0.23$)

$Y = (-0.154)\text{Salinity}$

Restoration ($R^2 = 0.54$)

$Y = (-148)\text{Slope} + (0.111)\text{Shoreline Oysters} + (0.081)\text{Shoreline Manmade} - (0.083)\text{SAV}$

Water Quality ($R^2 = 0.23$)
\[ Y = (-0.154)\text{Bottom DO} \]

*Sciaenops ocellatus <20mm*

Surface-fed (\( W \ R^2 = 0.00 \))

All factors (\( R^2 = 0.58 \))

\[ Y = (0.325)\text{Salinity} + (0.085)\text{Turbidity} + (0.104)\text{Flow} + (0.087)\text{Flashiness} \]

Water Management (\( R^2 = 0.29 \))

\[ Y = (-0.217)\text{Salinity} - (0.051)\text{Flashiness} + (0.029)\text{Flow} \]

Restoration (\( R^2 = 0.38 \))

\[ Y = (-0.157)\text{Depth} + (0.120)\text{Shoreline Oysters} \]

Water Quality (\( R^2 = 0.15 \))

\[ Y = (-0.134)\text{Chlorophyll} \]

*Sciaenops ocellatus >69mm*

Spring-fed (\( W \ R^2 = 0.36 \))

All factors (\( R^2 = 0.83 \))

\[ Y = (0.121)\text{Bottom Manmade} + (0.077)\text{Color} \]

Restoration (\( R^2 = 0.59 \))

\[ Y = (0.116)\text{Bottom Manmade} \]

Surface-fed (\( W \ R^2 = 0.052 \))

All factors (\( R^2 = 0.38 \))

\[ Y = (-0.228)\text{Slope} - (0.097)\text{SAV} \]

Water Management (\( R^2 = 0.31 \))
Y = (-0.209)Salinity + (0.003)H2O Structure in Zone

Archosargus probatocephalus 150 to 199mm

Spring-fed (W R^2 = 0.015)

All factors (R^2 = 0.65)

Y = (-0.191)Depth

Water Management (R^2 = 0.65)

Y = (-0.191)Salinity

Surface-fed (W R^2 = 0.14)

All factors (R^2 = 0.098)

Y = (-0.061)Turbidity

Water Quality model not significant

Archosargus probatocephalus 50 to 99mm

Surface-fed (W R^2 = 0.009)

Restoration (R^2 = 0.14)

Y = (0.113)Shoreline Manmade

Archosargus probatocephalus >199mm

None in Spring

Surface-fed (W R^2 = 0.42)

All factors (R^2 = 0.18)

Y = (-0.128)pH
\textit{Restoration} (R^2 = 0.13)

\[ Y = (0.092) \text{Depth} \]

\textit{Water Quality} (R^2 = 0.13)

\[ Y = (0.092) \text{Bottom DO} \]

\textbf{Brevoortia spp}

\textit{Spring-fed} (W R^2 = 0.33)

\textit{All factors} (R^2 = 0.999)

\[ Y = (0.166) \text{Flushing time} + (0.035) \text{Flow} + (0.025) \text{Temperature} \]

\textit{Water Management} (R^2 = 0.95)

\[ Y = (0.071) \text{Flushing time} - (0.222) \text{Flow} \]

\textit{Restoration} (R^2 = 0.85)

\[ Y = (-0.170) \text{Slope} \]

\textit{Surface-fed} (W R^2 = 0.0030)

\textit{All factors} (R^2 = 0.24)

\[ Y = (0.087) \text{Turbidity} \]

Water Quality model not significant

\textbf{Cynoscion arenarius 20 to 29mm}

None in Spring-fed

\textit{Surface-fed} (W R^2 = 0.070)

\textit{All factors} (R^2 = 0.46)

\[ Y = (0.253) \text{Temperature} + (0.269) \text{Bottom Mud} - (0.216) \text{Depth} \]
Water Management (R^2 = 0.33)
Y = (-0.241)Flow + (0.362)H2O Structure

Water Quality (R^2 = 0.20)
Y = (0.266)Color

*Cynoscion arenarius 30 to 39mm*

None in Spring-fed

Surface-fed (W R^2 = 0.19)

All factors (R^2 = 0.59)
Y = (-0.275)Shoreline Terrestrial – (0.200)Bottom Manmade + (0.160)Turbidity + (0.148)Flow

Restoration (R^2 = 0.57)
Y = (-0.220)Shoreline Terrestrial - (0.270)Bottom Manmade + (0.234)Bottom Mud - (0.191)Shoreline Emergent

Water Quality (R^2 = 0.28)
Y = (0.324)Color – (0.164)Chlorophyll

*Cynoscion arenarius 40 to 49mm*

None in Spring-fed

Surface-fed (W R^2 = 0.19)

Water Quality (R^2 = 0.19)
Y = (0.240)Color – (0.204)Chlorophyll

*Cynoscion arenarius 50 to 59mm*
None in Spring-fed

Surface-fed (W $R^2 = 0.035$)

All factors ($R^2 = 0.25$)

$Y = (0.328)\text{pH} - (0.202)\text{SAV}$

Water Quality ($R^2 = 0.13$)

$Y = (0.159)\text{Chlorophyll} - (0.285)\text{Bottom DO}$

\textit{Cynoscion arenarius <20mm}

None in Spring-fed

Surface-fed (W $R^2 = 0.028$)

All factors ($R^2 = 0.40$)

$Y = (0.311)\text{Flow} + (0.207)\text{Flashiness} - (0.173)\text{Bottom Sand}$

Water Quality ($R^2 = 0.17$)

$Y = (0.224)\text{Color}$

\textit{Cynoscion arenarius >59mm}

None in Spring-fed

Surface-fed (W $R^2 = 0.002$)

All factors ($R^2 = 0.34$)

$Y = (-0.260)\text{Depth} + (0.156)\text{Flow}$

Restoration ($R^2 = 0.27$)

$Y = (-0.294)\text{Depth}$

Water Quality ($R^2 = 0.29$)
Y = (-0.387)Bottom DO + (0.117)Chlorophyll

**Cynoscion nebulosus**

**Spring-fed** (W $R^2 = 0.41$)

All factors ($R^2 = 0.98$)

Y = (0.699)Salinity – (0.328)Slope

*Water Quality* ($R^2 = 0.47$)

Y = (0.258)DO

**Surface-fed** (W $R^2 = 0.29$)

All factors ($R^2 = 0.16$)

Y = (0.126)Bottom Oysters

*Water Management* ($R^2 = 0.097$)

Y = (-0.097)Flow

**Callinectes sapidus 100 to 109mm**

**Spring-fed** (W $R^2 = 0.44$)

All factors ($R^2 = 0.83$)

Y = (-0.140)Flushing time

Water Management model not significant

*Restoration* ($R^2 = 0.93$)

Y = (0.143)Algae – (0.079)Depth

**Surface-fed** (W $R^2 = 0.065$)

All factors $R^2 = (0.30)$
\[ Y = (0.127)\text{Shoreline Manmade} - (0.101)\text{Depth} + (0.100)\text{Flashiness} \]

*Restoration* \((R^2 = 0.37)\)

\[ Y = (0.173)\text{Shoreline Manmade} - (0.184)\text{Depth} + (0.137)\text{Bottom Mud} + (0.122)\text{Shoreline Terrestrial} \]

\[ Y = (0.049)\text{Salinity} \]

*Water Quality* \((R^2 = 0.88)\)

\[ Y = (0.049)\text{Turbidity} \]

*Surface-fed* \((W \ R^2 = 0.15)\)

\[ Y = (-0.165)\text{Tidal\_H2O\_Structure} - (0.104)\text{Bottom Sand} \]

*Restoration* \((R^2 = 0.091)\)

\[ Y = (-0.091)\text{Bottom Manmade} \]

*Water Quality* \((R^2 = 0.071)\)

\[ Y = (-0.078)\text{Bottom DO} \]

\[ \text{Callinectes sapidus 120 to 129mm} \]

*Spring-fed* \((W \ R^2 = 0.81)\)

*Water Management* \((R^2 = 0.88)\)

\[ Y = (0.049)\text{Salinity} \]

*Water Quality* \((R^2 = 0.88)\)

\[ Y = (0.049)\text{Turbidity} \]

\[ Y = (-0.078)\text{Bottom DO} \]

\[ \text{Callinectes sapidus 130 to 139mm} \]

*Spring-fed* \((W \ R^2 = 0.39)\)

*Restoration* \((R^2 = 0.85)\)

\[ Y = (0.305)\text{Slope} \]
Surface-fed \( (W \, R^2 = 0.029) \)

*All factors* \( (R^2 = 0.41) \)

\[
Y = (-0.140)\text{Slope} - (0.144)\text{Bottom Sand} + (0.121)\text{Bottom DO}
\]

*Restoration* \( (R^2 = 0.36) \)

\[
Y = (-0.177)\text{Slope} - (0.170)\text{Bottom Sand} - (0.091)\text{Bottom Oysters}
\]

*Water Quality* \( (R^2 = 0.14) \)

\[
Y = (-0.105)\text{Bottom DO} + (0.092)\text{Color}
\]

*Callinectes sapidus 30 to 39mm*

Spring-fed \( (W \, R^2 = 0.005) \)

*All factors* \( (R^2 = 0.75) \)

\[
Y = (0.197)\text{Bottom Sand}
\]

Surface-fed \( (W \, R^2 = 0.006) \)

*All factors* \( (R^2 = 0.38) \)

\[
Y = (0.175)\text{Bottom Oysters} - (0.145)\text{Depth}
\]

*Callinectes sapidus 40 to 49mm*

Spring-fed \( (W \, R^2 = 0.47) \)

*All factors* \( (R^2 = 0.61) \)

\[
Y = (0.121)\text{pH}
\]

Surface-fed \( (W \, R^2 = 0.008) \)

*All factors* \( (R^2 = 0.26) \)

\[
Y = (0.229)\text{Shoreline Manmade} - (0.169)\text{Bottom Manmade} + (0.102)\text{Shoreline Oysters}
\]
**Callinectes sapidus 50 to 59mm**

Spring-fed (W $R^2 = 0.31$)

*All factors* ($R^2 = 0.98$)

$Y = (0.181)\text{Shoreline Manmade} - (0.121)\text{Shoreline Mangroves}$

*Water Quality* ($R^2 = 0.80$)

$Y = (-0.173)\text{Color} - (0.049)\text{Chlorophyll}$

Surface-fed (W $R^2 = 0.0020$)

*All factors* ($R^2 = 0.25$)

$Y = (-0.127)\text{Depth} - (0.113)\text{Shoreline Emergent}$

**Callinectes sapidus 60 to 69mm**

Spring-fed (W $R^2 = 0.42$)

*Restoration* ($R^2 = 0.99$)

$Y = (-0.214)\text{Shoreline Emergent}$

Surface-fed (W $R^2 = 0.037$)

*All factors* ($R^2 = 0.37$)

$Y = (-0.138)\text{Depth} - (0.111)\text{SAV} + (0.106)\text{Shoreline Manmade} + (0.099)\text{Flow}$

*Water Management* ($R^2 = 0.095$)

$Y = (-0.108)\text{Flow}$

*Restoration* ($R^2 = 0.30$)

$Y = (-0.160)\text{Depth} - (0.111)\text{SAV} + (0.094)\text{Shoreline Manmade}$
**Callinectes sapidus 70 to 79mm**

Surface-fed (W $R^2 = 0.026$)

All factors ($R^2 = 0.33$)

\[ Y = (-0.133)\text{Shoreline Emergent} + (0.105)\text{Flow} - (0.094)\text{Shoreline Terrestrial} \]

Water Management ($R^2 = 0.14$)

\[ Y = (-0.058)\text{Flow} - (0.081)\text{Salinity} \]

Restoration ($R^2 = 0.25$)

\[ Y = (-0.135)\text{Shoreline Emergent} - (0.117)\text{Shoreline Terrestrial} \]

---

**Callinectes sapidus 80 to 89mm**

Spring-fed (W $R^2 = 0.52$)

Restoration ($R^2 = 0.85$)

\[ Y = (0.124)\text{Slope} + (0.083)\text{Bottom Sand} \]

Surface-fed (W $R^2 = 0.0020$)

All factors ($R^2 = 0.41$)

\[ Y = (-0.170)\text{Shoreline Emergent} - (0.119)\text{Depth} \]

Water Management ($R^2 = 0.22$)

\[ Y = (-0.151)\text{Salinity} - (0.021)\text{Flow} \]

---

**Callinectes sapidus 90 to 99mm**

Spring-fed (W $R^2 = 0.17$)

All factors ($R^2 = 0.81$)

\[ Y = (0.128)\text{Color} \]


Restoration \( R^2 = 0.93 \)

\[ Y = (0.159) \text{Algae} + (0.121) \text{Bottom Mud} \]

Water Quality model not significant

Surface-fed \( (W \ R^2 = 0.000) \)

All factors \( (R^2 = 0.47) \)

\[ Y = (-0.184) \text{Shoreline Emergent} - (0.201) \text{Depth} - (0.140) \text{Bottom Sand} - (0.112) \text{Shoreline Mangroves} \]

Water Management \( (R^2 = 0.20) \)

\[ Y = (-0.159) \text{Salinity} \]

\textit{Callinectes sapidus} \(<30\text{mm}\)

Surface-fed \( (W \ R^2 = 0.10) \)

All factors \( (R^2 = 0.13) \)

\[ Y = (-0.137) \text{Shoreline Terrestrial} \]

\textit{Callinectes sapidus} \(>159\text{mm}\)

Spring-fed \( (W \ R^2 = 0.10) \)

All factors \( (R^2 = 1.0) \)

\[ Y = (0.186) \text{Depth} + (0.240) \text{Shoreline Mangroves} + (0.040) \text{Flushing time} \]

Restoration \( (R^2 = 0.999) \)

\[ Y = (0.186) \text{Depth} + (0.305) \text{Shoreline Mangroves} - (0.062) \text{Algae} \]

Surface-fed \( (W \ R^2 = 0.021) \)

All factors \( (R^2 = 0.51) \)
Y = (-0.207)Bottom Sand – (0.162)Slope – (0.109)Bottom Manmade + (0.105)Shoreline Terrestrial

Water Quality (R^2 = 0.31)
Y = (-0.197)Turbidity

Centropomus undecimalis

None in Spring-fed
Surface-fed (W R^2 = 0.096)
All factors (R^2 = 0.59)
Y = (0.075)H2O Structure in Zone – (0.083)pH + (0.131)Bottom Mud – (0.093)Shoreline Emergent + (0.069)Shoreline Terrestrial
Restoration (R^2 = 0.51)
Y = (0.065)Depth + (0.138)Bottom Mud + (0.096)Shoreline Terrestrial – (0.082)Shoreline Emergent
Water Quality (R^2 = 0.24)
Y = (0.111)Bottom DO

Farfantepeaeus duorarum 10 to 14mm
Spring-fed (W R^2 = 0.31)
All factors (R^2 = 0.78)
Y = (0.130)Shoreline Oysters
Surface-fed (W R^2 = 0.15)
All factors (R^2 = 0.53)
\[ Y = (0.213)\text{Shoreline Mangroves} + (0.213)\text{Turbidity} - (0.192)\text{Shoreline Terrestrial} + (0.219)\text{Flow} \]

*Water Management* \((R^2 = 0.15)\)

\[ Y = (-0.056)\text{Flow} - (0.169)\text{Salinity} \]

*Restoration* \((R^2 = 0.48)\)

\[ Y = (0.238)\text{Shoreline Mangroves} + (0.301)\text{Bottom Mud} - (0.181)\text{Shoreline Emergent} - (0.159)\text{Slope} \]

**Farfantepenaeus duorarum 15 to 19mm**

*Spring-fed* \((W \ R^2 = 0.096)\)

*All factors* \((R^2 = 0.97)\)

\[ Y = (0.511)\text{Depth} - (0.282)\text{Bottom Manmade} \]

*Water Management* \((R^2 = 0.79)\)

\[ Y = (0.634)\text{Flushing time} + (0.564)\text{Flashiness} \]

*Surface-fed* \((W \ R^2 = 0.18)\)

*All factors* \((R^2 = 0.48)\)

\[ Y = (0.217)\text{Shoreline Mangroves} + (0.251)\text{pH} - (0.127)\text{SAV} \]

*Water Management* \((R^2 = 0.17)\)

\[ Y = (-0.200)\text{Salinity} - (0.001)\text{Flow} \]

*Restoration* \((R^2 = 0.35)\)

\[ Y = (0.314)\text{Shoreline Mangroves} \]

**Farfantepenaeus duorarum 20 to 24mm**
Spring-fed \( (W R^2 = 0.46) \)

All factors \( (R^2 = 0.96) \)

\[ Y = (0.420)\text{Flushing time} - (0.267)\text{Flow} \]

Water Management model not significant

Restoration \( (R^2 = 0.998) \)

\[ Y = (0.765)\text{Bottom Mud} - (0.437)\text{Shoreline Emergent} - (0.078)\text{Bottom Sand} \]

Surface-fed \( (W R^2 = 0.065) \)

All factors \( (R^2 = 0.68) \)

\[ Y = (0.109)\text{Flushing time} + (0.135)pH + (0.254)\text{Salinity} + (0.104)\text{Color} \]

Water Management \( (R^2 = 0.37) \)

\[ T = (0.119)\text{Flushing time} - (0.228)\text{Salinity} + (0.003)\text{Flow} \]

Restoration \( (R^2 = 0.64) \)

\[ Y = (-0.167)\text{Shoreline Emergent} - (0.234)\text{Shoreline Terrestrial} + (0.173)\text{Bottom Sand} \]

Water Quality \( (R^2 = 0.35) \)

\[ Y = (-0.082)\text{Chlorophyll} + (0.096)\text{Turbidity} - (0.117)\text{Bottom DO} \]

Farfantepenaeus duorarum 5 to 9mm

Spring-fed \( (W R^2 = 0.10) \)

All factors \( (R^2 = 0.81) \)

\[ Y = (0.549)pH \]

Surface-fed \( (W R^2 = 0.17) \)

All factors \( (R^2 = 0.36) \)

\[ Y = (-0.253)\text{Shoreline Terrestrial} + (0.212)\text{Turbidity} \]
Water Management \( (R^2 = 0.087) \)
\[ Y = (-0.160) \text{Flashiness} \]

Water Quality \( (R^2 = 0.096) \)
\[ Y = (-0.152) \text{Turbidity} \]

**Farfantepenaeus duorarum <5mm**

Surface-fed \( (W \ R^2 = 0.10) \)

All factors \( (R^2 = 0.16) \)
\[ Y = (0.128) \text{Bottom Oysters} \]

Water Quality \( (R^2 = 0.099) \)
\[ Y = (-0.100) \text{Turbidity} \]

**Farfantepenaeus duorarum >24mm**

Spring-fed \( (W \ R^2 = 0.27) \)

All factors \( (R^2 = 0.98) \)
\[ Y = (0.328) \text{Depth} - (0.384) \text{Temperature} \]

Restoration \( (R^2 = 0.92) \)
\[ Y = (0.474) \text{Depth} - (0.523) \text{Shoreline Mangroves} \]

Surface-fed \( (W \ R^2 = 0.011) \)

All factors \( (R^2 = 0.37) \)
\[ Y = (0.098) \text{Residence}_\text{Time} - (0.220) \text{Salinity} \]

Restoration \( (R^2 = 0.29) \)
\[ Y = (-0.177) \text{Shoreline Emergent} - (0.165) \text{Depth} \]
Water Quality ($R^2 = 0.31$)

\[ Y = (-0.216)\text{Chlorophyll} \]

**Ictalurus punctatus**

None in Spring-fed

Surface-fed ($W \ R^2 = 0.17$)

All factors $R^2 = (0.55)$

\[ Y = (0.191)\text{Shoreline Emergent} + (0.186)\text{Shoreline Terrestrial} + (0.141)\text{Color} - (0.129)\text{Tidal H2O Structure} + (0.114)\text{Bottom Oysters} \]

Restoration ($R^2 = 0.35$)

\[ Y = (0.185)\text{Shoreline Emergent} + (0.139)\text{Shoreline Terrestrial} \]

**Lutjanus griseus**

Spring-fed ($W \ R^2 = 0.35$)

All factors ($R^2 = 0.999$)

\[ Y = (-0.143)\text{Shoreline Mangroves} - (0.088)pH - (0.034)\text{Depth} \]

Restoration ($R^2 = 0.82$)

\[ Y = (-0.212)\text{Shoreline Mangroves} \]

**Lutjanus synagris**

Spring-fed ($W \ R^2 = 0.33$)

All factors ($R^2 = 0.999$)

\[ Y = (0.192)\text{Flushing time} + (0.041)\text{Flow} + (0.029)\text{Temperature} \]
Water Management ($R^2 = 0.95$)

$Y = (0.083) \text{Flushing time} - (0.258) \text{Flow}$

Restoration ($R^2 = 0.85$)

$Y = (-0.198) \text{Slope}$

Surface-fed ($R^2 = 0.41$)

All factors ($R^2 = 0.33$)

$Y = (-0.105) \text{Flashiness} - (0.067) \text{Shoreline Emergent}$

Water Management ($R^2 = 0.18$)

$Y = (0.074) \text{Flashiness} + (0.073) \text{Flushing time}$

Restoration ($R^2 = 0.098$)

$Y = (-0.064) \text{Slope}$

Leiostomus xanthurus 20 to 29mm

Surface-fed ($R^2 = 0.14$)

All factors ($R^2 = 0.27$)

$Y = (-0.311) \text{Flow} - (0.259) \text{H2O\_Structure}$

Restoration ($R^2 = 0.13$)

$Y = (0.260) \text{Shoreline Emergent} - (0.228) \text{Bottom Mud}$

Leiostomus xanthurus 40 to 49mm

Spring-fed ($R^2 = 0.053$)

All factors ($R^2 = 0.74$)

$Y = (-0.310) \text{Depth}$
*Leiostomus xanthurus* 50 to 59mm (not in table)

None in Spring-fed

Surface-fed ($W R^2 = 0.025$)

*All factors* ($R^2 = 0.16$)

$Y = (0.104)\text{Flashiness}$

Water Management model not significant

*Leiostomus xanthurus* 60 to 69mm (not in table)

None in Spring-fed

Surface-fed ($W R^2 = 0.012$)

*All factors* ($R^2 = 0.21$)

$Y = (0.109)\text{Flashiness}$

Water Management model not significant

Restoration ($R^2 = 0.061$)

$Y = (-0.056)\text{Depth}$

*Leiostomus xanthurus* 70 to 79mm (not in table)

Spring-fed ($W R^2 = 0.10$)

*All factors* ($R^2 = 0.96$)

$Y = (-0.346)\text{pH} + (0.216)\text{Shoreline Mangroves}$

Surface-fed ($W R^2 = 0.0030$)

$Y = (0.081)\text{Flashiness}$
Water Management model not significant

*Leiostomus xanthurus* <20mm

Spring-fed (W R^2 = 0.35)

All factors (R^2 = 1.0)

Y = (-0.378)Head Spring Sampled + (0.097)Flushing time + (0.045)Shoreline Mangroves

Water Management (0.91)

Y = (0.412)Flashiness

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*Leiostomus xanthurus* >79mm

Spring-fed (W R^2 = 0.17)

All factors (R^2 = 0.997)

Y = (0.290)Depth + (0.068)Color

Water Management (R^2 = 0.95)

Y = (0.307)Salinity

Restoration (R^2 = 1.0)

Y = (0.317)Depth – (0.110)SAV – (0.048)Bottom Manmade

Surface-fed (W R^2 = 0.0010)

All factors (R^2 = 0.47)

Y = (0.160)Turbidity – (0.157)Depth + (0.130)Flashiness

Restoration (R^2 = 0.24)

Y = (-0.213)Depth + (0.126)Bottom Mud
**Menticirrhus americanus 20 to 29mm**

None in Spring-fed

**Surface-fed** \((W \ R^2 = 0.008)\)

**All factors** \((R^2 = 0.52)\)

\[ Y = (-0.262)\text{Shoreline Emergent} + (0.182)\text{DO} - (0.145)\text{Shoreline Terrestrial} \]

**Water Management** \((R^2 = 0.12)\)

\[ Y = (0.154)\text{Flushing time} \]

**Restoration** \((R^2 = 0.46)\)

\[ Y = (-0.270)\text{Shoreline Emergent} - (0.153)\text{Shoreline Terrestrial} - (0.133)\text{Bottom Manmade} \]

**Water Quality** \((R^2 = 0.11)\)

\[ Y = (-0.143)\text{Bottom DO} \]

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**Menticirrhus americanus 30 to 39mm**

None in Spring-fed

**Surface-fed** \((W \ R^2 = 0.005)\)

**All factors** \((R^2 = 0.56)\)

\[ Y = (-0.138)\text{Depth} - (0.139)\text{Shoreline Terrestrial} + (0.135)\text{Flow} - (0.119)\text{Shoreline Emergent} - (0.123)\text{SAV} \]

**Water Management** \((R^2 = 0.22)\)

\[ Y = (0.017)\text{Flushing time} - (0.196)\text{Flow} \]

**Restoration** \((R^2 = 0.37)\)

\[ Y = (-0.161)\text{Depth} - (0.161)\text{Shoreline Terrestrial} \]

**Water Quality** \((R^2 = 0.26)\)
\[ Y = (-0.223)DO \]

**Menticirrhus americanus 40 to 49mm**

None in Spring-fed

Surface-fed (W \( R^2 = 0.0030 \))

All factors (\( R^2 = 0.32 \))

\[ Y = (0.214)\text{Flow} + (0.174)\text{Shoreline Mangroves} \]

Water Management (\( R^2 = 0.17 \))

\[ Y = (-0.030)\text{Flow} - (0.169)\text{Salinity} \]

Restoration (\( R^2 = 0.17 \))

\[ Y = (-0.192)\text{Depth} \]

Water Quality (0.17)

\[ Y = (-0.192)\text{Bottom DO} \]

**Menticirrhus americanus 50 to 59mm**

None in Spring-fed

Surface-fed (W \( R^2 = 0.0020 \))

All factors (\( R^2 = 0.28 \))

\[ Y = (0.161)\text{Flow} + (0.123)\text{Flushing time} \]

Restoration (\( R^2 = 0.12 \))

\[ Y = (-0.148)\text{Depth} \]

Water Quality (\( R^2 = 0.12 \))

\[ Y = (-0.148)\text{Bottom DO} \]
Menticirrhus americanus 60 to 69mm

None in Spring-fed

Surface-fed (W $R^2 = 0.029$)

All factors ($R^2 = 0.36$)

$Y = (0.202)\text{Flow} + (0.115)\text{Shoreline Mangroves}$

Restoration ($R^2 = 0.12$)

$Y = (-0.131)\text{Depth}$

Menticirrhus americanus 70 to 79mm

None in Spring-fed

Surface-fed (W $R^2 = 0.005$)

All factors ($R^2 = 0.38$)

$Y = (0.156)\text{Flow} + (0.123)\text{Shoreline Mangroves}$

Water Management ($R^2 = 0.063$)

$Y = (-0.078)\text{Flow}$

Restoration ($R^2 = 0.15$)

$Y = (-0.120)\text{Depth}$

Water Quality ($R^2 = 0.15$)

$Y = (-0.120)\text{Bottom DO}$

Menticirrhus americanus <20mm

None in Spring-fed
Surface-fed (W $R^2 = 0.004$)

All factors ($R^2 = 0.48$)

\[ Y = (0.104)pH - (0.145)SAV + (0.196)\text{Bottom DO} - (0.192)\text{Shoreline Emergent} \]

Restoration ($R^2 = 0.32$)

\[ Y = (-0.152)\text{Depth} - (0.126)\text{Shoreline Emergent} - (0.125)\text{SAV} \]

Water Quality ($R^2 = 0.17$)

\[ Y = (-0.155)\text{Bottom DO} \]

**Menticirrhus americanus >79mm**

None in Spring-fed

Surface-fed (W $R^2 = 0.016$)

All factors ($R^2 = 0.49$)

\[ Y = (0.251)\text{Flushing time} + (0.134)\text{Flashiness} \]

Restoration ($R^2 = 0.47$)

\[ Y = (-0.114)\text{Depth} - (0.242)\text{Shoreline Emergent} - (0.142)\text{Bottom Oysters} - (0.108)\text{Bottom Oysters} \]

Manmade

Water Quality ($R^2 = 0.28$)

\[ Y = (-0.254)\text{DO} + (0.067)\text{Chlorophyll} \]

**Micropogonias undulatus**

None in Spring-fed

Surface-fed (W $R^2 = 0.12$)

Water Management ($R^2 = 0.16$)
\[ Y = (-0.090)\text{Salinity} + (0.111)\text{Flushing time} \]

**Paralichthys albigutta**

*Spring-fed* \( (W \ R^2 = 0.85) \)

*All factors* \( (R^2 = 0.68) \)

\[ Y = (-0.283)\text{Shoreline Mangroves} \]

*Surface-fed* \( (W \ R^2 = 0.31) \)

*All factors* \( (R^2 = 0.55) \)

\[ Y = (0.225)\text{pH} + (0.103)\text{Shoreline Manmade} - (0.148)\text{Flushing time} - (0.111)\text{Bottom Mud} + (0.079)\text{DO} \]

*Water Management* \( (R^2 = 0.10) \)

\[ Y = (-0.050)\text{Salinity} + (0.075)\text{Flashiness} \]

*Restoration* \( (R^2 = 0.15) \)

\[ Y = (-0.117)\text{Shoreline Emergent} \]

*Water Quality* \( (R^2 = 0.071) \)

\[ Y = (-0.078)\text{Color} \]

**Sciaenops ocellatus 20 to 29mm**

None in Spring-fed

*Surface-fed* \( (W \ R^2 = 0.070) \)

*All factors* \( (R^2 = 0.20) \)

\[ Y = (-0.124)\text{Bottom Sand} + (0.107)\text{Chlorophyll} \]
Sciaenops ocellatus <20mm

Surface-fed \((W \, R^2 = 0.026)\)

All factors \((R^2 = 0.26)\)

\[ Y = (-0.138)\text{Bottom Sand} + (0.110)\text{Turbidity} \]

Restoration \((R^2 = 0.16)\)

\[ Y = (-0.147)\text{Bottom Sand} \]

Water Quality \((R^2 = 0.16)\)

\[ Y = (-0.147)\text{Turbidity} \]