2826

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Fishery Resource Habitat Use Modeling in Florida Bay: Development and Application to Everglades Restoration Implementation (Phase 1)

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Executive Summary

The goal of this project is to develop methodology for assessing potential effects of Everglades restoration projects (i.e., CERP projects) on marine fishery resources under the responsibility of the National Park Service. Those water management projects that will affect coastal estuarine habitats include the Modified Waters Delivery Project, the C-111 Project, the C-111 Spreader Canal Project, and the Biscayne Bay Coastal Wetlands Project by altering the quantity, timing, and distribution of fresh water to Florida and Biscayne bays. The principal objectives of project Phase 1 were to: (1) develop GIS maps of important fish habitat features in Florida Bay, to permit mapping anticipated changes in these features due to Everglades restoration activities; (2) develop methods for analyzing and modeling fish habitat use utilizing synoptic fishery-independent survey data; (3) develop a methodology for applying fish habitat use models for evaluating spatial effects of salinity changes in Florida Bay; and (4) develop a prototype decision support tool to facilitate evaluation of forecasted hydrological (salinity) conditions on habitats in Florida Bay. Work was carried out by two collaborating teams of investigators, the Everglades National Park (ENP) team headed by Dr. William Perry, and the University of Miami-Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS) team headed by Drs. Jerald Ault and Steven Smith.

Florida Bay geo-referenced data for the important environmental variables bathymetry and bottom type were compiled from existing databases and transformed into GIS layers using ArcGIS software. Average monthly salinity values for spatial regions of Florida Bay for the period 1991-2002 were obtained from outputs of the FATHOM hydrodynamic model for Florida Bay. GIS layers with salinity data were created for each year-month of the 1991-2002 time series. A composite digital habitat map was created by overlaying a 200 by 200 m grid layer on the Florida Bay domain and interpolating values of bathymetry, bottom type, and salinity for each grid cell.

Restoration projects will likely alter the salinity dynamics along the northern portion of Florida Bay adjacent to the mainland, i.e., the region most influenced by freshwater inflows. In turn, these alterations may potentially affect Florida Bay populations of fish and macroinvertebrate species that predominately utilize 'estuarine' habitats, characterized by low to moderate salinities. Utilizing fishery-independent survey data, we evaluated two approaches for analyzing fish use of coastal bay habitats: (1) design-based estimation of habitat use, and (2)

regression modeling of habitat use. Spatially synoptic co-occurrent biological (species abundance, size composition) and environmental (bathymetry, bottom type, salinity) data from fishery-independent surveys were compiled for two southern Florida estuaries, Charlotte Harbor and Biscayne Bay. Comparable data for Florida Bay were not available at the outset of this study. Sampling design-based procedures were employed to estimate three measures of habitat use: (1) probability of use (presence-absence), (2) per unit amount of use (catch-per-unit-effort CPUE) and (3) population amount of use (abundance). This analysis was applied to five important forage and/or fishery species in southern Florida coastal bays. Results indicated that spotted seatrout, pink shrimp, pinfish, and gray snapper exhibited high levels of use of estuarine habitats, whereas bluestriped grunt exhibited high levels of use in near-oceanic salinity environments. This analysis approach appears to be an effective method for identifying potential indicator species for evaluating potential effects of restoration projects on fishery resources.

Juvenile spotted seatrout were selected for example calculations. Catch-per-unit effort (CPUE, i.e., relative animal density) data from fish surveys were modeled as a function of the environmental covariates bathymetry, bottom type, and salinity. To satisfy error assumptions of the generalized linear modeling procedure, estimation of the abundance-habitat relationship was carried out in two stages. One stage utilized presence-absence data to fit a logistic regression model, and the other stage utilized non-zero CPUE observations to fit a generalized linear regression model. Multiplying the probability of occurrence predicted by logistic regression with the predicted non-zero CPUE from generalized linear regression yielded the predicted CPUE as a function of habitat variables. This two-stage procedure was necessary due to the high frequency of zero catches common in fishery-independent survey data. The regression analysis approach enables elucidation of influential habitat variables in explaining the variation of fish habitat use, and provides quantitative functional relationships between measures of habitat use and influential habitat variables. Animal-habitat regression models were used to develop various habitat suitability metrics for evaluating Restudy impacts on Florida Bay fish and macroinvertebrate populations. A prototype process was developed to carry out the computations and for displaying habitat suitability metrics with a series of maps, tables, and graphs.

A suite of mapping, analysis, and modeling methods were developed in project Phase 1 as a prototype for evaluating spatial impacts of proposed restoration activities on populations of fish

and macroinvertebrates in Florida Bay. The next research phase will include the following steps: (1) application of design-based habitat use analysis to identify the full set of fish and macroinvertebrate indicator species for Restudy scenario testing; (2) development of two-stage animal-habitat regression models for indicator species, and application of these models for analyzing Restudy impacts on habitat suitability metrics; (3) refinement and enhancement of the decision support tool; (4) development of a statistical sampling design and implementation of fishery-independent monitoring surveys for indicator species in Florida Bay.

Table of Contents

Executive Summary..... 2

1.0 Goals and Background..... 6

2.0 Phase 1 Objectives and Research Coordination..... 7

3.0 Habitat Mapping and Modeling..... 7

4.0 Fish Habitat Use Analysis..... 7

4.1 Data Sources..... 7

4.2 Design-Based Estimation of Habitat Use..... 8

4.3 Regression Modeling of Habitat Use..... 10

5.0 Modeling of Fish Habitat Suitability in Florida Bay..... 12

6.0 Prototype Decision Support Tool..... 14

7.0 Next Research Steps..... 14

8.0 Literature Cited..... 15

Tables, Figures & Appendices..... 16

1.0 Goals and Background

The goal of this project was to develop methodology for an environmental assessment application that will permit quantitative evaluation of the potential effects of Everglades restoration projects on marine fishery resources under the responsibility of the National Park Service. Those water management projects that will affect coastal estuarine habitats include the Modified Waters Delivery Project (presently part of the combined structural and operational plan), the C-111 Project, the C-111 Spreader Canal Project, and the Biscayne Bay Coastal Wetlands Project by altering the quantity, timing, and distribution of fresh water to the bay. Additionally, the Florida Bay Feasibility Study will require an evaluation of water management proposals on habitat and standing stocks of recreational fish species. This study developed analytical and statistical procedures for using fishery-independent survey data to quantitatively asses and map fish habitat use from resource surveys conducted in Biscayne Bay, Tampa Bay, and Charlotte Harbor, where many of the same resource management and environmental assessment issues exist (Ault et al. 1999, 2002).

2.0 Phase 1 Objectives and Research Coordination

The principal objectives of project Phase 1 were:

(1) To develop GIS maps of important fish habitat features in Florida Bay, and methods for mapping anticipated changes in these features due to Restudy activities.

(2) To develop methods for analyzing and modeling fish habitat use utilizing synoptic fishery-independent survey data.

(3) To develop a methodology for applying fish habitat use models for evaluating spatial impacts of Restudy activities in Florida Bay.

(4) To develop a prototype decision support tool to facilitate evaluation of forecasted hydrological conditions on spatial fish habitats in Florida Bay.

This work was conducted by two collaborating teams of investigators from: (1) the Everglades National Park (ENP) by a team headed by Dr. William Perry, who was the project manager and a co-principal investigator; and (2) the University of Miami's Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS) by a team headed by Drs. Jerald Ault and Steven Smith, the project's principal investigators.

3.0 Habitat Mapping and Modeling

Geo-referenced physical and biological data for important environmental variables from Florida Bay were compiled from existing databases and transformed into geographic information system (GIS) layers using the ArcGIS software. Examples are shown for bathymetry (**Figure 1**) and bottom habitat type (**Figure 2**) Average monthly salinity values for 40 model-defined spatial regions of Florida Bay for the period 1991-2002 were obtained from outputs of the mass balance FATHOM hydrodynamic circulation model (Cosby et al. 2004). Salinity GIS layers were created for each year-month of the 1991-2002 time series. Example salinity maps for April 2001 (late dry season), June 2001 (early wet season), and September 2001 (wet season) are shown in **Figures 3**, **4**, and **5**, respectively. A composite digital habitat map was created by overlaying a 200 by 200 m grid layer on the Florida Bay domain (see **Figure 2**), and spatially interpolating values of bathymetry, bottom type, and salinity for each grid cell.

4.0 Fish Habitat Use Analysis

Everglades restoration projects will likely alter the salinity dynamics along the northern portion of Florida Bay adjacent to the mainland, i.e., the region most influenced by freshwater inflows. In turn, it is hypothesized that these alterations of freshwater inflows and resultant salinity regimes may potentially affect Florida Bay populations of fish and macroinvertebrate species that predominately utilize 'estuarine' habitats, characterized by salinities somewhat higher than 0 (freshwater) and somewhat lower than 35 (oceanic), for all or some portion of their lifespan, e.g., early juvenile, adult, etc.

To address these issues, utilizing fishery-independent survey data we evaluated two approaches for analyzing fish use of coastal bay habitats: (1) design-based estimation of habitat use, and (2) regression modeling of habitat use.

4.1 Data Sources

Spatially synoptic co-occurrent biological (species abundance, size composition) and environmental (bathymetry, bottom type, salinity) data from fishery-independent surveys were compiled for two southern Florida estuaries, Charlotte Harbor and Biscayne Bay. Comparable data for Florida Bay were not available at the outset of this study. Stratified random fishery-

independent surveys for Charlotte Harbor were conducted by Florida's Fish and Wildlife Research Institute (FWRI) (McMichael 1991). These surveys utilized a variety of sampling gears, including seines, trawls, and dropnets. Synoptic spatial coverage of Charlotte Harbor was carried out primarily with small-meshed gears (3 mm square mesh) that targeted smaller animals, usually less than 100 mm total length (TL) for principal species. Catch-per-unit-effort (CPUE) observations were inter-calibrated among sampling gears using a modified fishing power procedure (Robson 1966; Ault et al. 2002). Sampling was mostly conducted on a seasonal basis with emphasis on spring (March-May) and fall (September-November). Descriptions of habitat strata for the Charlotte Harbor sampling domain are given in **Table 1**. Sample sizes by habitat strata for Charlotte Harbor fall surveys during 1991-2000 are provided in **Table 2**.

Seasonal stratified random fishery-independent surveys for Biscayne Bay were conducted by UM-RSMAS utilizing a roller-frame trawl gear (Ault et al. 1999). Sampling was conducted at night and primarily targeted pink shrimp (*Farfantepenaeus duorarum*). The trawl gear (10 mm square mesh) also captured over 150 fish species, mostly targeting smaller size classes less than 200 mm. Descriptions of habitat strata for the Biscayne Bay sampling domain are given in **Table 3**. Sample sizes by habitat strata for Biscayne Bay seasonal surveys during 1996-2000 are provided in **Table 4**.

4.2 Design-Based Estimation of Habitat Use

Drawing upon resource selection theory (Manly et al. 1993), three measures of habitat use were estimated for a given habitat stratum: (1) probability of use $\overline{p}$, i.e., the proportion of habitat units (or sample units) occupied by at least one animal; (2) per unit amount of use, i.e., animal density D or CPUE; and (3) population amount of use, i.e., animal abundance Y. Sampling design-based procedures (Cochran 1977; Ault et al. 1999) were employed to estimate the mean and variance of each measure (**Table 5**). A formal test for habitat selection was made by comparing the population proportion $p(\hat{Y}_h)$ against the proportion of area $p(A_h)$ for a given habitat h. Estimates of stratum abundance $\hat{Y}_h$ were divided by domain-wide abundance $\hat{Y}_{st}$ to convert to population proportion $p(\hat{Y}_h)$. Statistical differences between $p(\hat{Y}_h)$ and $p(A_h)$ were evaluated with a confidence interval-based t-test, with outcomes interpreted as follows:

$$p(\hat{Y}_h) > p(A_h): \text{ positive habitat selection;}$$

$$p(\hat{Y}_h) = p(A_h): \text{ neutral selection;}$$
$$p(\hat{Y}_h) < p(A_h): \text{ negative selection.}$$

Example SAS program code for estimation of probability of use is given in **Appendix A-1**. Example SAS program code for estimation of per unit and population amount of use is given in **Appendix A-2**.

We illustrate this analysis approach for five fish-macroinvertebrate species that represent important forage and/or fishery species in southern Florida coastal bays: spotted seatrout (*Cynoscion nebulosus*), pink shrimp, pinfish (*Lagodon rhomboides*), gray snapper (*Lutjanus griseus*), and bluestriped grunt (*Haemulon sciurus*). Results for juvenile spotted seatrout (≤80 mm TL) in Charlotte Harbor during fall are given in **Figure 6** and **Table 6**. Both probability of use and per unit amount of use were higher in shallow, moderate salinity, vegetated habitats relative to other available habitats. Relatively low probability and per unit amount of use were evident in low salinity environments and at deeper depths. Of particular interest are habitats 3, 4, and 5 (**Table 1**), the principal shallow estuarine habitats of Charlotte Harbor. While these habitats account for about 20% of the available area, about 50% or more of the juvenile spotted seatrout population consistently resided in these habitats among survey years.

In Biscayne Bay, habitats along the western shoreline (SW, HW, and BWC; see **Table 3**) are the principal estuarine habitats. Both juvenile pink shrimp (<18 mm carapace width CW; **Figure 7**, **Table 7**) and pinfish (≤200 mm TL; **Figure 8**, **Table 8**) exhibited high probability of use, per unit amount of use, and positive selection for shallow, lower salinity, vegetated environments (SW) relative to other available habitats. Juvenile gray snapper exhibited high probability and per unit amount of use in vegetated habitats of both lower (SW) and moderate (SC) salinities. In contrast, juvenile bluestriped grunt (≤165 mm TL; **Figure 10**, **Table 10**) exhibited high probability and per unit amount of use in vegetated, near-oceanic salinity environments (SE) and mostly negative selection for estuarine habitats.

This analysis approach appears to be an effective method for identifying potential indicator species for evaluating Everglades restoration project impacts. Our results suggest that spotted seatrout, pink shrimp, pinfish, and to a lesser extent gray snapper would be good candidates for restoration project scenario testing, whereas bluestriped grunt would not be a good candidate.

4.3 Regression Modeling of Habitat Use

The relationship between animal abundance indices dependent on environmental habitat variables was analyzed using general multiple linear regression models of the form

$$y = b_0 + b_1 X_1 + b_2 X_2 + \cdots + b_k X_k + \varepsilon \qquad (1)$$

where the response variable is y, explanatory variables (i.e., habitat covariates) are $X_1, X_2, \ldots, X_k$, parameters to be estimated are the coefficients $b_0, b_1, \ldots, b_k$, and the additive error term is ε. We illustrate this approach for spotted seatrout (≤80 mm TL) CPUE in Charlotte Harbor during fall. To satisfy error assumptions of the generalized linear modeling procedure (McCullagh and Nelder 1989; Greene 1993; Neter et al. 1996), estimation was carried out in two stages: the first stage fit frequency of occurrence (presence-absence) data to a logistic regression model; and, second, the second stage fit non-zero CPUE observations, denoted as u, to a generalized linear regression model.

Single regression models were first developed for each separate habitat variable. Seatrout logistic regression models for habitat variables depth, bottom vegetation, salinity, and temperature are shown in **Figure 11**. For logistic regression, the response variable y is the logit function $\log[p/(1-p)]$, where p is the proportion of nonzero CPUEs. Positive CPUE regression functions for separate habitat variables are shown in **Figure 12**. For positive CPUE regression, the response variable was the natural logarithm of positive CPUE, $\log(u)$. We used polynomial functions (e.g., linear, quadratic, cubic) as a convenient method for describing nonlinear y-X relationships within the framework of general linear regression models (Neter et al. 1996). Logistic regression analysis of the logit(p)-salinity relationship revealed an abrupt decline at salinities below 1. This suggests that a minimum physiological threshold for salinity may occur between 0 and 1 for juvenile spotted seatrout. This abrupt discontinuity in the logit(p)-salinity relationship was modeled with a categorical variable with salinities below 1 designated as one category and all other salinities designated as a second category. A continuous function for logit(p)-salinity was then fit for salinities above 1.

Figure 13 illustrates the use of the two-stage procedure to satisfy the distributional assumptions of generalized linear regression modeling of CPUE-habitat data. CPUE observations from fishery-independent surveys commonly exhibit a highly skewed frequency distribution due to the high frequency of zero and low catches together with the low frequency of very high catches. Separating the CPUE observations into a presence-absence component yields

a discrete Bernoulli-binomial distribution appropriate for logistic regression. Eliminating the zero observations alleviates much of the skewness problem for constructing CPUE-habitat linear regression models, but the error residuals of positive CPUE models still usually exhibit asymmetric, non-normal frequency distributions. In many cases, as was the case for spotted seatrout, further log-transformation of the positive CPUE observations satisfies the normality assumption of model error residuals. The procedure for developing an overall predictive function for CPUE for two-stage regression models is illustrated in **Figure 14**. Predicted values of logit(p) from the logistic regression model are first back-transformed to obtain predicted values of p, the probability of occurrence. Likewise, predicted values of log(u) from the general linear regression model are back-transformed to obtain predicted values of u, positive CPUE. Multiplying predicted values of p and u yields the predicted CPUE as a function of habitat variables.

Taken together, the regression functions in **Figures 11** and **12** suggest that CPUE of juvenile spotted seatrout is higher in vegetated compared to non-vegetated substrates, in shallower vs. deeper depths, and in moderate vs. high or low salinities. These results corroborate the findings of design-based habitat use analysis shown in **Table 6** and **Figure 6**. Functions involving the habitat covariate temperature exhibited generally increasing relationships for both logit(p) and log(u) response variables; however, there was little spatial variation in temperature in Charlotte Harbor at a given time period. The regression models are likely describing a within-season time change in the abundance of spotted seatrout during the fall season (September to November), during which the influx of new recruits to the juvenile life stage (≤80 mm TL) is minimal whereas animals are growing out of this life stage as well as dying, leading to a decline in abundance through the season that corresponds to a decrease in water temperature.

Single regression functions for logit(p) and log(u) were then combined into respective multiple habitat variable models. Example SAS program code for developing logistic regression models of fish habitat use is given in **Appendix A-3**. Example SAS program code for developing positive CPUE regression models of fish habitat use is given in **Appendix A-4**. Backward selection was employed to eliminate non-significant regression coefficients to arrive at final models for both logit(p) and log(u) (**Table 11**). Note that for polynomial regression functions, the highest-order significant term is included for a given habitat variable as well as all lower-order terms irrespective of their significance. Quadratic functions for salinity and linear

functions for temperature were incorporated into both the log(u) and logit(p) models. Interestingly, depth was not included in the log(u) model, but was described by a quadratic polynomial in the logit(p) model. This suggests that depth mainly affects the probability of use but not the per unit amount of use of juvenile spotted seatrout in Charlotte Harbor during fall. The regression analysis approach enables elucidation of influential habitat variables in explaining the variation of both the probability of use p and per unit amount of use CPUE. Moreover, these models provided quantitative functional relationships between measures of habitat use and influential habitat variables.

5.0 Models of Fish Habitat Suitability in Florida Bay

A method was developed for predicting fish habitat suitability in Florida Bay using the two-stage animal-habitat regression models described above. We illustrate this procedure for juvenile spotted seatrout (**Table 11**). The models were initially applied to the full range of environmental conditions for Florida Bay with respect to the principal habitat variables depth, bottom type, and salinity to examine the possible range of predicted CPUE values. The salinity range for the models was extended beyond the upper bound of 36.5 for Charlotte Harbor conditions to predict CPUEs in the hypersaline conditions found in Florida Bay. Near-zero CPUEs were predicted at a salinity of 44, and this was set as the upper bound of salinity in the model. A habitat suitability index (HSI) value was computed as

$$HSI = \frac{\hat{CPUE}}{\max(\hat{CPUE})} \qquad (2)$$

in which model-predicted $\hat{CPUE}$ is scaled to the global maximum model-predicted $\hat{CPUE}$ for Florida Bay environmental conditions. Values of HSI thus range from 0 to 1 and represent relative per unit amount of habitat use. Maximum values of HSI in Florida Bay are predicted to occur in shallow, vegetated substrates within a salinity range of 15.5 to 18.2 (**Table 12**). Likewise, high values of HSI above 0.9 are predicted to occur in moderately shallow, vegetated substrates within a salinity range of 10.4 to 23.3. Very low values of HSI below 0.1 are predicted to occur in either very low or above-oceanic salinities and in deeper, non-vegetated substrates.

Habitat use maps for Florida Bay were developed by predicting HSI values for each 200 by 200 m grid cell of the digital composite habitat map. Example maps of juvenile spotted

seatrout HSI are shown for June 2001 and September 2001 in **Figures 15** and **16**, respectively. These correspond to the FATHOM model-predicted salinity maps of **Figures 4** and **5**. Predicted HSI values were generally low in June 2001 during the early portion of the wet season in which salinities were predicted to be generally high throughout Florida Bay. In contrast, HSI values were predicted to be fairly high in many portions of the Bay in September 2001 where salinities were predicted to be more or less 'estuarine' during the middle of the wet season.

Two metrics were developed to provide Bay-wide summary measures of habitat suitability. The first was computed by summing predicted HSI values for all grid cells *i* in the digital composite habitat map,

$$HSAI = \sum_i HSI_i \qquad (3)$$

where HSAI is termed the habitat suitability abundance index, a relative measure of population abundance. Estimated monthly values of HSAI for juvenile spotted seatrout for June through November 2001 are given in **Table 13**. This six-month time frame corresponds to the period when the juvenile life stage (≤80 mm TL) of spotted seatrout is present in southern Florida coastal bays (peak spawning for this species occurs in late spring and summer; Rutherford 1982). The estimated age of this life stage is ≤4 months (McMichael and Peters 1989). For 2001, values of HSAI were lowest in June and July, and then progressively increased from August to November, generally tracking the monthly changes in salinity conditions from high to hypersaline in June to low salinities in November at the end of the wet season.

A second summary metric of habitat suitability was computed by multiplying grid cell HSI values over a selected time period, t=1, 2,…,m, and then summing these products over all grid cells *i* in the habitat map:

$$HSCI = \sum_i \left(\prod_{t=1}^{t=m} HSI_{it} \right) \qquad (4)$$

where HSCI is termed the habitat suitability composite index. For application to juvenile spotted seatrout, HSCI was computed for cohorts recruiting in June, July, and August and presumed to occupy Florida Bay habitats for a 4-month time period (**Table 14**). HSCI is thus computed in a similar fashion to survivorship over a specified time interval. Our results suggest that late-season (August) recruits in 2001 would have experienced more favorable habitat conditions, i.e., low to moderate salinities, compared to early-season recruits (June) during the juvenile life stage.

6.0 Prototype Decision Support Process

A prototype decision support process was developed to facilitate scenario-testing of restoration impacts on Florida Bay fish habitats and populations. The flow diagram for the prototype version is shown in **Figure 17**. A SAS program (**Appendix A-5**) reads in a datafile (format .dbf) of FATHOM model-predicted monthly salinities for Florida Bay and a datafile (format .dbf) of the Florida Bay digital composite habitat map produced by ArcGIS. The SAS program computes the regression model-predicted HSI map grid for specified monthly time periods, as well as the summary metrics HSAI and HSCI described above. The HSI map grids and summary metrics are output to Excel files (format .xls). Map grid files are modified if necessary and subsequently output from Excel (format .dbf) to ArcGIS for development and display of predicted HSI maps. Excel is also used to develop and display tables and graphs of habitat suitability summary metrics.

7.0 Next Steps in the Research

A suite of mapping, analysis, and modeling methods were developed in project Phase1 for evaluating spatial effects of Everglades restoration activities on populations of fish and macroinvertebrates, and their habitats in Florida Bay. The next research phase will likely include the following steps:

(1) application of design-based habitat use analysis to identify the full set of fish and macroinvertebrate indicator species for restoration scenario testing;

(2) development of two-stage animal-habitat regression models for indicator species, and application of these models for analyzing potential effects of restoration on habitat suitability metrics;

(3) refinement and enhancement of the decision support tool;

(4) development of a statistical sampling design and implementation of fishery-independent monitoring surveys for indicator species in Florida Bay; and,

(5) comparison of the decision support process to include metrics identified above that allow a flexible quantitative evaluation of Everglades restoration effects.

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Table 1. Habitat strata descriptions for Charlotte Harbor fishery-independent surveys during fall (database source: FWRI Fishery Independent Monitoring Program).

Habitat Class	Description	Habitat Area (km^2)
1	Salinity <1	5.52
2	Salinity 1-8	12.37
3	Salinity 8-28, depth <1.5 m, non-vegetated	58.41
4	Salinity 8-28, depth <0.5 m, SAV	30.08
5	Salinity 8-28, depth 0.5-1.5 m, SAV	26.57
6	Salinity 8-28, depth 1.5-3.0 m	123.33
7	Salinity 28-36.5; depth <1.5 m and non-vegetated, or depth 1.5-3.0 m all substrates	72.98
8	Salinity 28-36.5, depth <0.5 m, SAV	31.81
9	Salinity 28-36.5, depth 0.5-1.5 m, SAV	23.62
10	Depth >3.0 m	145.26
Total		529.95

Table 2. Sample sizes by habitat strata for Charlotte Harbor fishery-independent surveys during fall in years 1991-2000(database source: FWRI Fishery Independent Monitoring Program). Habitat descriptions are given in Table 1.

Habitat Class	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000
1	9	9	2	13	34	19	60	72	1	9
2	12	14	16	15	19	32	60	30	31	17
3	14	16	12	8	36	25	36	25	25	30
4	5	3	13	10	13	4	13	15	4	6
5	25	25	28	29	33	37	21	30	22	19
6	12	13	20	17	43	17	21	19	20	18
7	9	13	3	5	5	6	10	4	9	8
8	3	7	7	4	5	7	5	3	3	3
9	16	14	5	18	4	16	16	4	12	16
10	21	21	24	25	29	12	12	9	5	6
Total	126	135	130	144	221	175	254	211	132	132

Table 3. Habitat strata descriptions for Biscayne Bay fishery-independent seasonal surveys during 1996-2000 (source: Ault et al. 1999).

Habitat Code	Description	Area (km^2)
SW	Seagrass, western Bay, depth 1-2 m	81.19
SC	Seagrass, central Bay, depth >2 m	192.00
SE	Seagrass, eastern Bay, depth 1-2 m	25.31
HW	Hardbottom, western Bay, depth 1-2 m	31.49
HCE	Hardbottom, central & eastern Bay, depth >1 m	30.07
BWC	Bare (not vegetated) substrate, western & central Bay, depth >1 m	20.33
BE	Bare substrate, eastern Bay, depth 1-2 m	5.84
Total		386.23

Table 4. Sample sizes by habitat strata for Biscayne Bay fishery-independent seasonal surveys during 1996-2000 (database source: Ault et al. 1999, 2001). Habitat code descriptions are given in Table 3.

Habitat Code	Spring 1996	Summer 1996	Fall 1996	Spring 1997	Summer 1997	Fall 1997	Fall 1999	Spring 2000
SW	23	18	32	43	57	34	31	38
SC	47	25	74	52	64	53	64	52
SE	10	15	9	7	8	11	6	1
HW	6	6	11	5	4	8	9	4
HCE	12	10	13	6	9	5	6	12
BWC	12	11	9	6	4	9	3	3
BE	4	8	2	3	5	0	0	0
Total	114	93	150	122	151	120	119	110

Table 5. Variable definitions and computational formulas for stratified random sampling design estimation.

Symbol	Definition	Computational Formula
H	Stratum subscript	
J	Sample unit subscript	
A_h	Area of stratum h	
A	Area of entire survey domain	$A = \sum_h A_h$
T_{hj}	Area of jth sample unit in stratum h	
N_h	Total number of sample units in stratum h	$N_h = \frac{A_h}{T_{hj}}$
N	Total number of sample units in survey domain	$N = \sum_h N_h$
n_h	Number of sampled units j in stratum h	
f_h	Sampling fraction for stratum h	$f_h = \frac{n_h}{N_h}$
w_h	Stratum h weighting factor	$w_h = \frac{N_h}{N}$
y_{hj}	Presence (y=1) or absence (y=0) for sample unit j in stratum h	
$\overline{p}_h$	Mean proportion of non-zero units j in stratum h	$\overline{p}_h = \frac{\sum_j y_{hj}}{n_h}$
$\mathrm{var}(\overline{p}_h)$	Variance of mean proportion of non-zero sample units in stratum h	$(1-f_h)\frac{p_h(1-p_h)}{n_h-1}$
$\overline{p}_{st}$	Domain-wide mean proportion of non-zero sample units for a stratified random survey	$\overline{p}_{st} = \sum_h w_h \overline{p}_h$
$\mathrm{var}(\overline{p}_{st})$	Variance of domain-wide mean proportion of non-zero sample units for a stratified random survey	$\mathrm{var}(\overline{p}_{st}) = \sum_h w_h^2 \,\mathrm{var}(\overline{p}_h)$

Table 5. (cont.)

Symbol	Definition	Computational Formula
D_{hj}	Density (number of individuals per sample unit) or catch per unit effort (CPUE) in sample unit *j* in stratum *h*	
$\overline{D}_h$	Mean density in stratum *h*	$\overline{D}_h = \frac{1}{n_h}\sum_j D_{hj}$
$\text{var}(\overline{D}_h)$	Variance of mean density in stratum *h*	$\text{var}(\overline{D}_h) = (1 - f_h)\frac{\sum_j (D_{hj} - \overline{D}_h)^2}{n_h(n_h - 1)}$
$\overline{D}_{st}$	Domain-wide mean density for a stratified random survey	$\overline{D}_{st} = \sum_h w_h \overline{D}_h$
$\text{var}(\overline{D}_{st})$	Variance of domain-wide mean density for a stratified random survey	$\text{var}(\overline{D}_{st}) = \sum_h w_h^2 \text{var}(\overline{D}_h)$
$\hat{Y}_h$	Abundance (number of animals) in stratum *h*	$\hat{Y}_h = N_h \overline{D}_h$
$\text{var}(\hat{Y}_h)$	Variance of abundance in stratum *h*	$\text{var}(\hat{Y}_h) = N_h^2 \text{var}(\overline{D}_h)$
$\hat{Y}_{st}$	Domain-wide abundance for a stratified random survey	$\hat{Y}_{st} = \sum_h \hat{Y}_h$
$\text{var}(\hat{Y}_{st})$	Variance of domain-wide abundance for a stratified random survey	$\text{var}(\hat{Y}_{st}) = \sum_h \text{var}(\hat{Y}_h)$
SE( )	Standard error of an estimate; computed by taking square root of variance of an estimate.	

Table 6. Spotted seatrout (≤80 mm TL) habitat selection in Charlotte Harbor during fall for years 1991, 1992, and 1996 (database source: FWRI Fishery Independent Monitoring Program). See Table 1 for habitat descriptions; p(A) is proportion of baywide area in a given habitat; p(Y) is proportion of total seatrout population in a given habitat; LCI and UCI are respective lower and upper 95% confidence intervals.

Year	Habitat Class	p(A)	p(Y)	LCI_p(Y)	UCI_p(Y)	Habitat Selection
1991	1	1.04%	0.00%	0.00%	0.00%	negative
1991	2	2.34%	2.09%	-1.49%	5.66%	neutral
1991	3	11.02%	28.85%	14.49%	43.21%	positive
1991	4	5.68%	10.78%	-1.82%	23.38%	neutral
1991	5	5.01%	28.88%	8.47%	49.28%	positive
1991	6	23.27%	2.24%	-2.69%	7.18%	negative
1991	7	13.77%	2.59%	-3.38%	8.56%	negative
1991	8	6.00%	11.88%	-14.48%	38.23%	neutral
1991	9	4.46%	12.70%	5.50%	19.90%	positive
1991	10	27.41%	0.00%	0.00%	0.00%	negative
1992	1	1.04%	0.15%	-0.08%	0.37%	negative
1992	2	2.34%	2.21%	0.03%	4.39%	neutral
1992	3	11.02%	15.18%	3.22%	27.15%	neutral
1992	4	5.68%	7.24%	-10.63%	25.12%	neutral
1992	5	5.01%	23.24%	11.28%	35.21%	positive
1992	6	23.27%	19.67%	-7.01%	46.35%	neutral
1992	7	13.77%	2.19%	-2.58%	6.96%	negative
1992	8	6.00%	18.60%	-15.04%	52.23%	neutral
1992	9	4.46%	11.52%	1.51%	21.54%	neutral
1992	10	27.41%	0.00%	0.00%	0.00%	negative
1996	1	1.04%	0.36%	-0.40%	1.12%	neutral
1996	2	2.34%	6.24%	-1.05%	13.53%	neutral
1996	3	11.02%	2.90%	-3.09%	8.89%	negative
1996	4	5.68%	3.50%	-7.64%	14.64%	neutral
1996	5	5.01%	59.41%	25.19%	93.63%	positive
1996	6	23.27%	0.00%	0.00%	0.00%	negative
1996	7	13.77%	0.00%	0.00%	0.00%	negative
1996	8	6.00%	11.35%	-0.92%	23.62%	neutral
1996	9	4.46%	16.24%	2.28%	30.20%	neutral
1996	10	27.41%	0.00%	0.00%	0.00%	negative

Table 7. Pink shrimp (<18 mm CW) habitat selection in Biscayne Bay during fall, spring, and summer seasons (database source: FWRI Fishery Independent Monitoring Program). See Table 3 for habitat descriptions; p(A) is proportion of baywide area in a given habitat; p(Y) is proportion of total pink shrimp population in a given habitat; LCI and UCI are respective lower and upper 95% confidence intervals.

Season	Habitat Code	p(A)	p(Y)	LCI_p(Y)	UCI_p(Y)	Habitat Selection
Fall	SW	21.22%	44.55%	32.88%	56.23%	positive
	SC	49.16%	41.57%	28.19%	54.94%	neutral
	SE	6.66%	4.34%	-3.18%	11.87%	neutral
	HW	8.34%	5.15%	2.99%	7.32%	negative
	HCE	7.89%	2.48%	0.97%	3.99%	negative
	BWC	5.19%	1.78%	0.19%	3.37%	negative
	BE	1.56%	0.13%	-0.78%	1.03%	negative
Spring	SW	21.19%	46.10%	35.79%	56.42%	positive
	SC	50.09%	43.15%	27.40%	58.89%	neutral
	SE	6.57%	0.71%	-0.63%	2.05%	negative
	HW	8.03%	5.99%	1.39%	10.60%	neutral
	HCE	7.77%	2.70%	1.03%	4.37%	negative
	BWC	5.24%	1.15%	0.02%	2.29%	negative
	BE	1.12%	0.20%	-0.32%	0.71%	negative
Summer	SW	21.04%	37.20%	26.33%	48.06%	positive
	SC	49.79%	46.20%	33.06%	59.34%	neutral
	SE	6.53%	1.76%	-1.19%	4.71%	negative
	HW	8.20%	7.67%	1.56%	13.77%	neutral
	HCE	7.49%	2.47%	0.43%	4.52%	negative
	BWC	5.36%	3.45%	0.66%	6.23%	neutral
	BE	1.60%	1.27%	-0.11%	2.65%	neutral

Table 8. Pinfish (≤200 mm TL) habitat selection in Biscayne Bay during fall, spring, and summer seasons (source: Ault et al. 1999, 2001). See Table 3 for habitat descriptions; p(A) is proportion of baywide area in a given habitat; p(Y) is proportion of total pinfish population in a given habitat; LCI and UCI are respective lower and upper 95% confidence intervals.

Season	Habitat Code	p(A)	p(Y)	LCI_p(Y)	UCI_p(Y)	Habitat Selection
Fall	SW	21.22%	62.51%	14.23%	110.80%	neutral
	SC	49.16%	31.72%	16.04%	47.40%	negative
	SE	6.66%	0.95%	-1.15%	3.05%	negative
	HW	8.34%	3.59%	-1.12%	8.30%	negative
	HCE	7.89%	0.42%	-0.19%	1.04%	negative
	BWC	5.19%	0.81%	-0.61%	2.23%	negative
	BE	1.56%	0.00%	0.00%	0.00%	negative
Spring	SW	21.19%	66.85%	33.26%	100.44%	positive
	SC	50.09%	21.51%	9.49%	33.52%	negative
	SE	6.57%	0.67%	-1.03%	2.36%	negative
	HW	8.03%	6.94%	-10.81%	24.68%	neutral
	HCE	7.77%	3.11%	-1.21%	7.43%	negative
	BWC	5.24%	0.87%	-1.00%	2.75%	negative
	BE	1.12%	0.05%	-0.21%	0.32%	negative
Summer	SW	21.04%	65.25%	21.63%	108.88%	positive
	SC	49.79%	29.82%	3.61%	56.02%	neutral
	SE	6.53%	0.38%	-0.06%	0.81%	negative
	HW	8.20%	4.02%	-3.50%	11.54%	neutral
	HCE	7.49%	0.05%	-0.07%	0.17%	negative
	BWC	5.36%	0.44%	-0.64%	1.53%	negative
	BE	1.60%	0.04%	-0.04%	0.12%	negative

Table 9. Gray snapper (≤165 mm TL) habitat selection in Biscayne Bay during fall, spring, and summer seasons (source: Ault et al. 1999, 2001). See Table 3 for habitat descriptions; p(A) is proportion of baywide area in a given habitat; p(Y) is proportion of total gray snapper population in a given habitat; LCI and UCI are respective lower and upper 95% confidence intervals.

Season	Habitat Code	p(A)	p(Y)	LCI_p(Y)	UCI_p(Y)	Habitat Selection
Fall	SW	21.22%	26.66%	9.46%	43.87%	neutral
	SC	49.16%	60.71%	28.69%	92.74%	neutral
	SE	6.66%	9.34%	-13.98%	32.67%	neutral
	HW	8.34%	0.87%	-1.56%	3.29%	negative
	HCE	7.89%	0.91%	-1.61%	3.43%	negative
	BWC	5.19%	1.51%	-3.37%	6.38%	neutral
	BE	1.56%	0.00%	0.00%	0.00%	negative
Spring	SW	21.19%	30.42%	8.28%	52.55%	neutral
	SC	50.09%	58.98%	21.54%	96.43%	neutral
	SE	6.57%	5.09%	-8.28%	18.45%	neutral
	HW	8.03%	2.64%	-6.34%	11.62%	neutral
	HCE	7.77%	1.50%	-2.47%	5.47%	negative
	BWC	5.24%	1.38%	-4.45%	7.20%	neutral
	BE	1.12%	0.00%	0.00%	0.00%	negative
Summer	SW	21.04%	34.81%	19.92%	49.69%	neutral
	SC	49.79%	59.85%	22.81%	96.88%	neutral
	SE	6.53%	1.73%	-2.72%	6.19%	negative
	HW	8.20%	2.42%	-3.07%	7.90%	negative
	HCE	7.49%	1.20%	-1.55%	3.95%	negative
	BWC	5.36%	0.00%	0.00%	0.00%	negative
	BE	1.60%	0.00%	0.00%	0.00%	negative

Table 10. Bluestriped grunt (≤165 mm TL) habitat selection in Biscayne Bay during fall, spring, and summer seasons (source: Ault et al. 1999, 2001). See Table 3 for habitat descriptions; p(A) is proportion of baywide area in a given habitat; p(Y) is proportion of total bluestriped grunt population in a given habitat; LCI and UCI are respective lower and upper 95% confidence intervals.

Season	Habitat Code	p(A)	p(Y)	LCI_p(Y)	UCI_p(Y)	Habitat Selection
Fall	SW	21.22%	13.23%	5.31%	21.14%	negative
	SC	49.16%	41.95%	23.87%	60.04%	neutral
	SE	6.66%	40.02%	-51.30%	131.33%	neutral
	HW	8.34%	1.69%	-1.04%	4.42%	negative
	HCE	7.89%	1.41%	-1.00%	3.81%	negative
	BWC	5.19%	1.71%	-0.62%	4.03%	negative
	BE	1.56%	0.00%	0.00%	0.00%	negative
Spring	SW	21.19%	21.65%	9.80%	33.49%	neutral
	SC	50.09%	55.87%	29.43%	82.32%	neutral
	SE	6.57%	11.97%	-12.77%	36.72%	neutral
	HW	8.03%	1.89%	-2.56%	6.34%	negative
	HCE	7.77%	7.67%	-3.20%	18.54%	neutral
	BWC	5.24%	0.72%	-1.47%	2.91%	negative
	BE	1.12%	0.23%	-0.91%	1.36%	neutral
Summer	SW	21.04%	9.21%	4.76%	13.65%	negative
	SC	49.79%	67.22%	41.56%	92.87%	neutral
	SE	6.53%	18.54%	-3.65%	40.74%	neutral
	HW	8.20%	2.20%	-2.52%	6.93%	negative
	HCE	7.49%	0.75%	-0.50%	2.01%	negative
	BWC	5.36%	1.26%	-1.52%	4.05%	negative
	BE	1.60%	0.82%	-0.36%	1.99%	neutral

Table 11. Animal-habitat multiple regression model summary for spotted seatrout (≤80 mm TL) in Charlotte Harbor during fall (database source: FWRI Fishery Independent Monitoring Program).

Multiple Regression Summary, nonzero CPUE

error pdf: normal

Explanatory Variables

Symbol	Description	Prediction Range
BV	bottom vegetation	N or V
S	salinity	0-36.5
T	temperature (C)	15.5-33.0 C

Final Model Parameters

Parameter	Description	Estimate	SE	p-value
b0	Intercept	-0.50027	0.49940	0.3170
b1	coeff for BV=V	0.14887	0.07039	0.0349
b2	coeff for BV=N	-0.14887	0.07039	0.0349
b3	coeff for S	0.04648	0.02393	0.0527
b4	coeff for S*S	-0.00146	0.00061	0.0170
b5	coeff for T	0.04378	0.01655	0.0084

Prediction Equations

Let y=logu

For BV=V: y=b0+b1+b3*S+b4*(S*S)+b5*T

For BV=N: y=b0+b2+b3*S+b4*(S*S)+b5*T

u=exp(y)

Multiple Logistic Regression Summary, presence-absence

Explanatory Variables

Symbol	Description	Prediction Range
BV	bottom vegetation	N or V
D	depth (m)	0-3.5 m; set D=3.5 for D>3.5m
S	salinity	<1.0, 1-36.5
T	temperature (C)	15.5-33.0 C

Final Model Parameters

Parameter	Description	Estimate	SE	p-value
b0	Intercept	-3.7594	0.6129	<0.0001
b1	coeff for S<1.0	-1.1248	0.1618	<0.0001
b2	coeff for BV=V	0.7116	0.0833	<0.0001
b3	coeff for BV=N	-0.7116	0.0833	<0.0001
b4	coeff for D	0.7633	0.4478	0.0883
b5	coeff for D*D	-0.6166	0.1606	0.0001
b6	coeff for S	0.1297	0.0293	<0.0001
b7	coeff for S*S	-0.0036	0.0008	<0.0001
b8	coeff for T	0.0998	0.0204	<0.0001

Prediction Equations

For S<1, BV=V: y=b0+b1+b2+b4*D+b5*(D*D)+b8*T

For S<1, BV=N: y=b0+b1+b3+b4*D+b5*(D*D)+b8*T

For S>1, BV=V: y=b0+b2+b4*D+b5*(D*D)+b6*S+b7*(S*S)+b8*T

For S>1, BV=N: y=b0+b3+b4*D+b5*(D*D)+b6*S+b7*(S*S)+b8*T

p=exp(y)/(1+exp(y))

Table 12. Environmental conditions in Florida Bay with respect to bottom vegetation (V is vegetated, N is non-vegetated), depth, and salinity corresponding to high and low model-predicted values of habitat suitability (HSI) for juvenile spotted seatrout (≤80 mm TL).

Bottom Vegetation	Depth (m)	Salinity range for HSI = 1.00	Salinity range for HSI = 0.90-0.99	Salinity range for HSI < 0.10
V	0.5	15.5 - 18.2	10.4-15.4, 18.3-23.3	>43.0
V	1.0	n/a	11.3 - 22.5	>42.7
V	1.5	n/a	n/a	>41.3
V	2.0	n/a	n/a	<1.0, >38.4
N	0.5	n/a	n/a	<1.0, >35.5
N	1.0	n/a	n/a	<1.0, >35.1
N	1.5	n/a	n/a	<1.8, >32.8
N	2.0	n/a	n/a	<6.9, >27.8

Table 13. Model-predicted values of the Habitat Suitability Abundance Index (HSAI) for juvenile spotted seatrout (≤80 mm TL) in Florida Bay during the period June to November 2001.

Year	Month	HSAI
2001	June	4444
2001	July	4775
2001	August	9140
2001	September	14037
2001	October	18927
2001	November	20918

Table 14. Model-predicted values of the Habitat Suitability Composite Index (HSCI) for spotted seatrout in Florida Bay for several 4-month time intervals in 2001 for the juvenile life stage (≤80 mm TL) corresponding to early- (Jun), mid- (Jul), and late-recruiting (Aug) cohorts.

Juvenile Life Stage Time Interval	HSCI
Jun-Sep 2001	117
Jul-Oct 2001	525
Aug-Nov 2001	2285

Figure 1. Bathymetry map of Florida Bay.

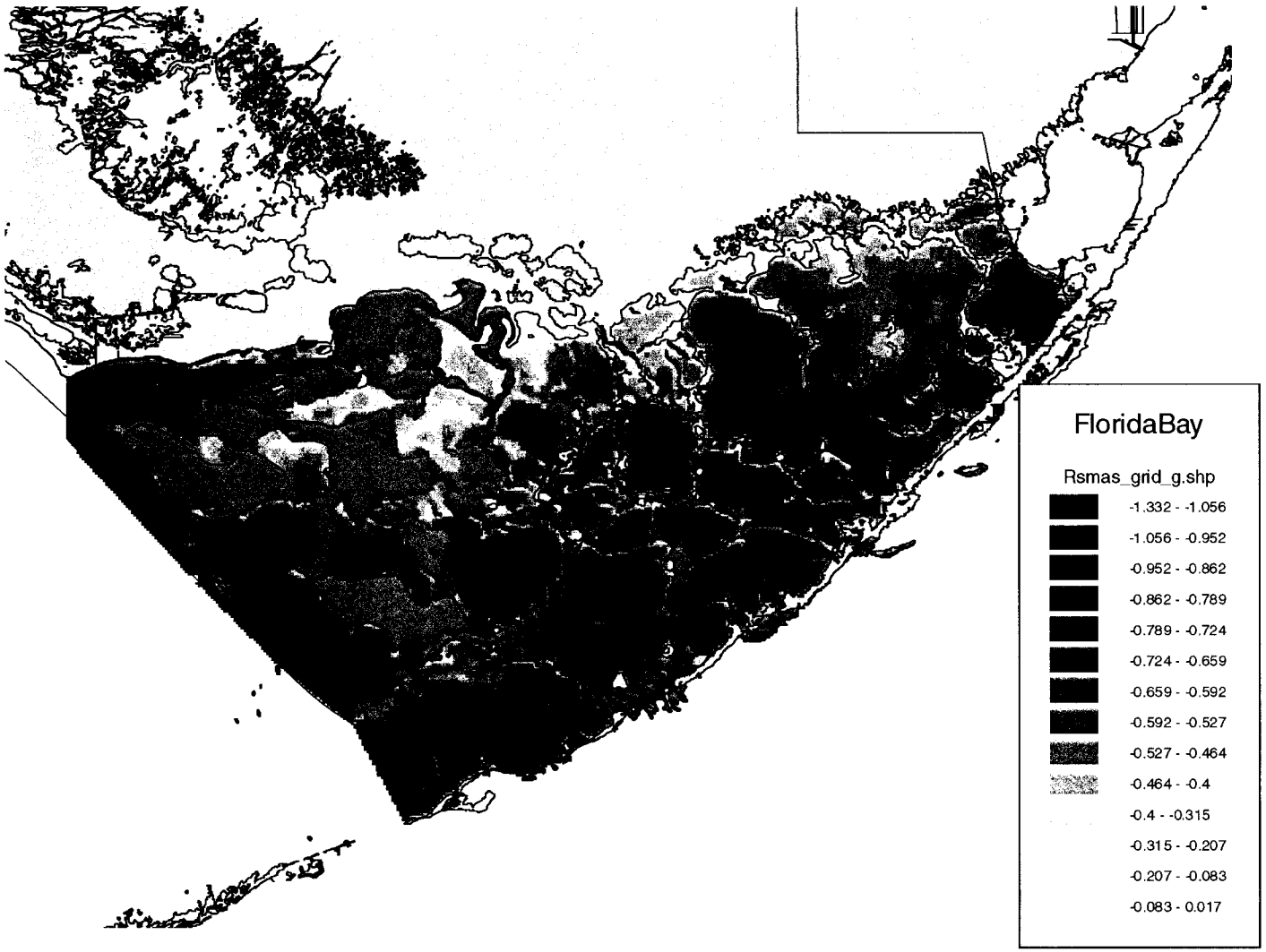


Figure 2. Map of Florida Bay bottom type; also shown is the 200 by 200 m model grid.

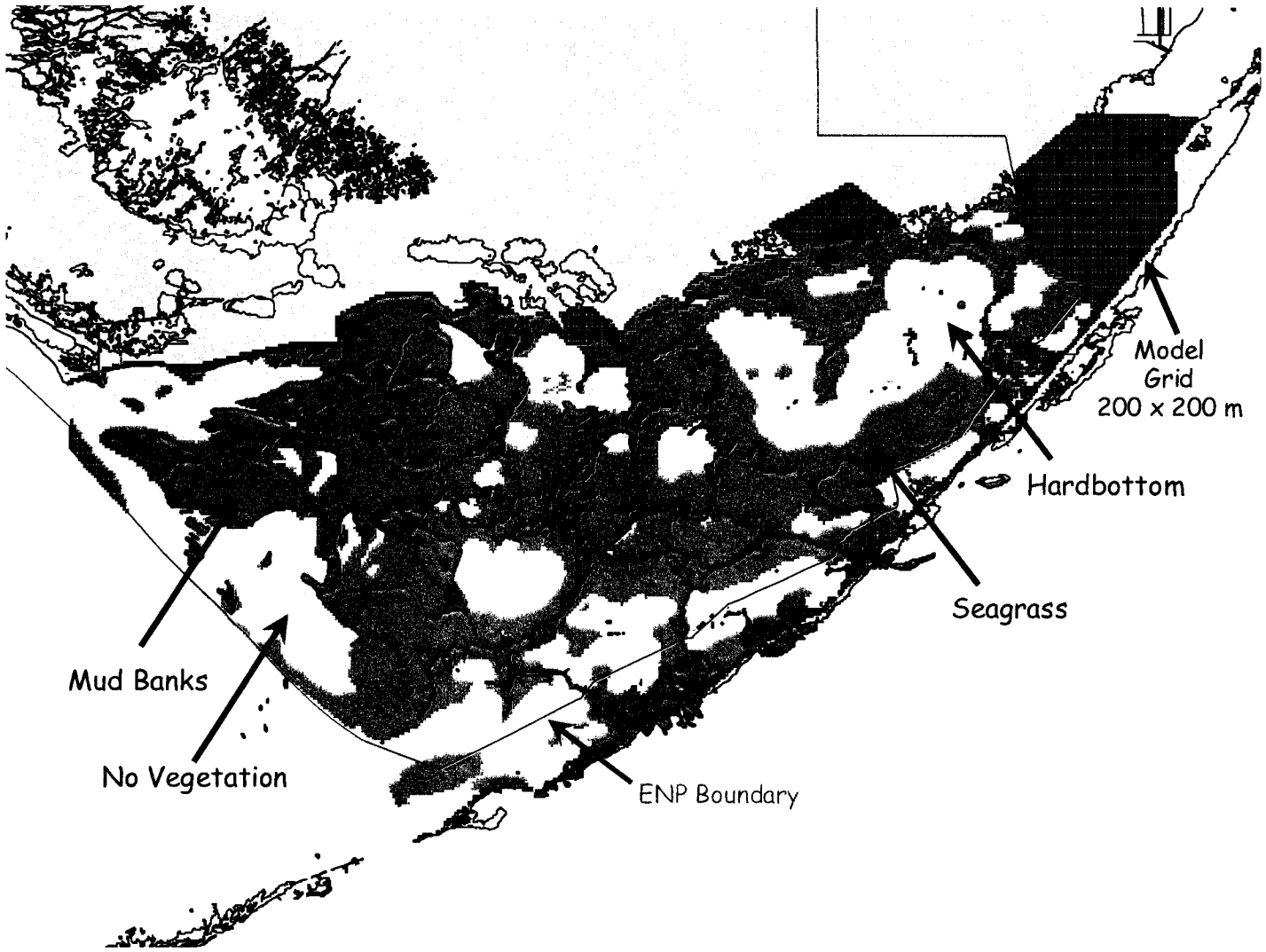


Figure 3. April 2001 salinities for Florida Bay based on FATHOM simulations.

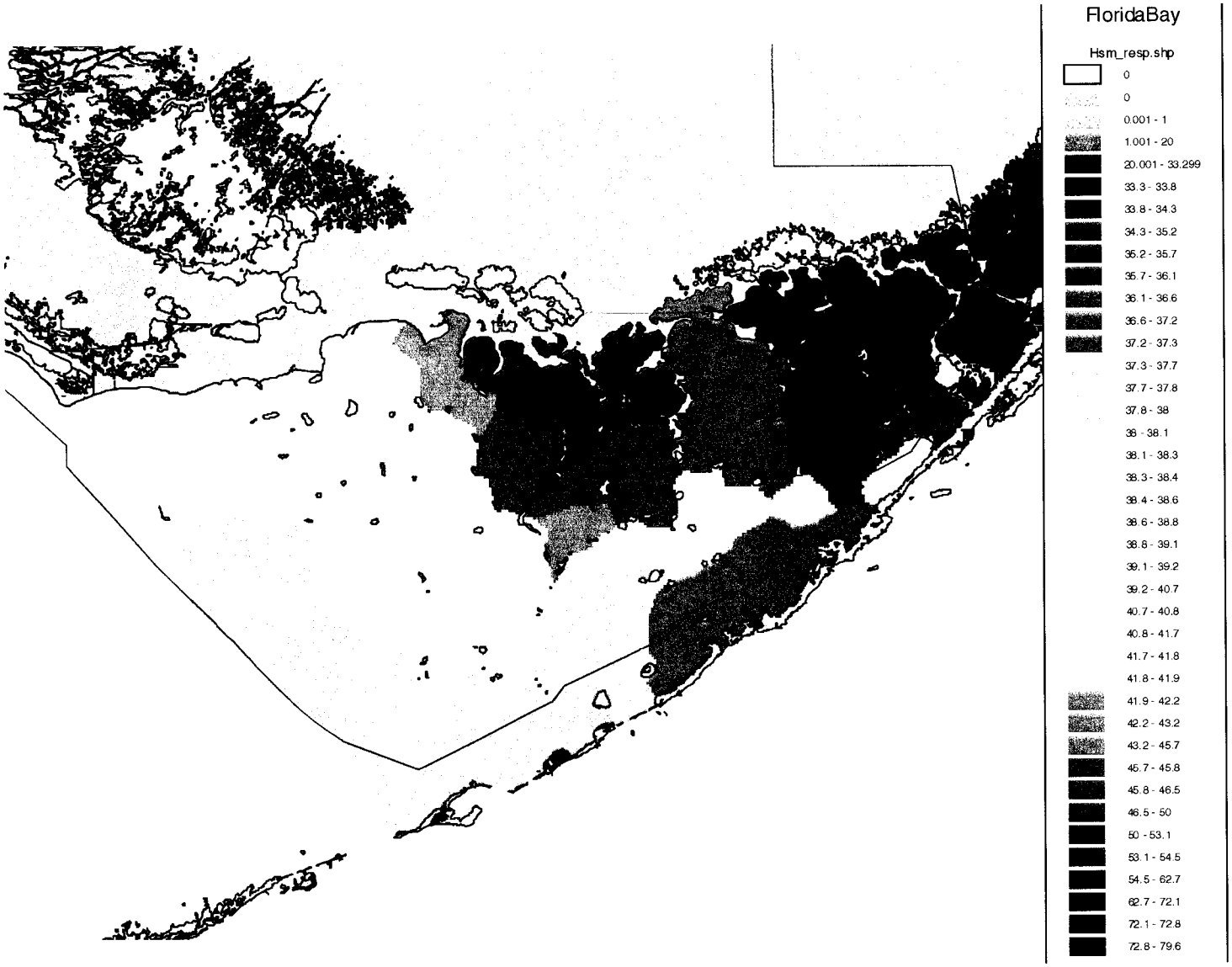


Figure 4. June 2001 salinities for Florida Bay based on FATHOM simulations.

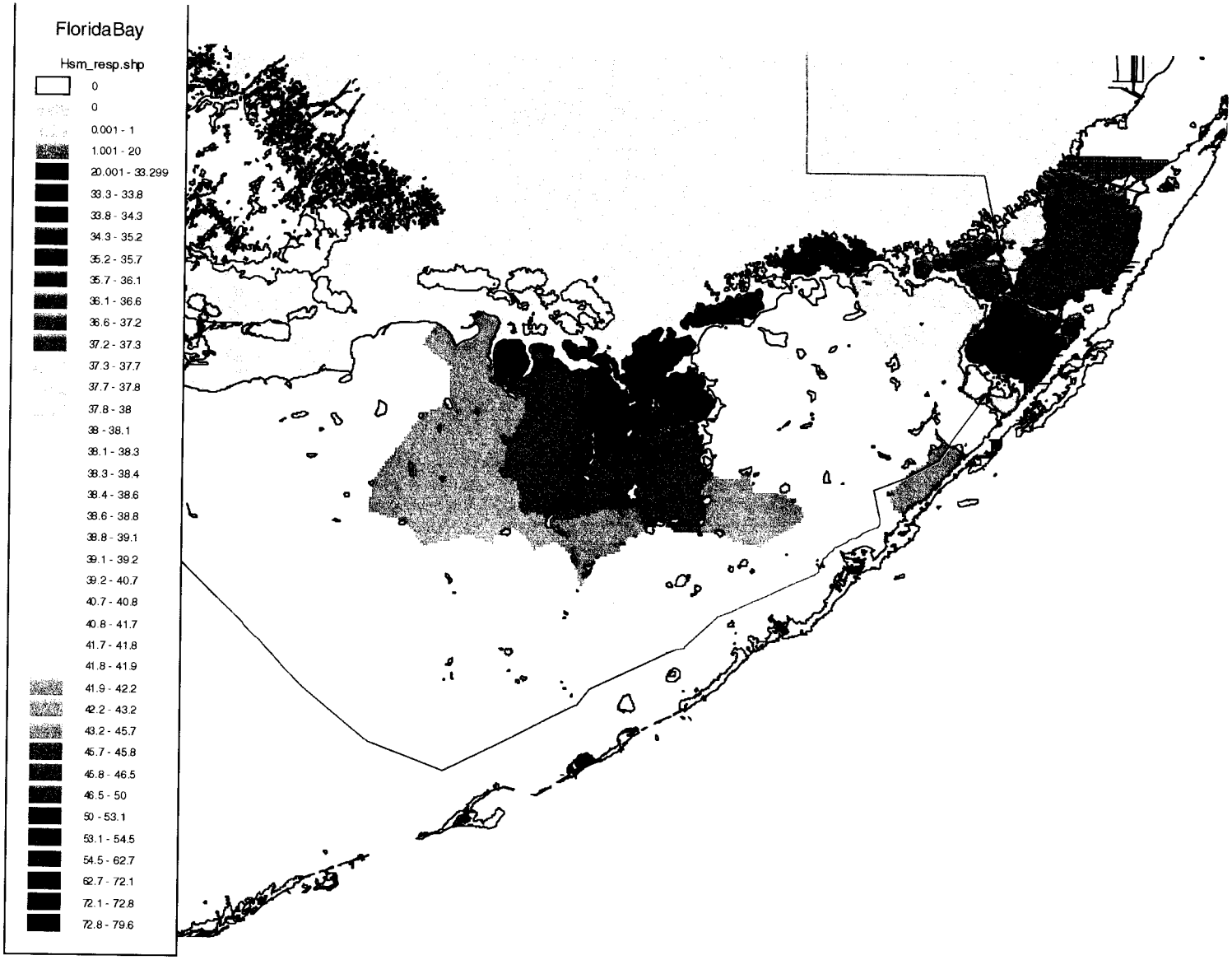


Figure 5. September 2001 salinities for Florida Bay based on FATHOM simulations.

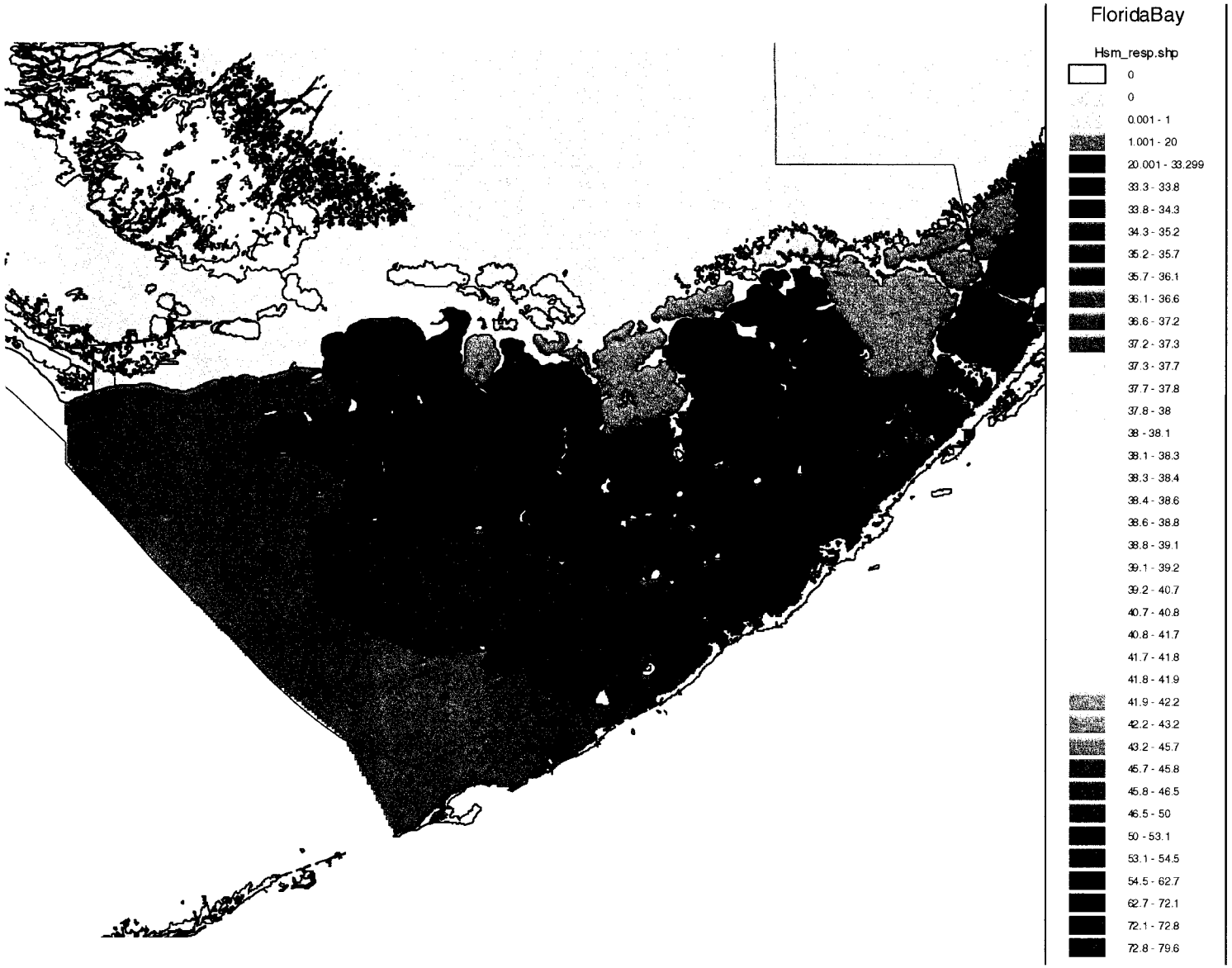


Figure 6. Spotted seatrout (≤80 mm TL) probability of use (left panels) and per-unit amount of use (right panels) among habitats in Charlotte Harbor for several fall surveys (database source: FWRI Fishery Independent Monitoring Program). Dashed lines denote domain-wide means. See Table 1 for habitat descriptions.

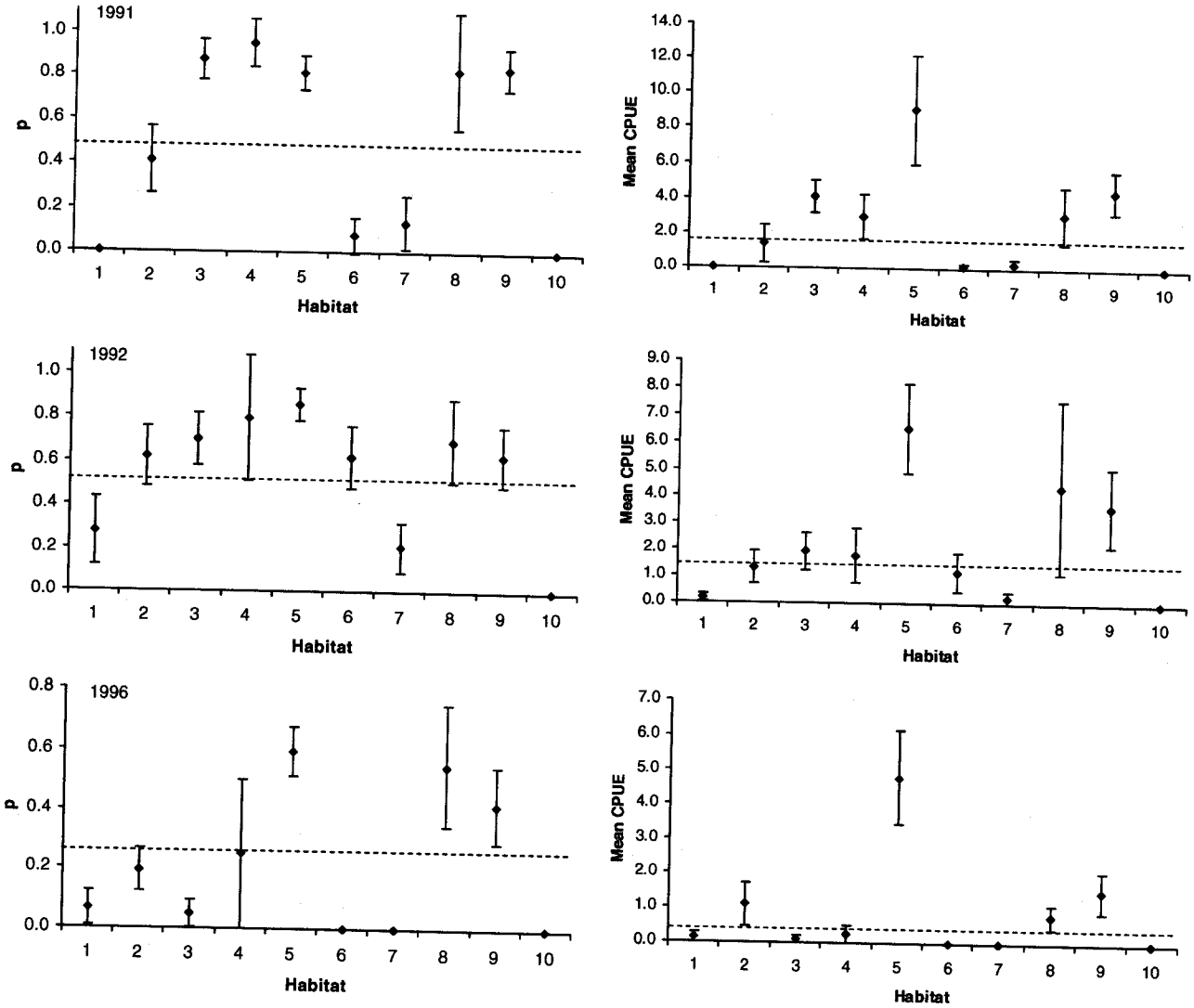


Figure 7. Pink shrimp (<18 mm CW) probability of use (left panels) and per-unit amount of use (right panels) among habitats in Biscayne Bay for seasonal surveys (database source: FWRI Fishery Independent Monitoring Program). Dashed lines denote domain-wide means. See Table 3 for habitat descriptions.

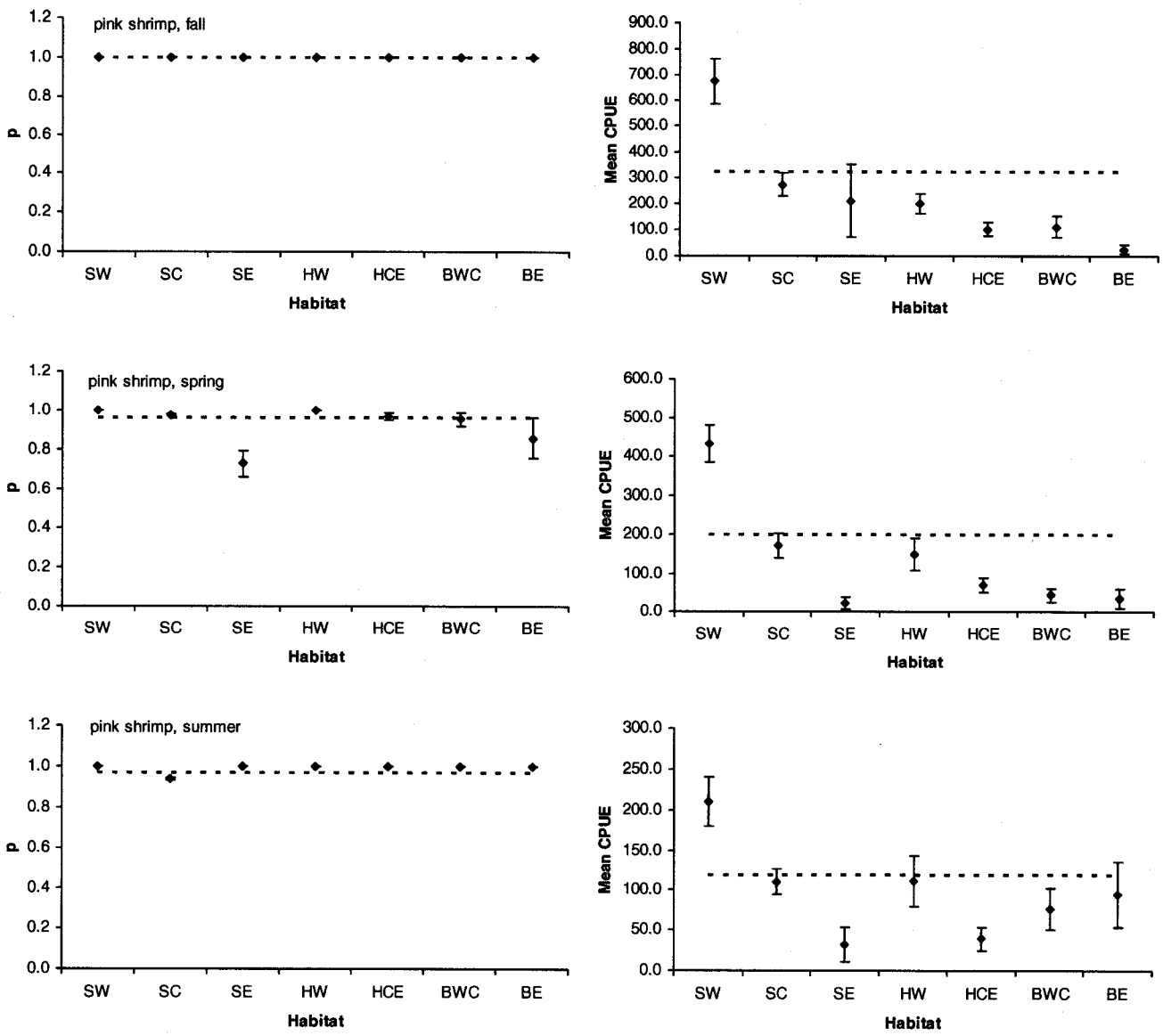


Figure 8. Pinfish (≤200 mm TL) probability of use (left panels) and per-unit amount of use (right panels) among habitats in Biscayne Bay for seasonal surveys (source: Ault et al. 1999, 2001). Dashed lines denote domain-wide means. See Table 3 for habitat descriptions.

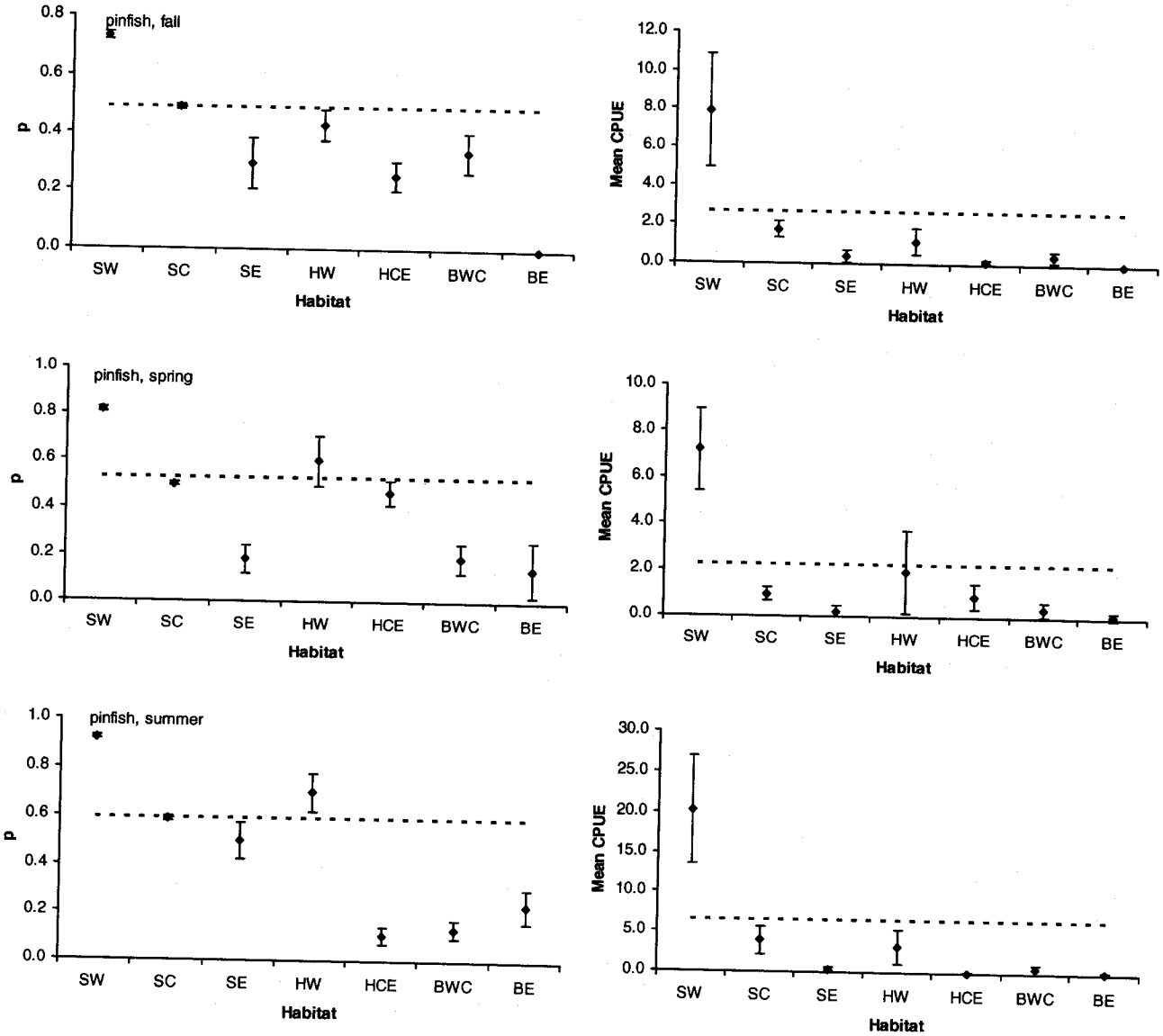


Figure 9. Gray snapper (≤165 mm TL) probability of use (left panels) and per-unit amount of use (right panels) among habitats in Biscayne Bay for seasonal surveys (source: Ault et al. 1999, 2001). Dashed lines denote domain-wide means. See Table 3 for habitat descriptions.

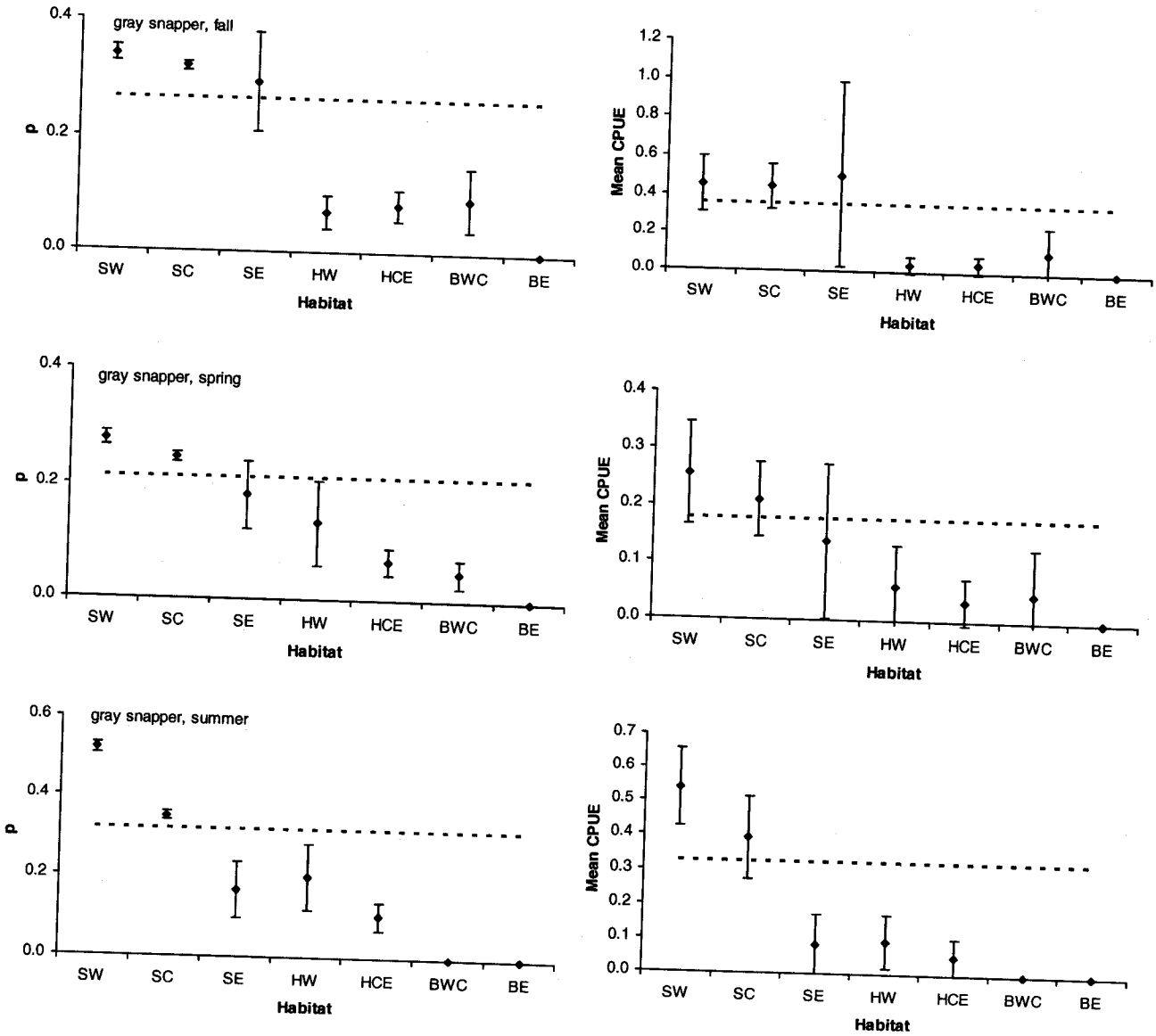


Figure 10. Bluestriped grunt (≤165 mm TL) probability of use (left panels) and per-unit amount of use (right panels) among habitats in Biscayne Bay for seasonal surveys (source: Ault et al. 1999, 2001). Dashed lines denote domain-wide means. See Table 3 for habitat descriptions.

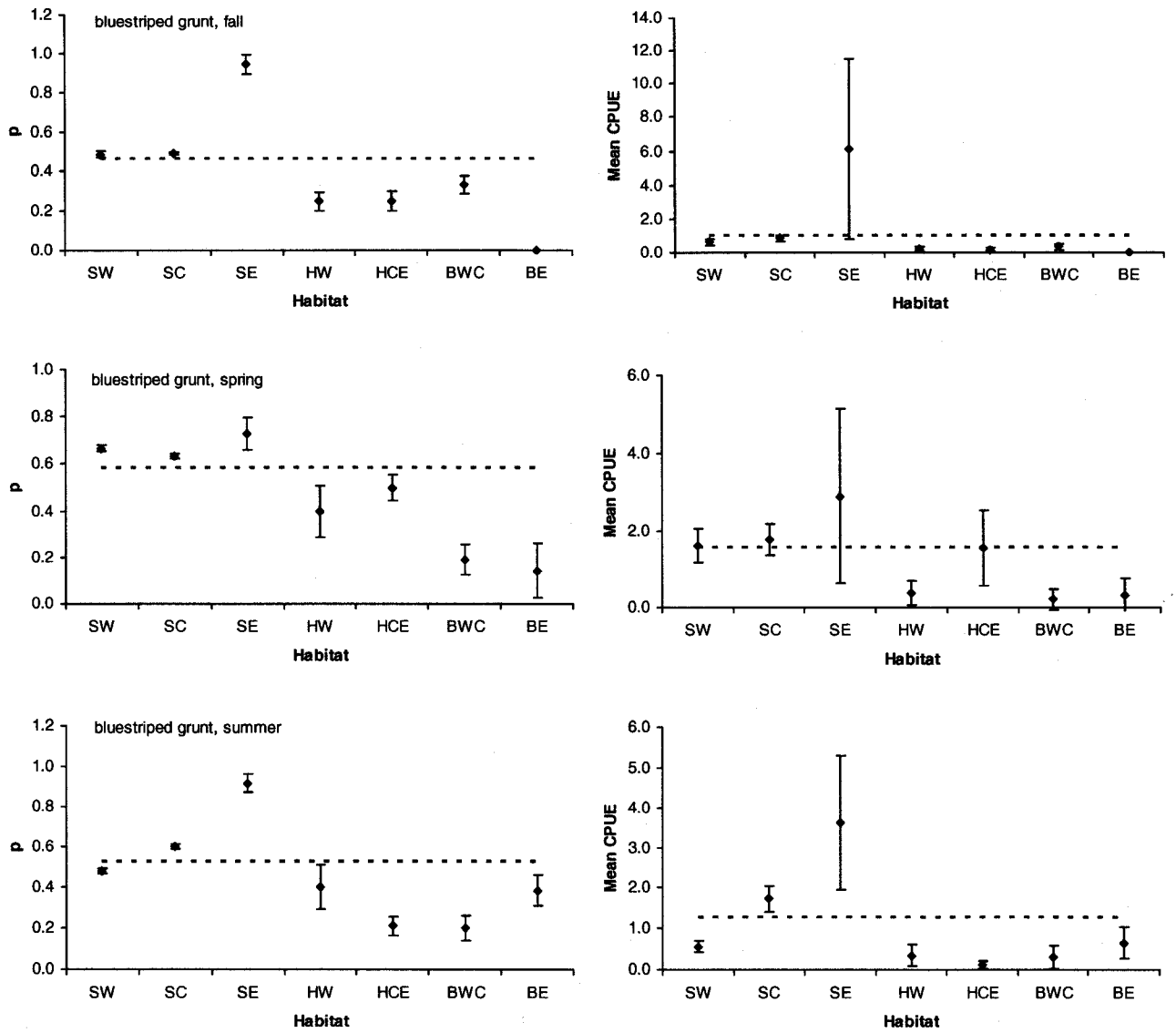


Figure 11. Single logistic regression functions (logit-transformed presence-absence) for habitat variables (a) depth, (b) bottom vegetation, (c) salinity, and (d) temperature for juvenile spotted seatrout (≤80 mm TL) in Charlotte Harbor during fall. Solid dots are mean values for habitat variable intervals.

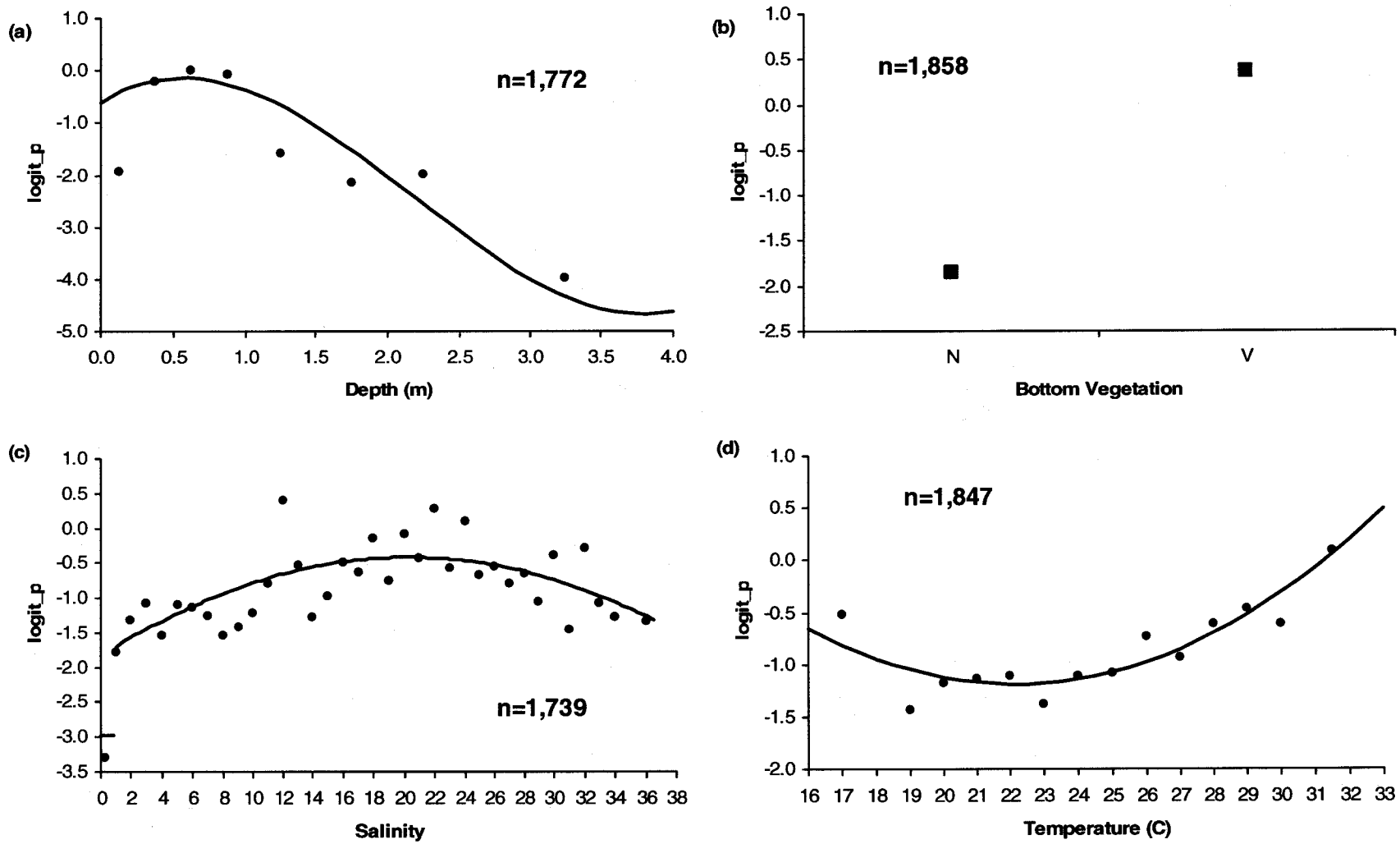


Figure 12. Positive CPUE (log-transformed) single regression functions for habitat variables (a) depth, (b) bottom vegetation, (c) salinity, and (d) temperature for juvenile spotted seatrout (≤80 mm TL) in Charlotte Harbor during fall. Solid dots are mean values for habitat variable intervals.

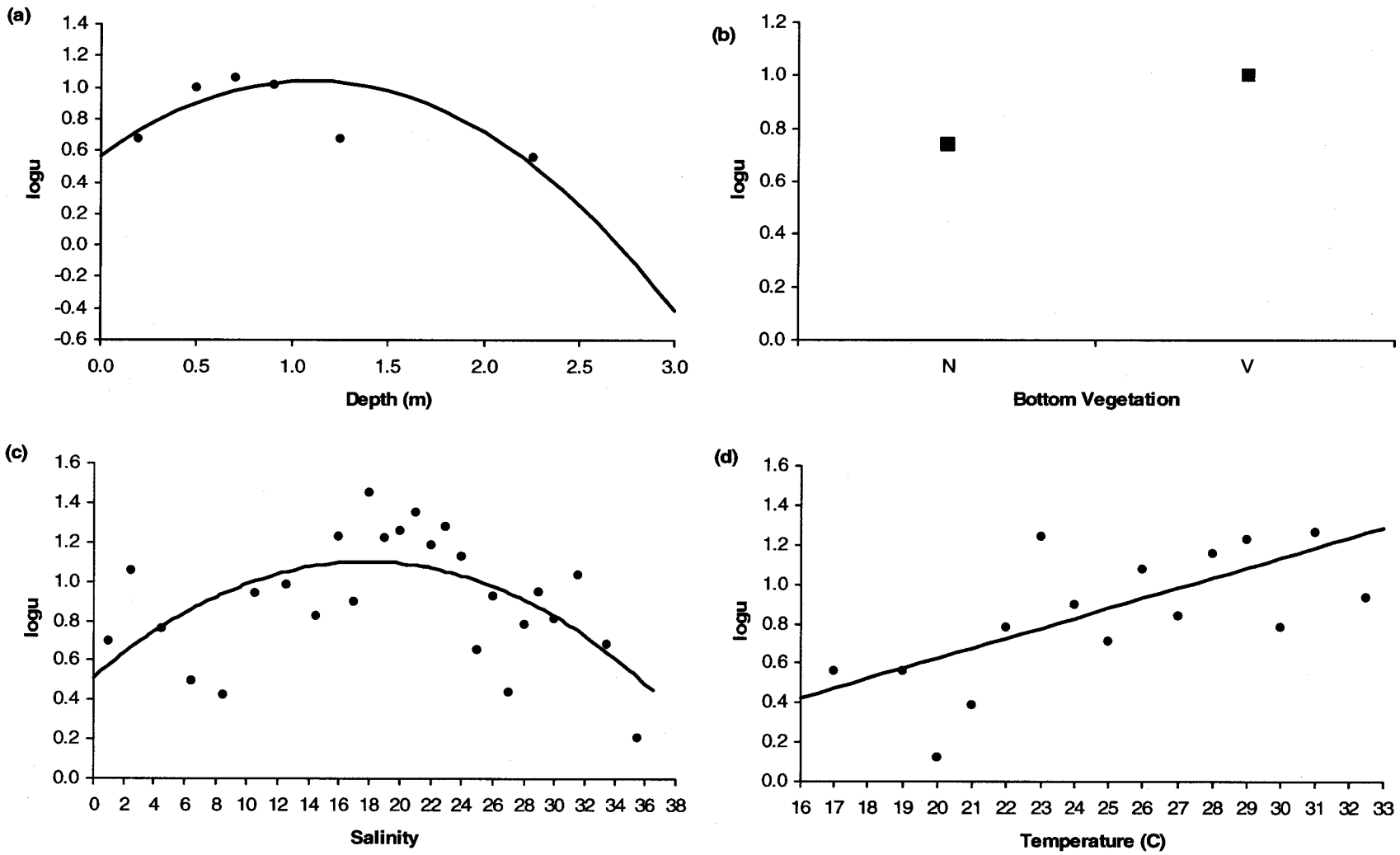


Figure 13. Illustration of two-stage regression modeling procedures with respect to distributional assumptions for response variable observations and error residuals.

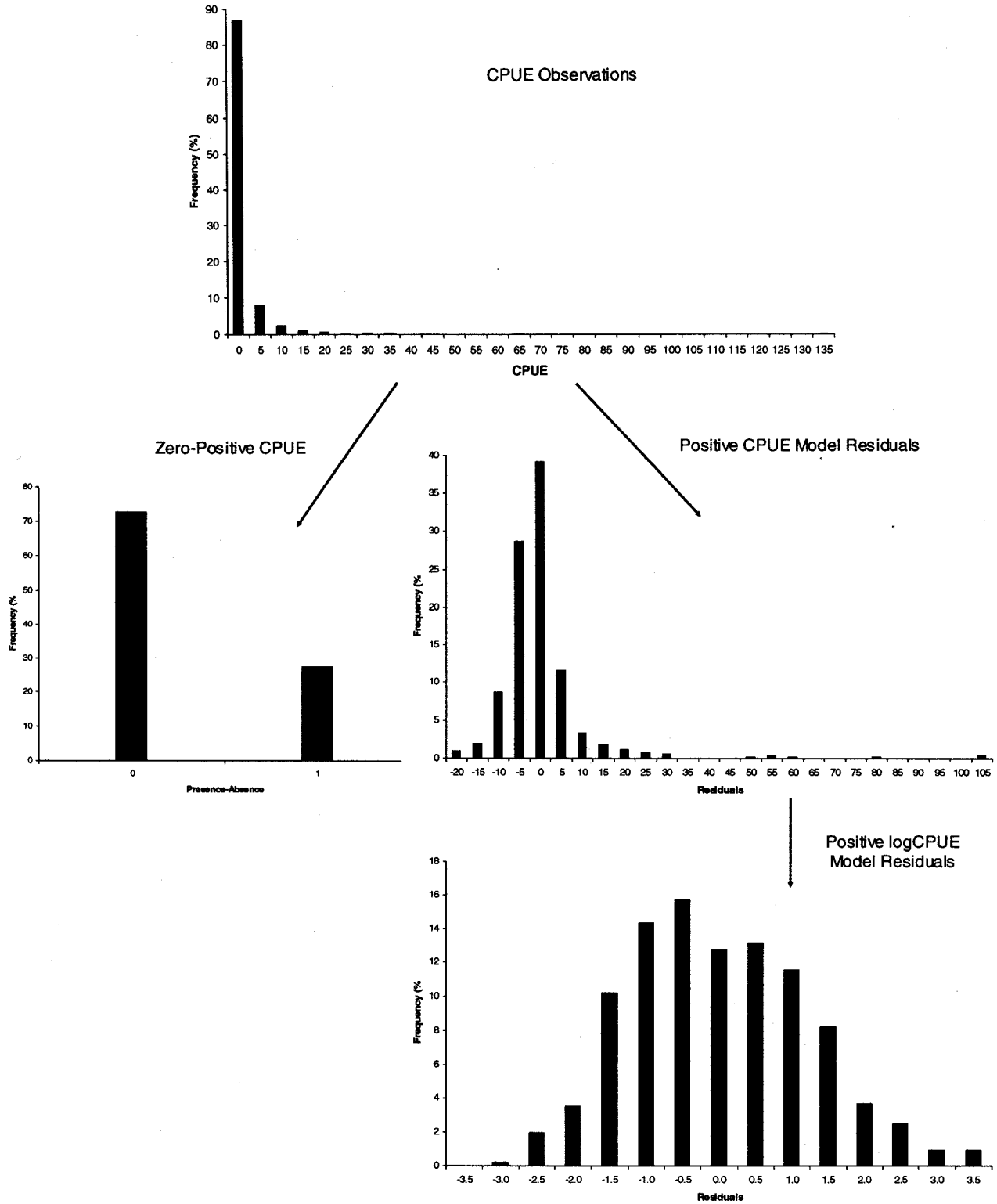


Figure 14. Illustration of two-stage regression modeling procedures with respect to developing predictive functions of CPUE.

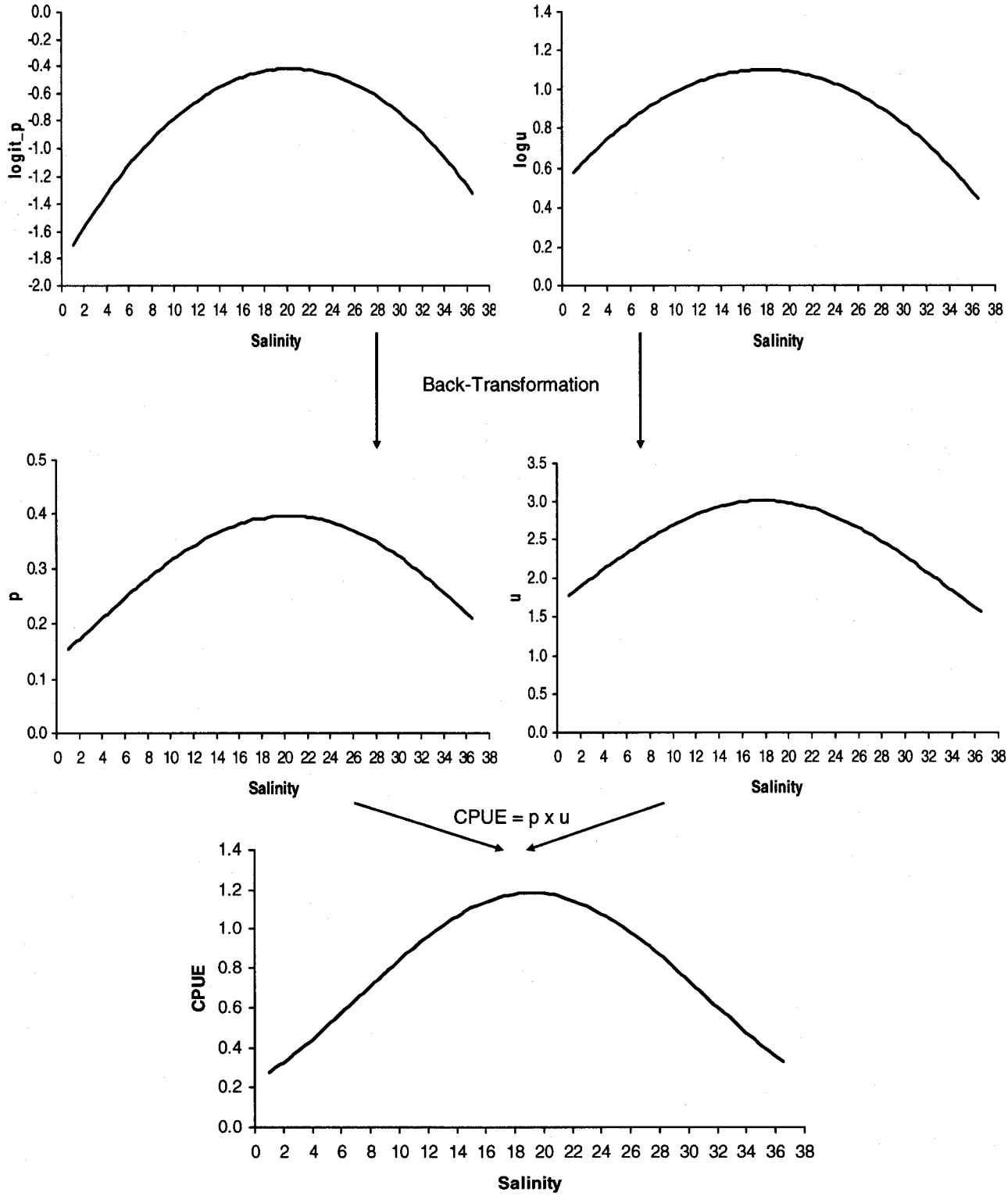


Figure 15. Model-predicted map of juvenile spotted seatrout habitat suitability (HSI) for June 2001.

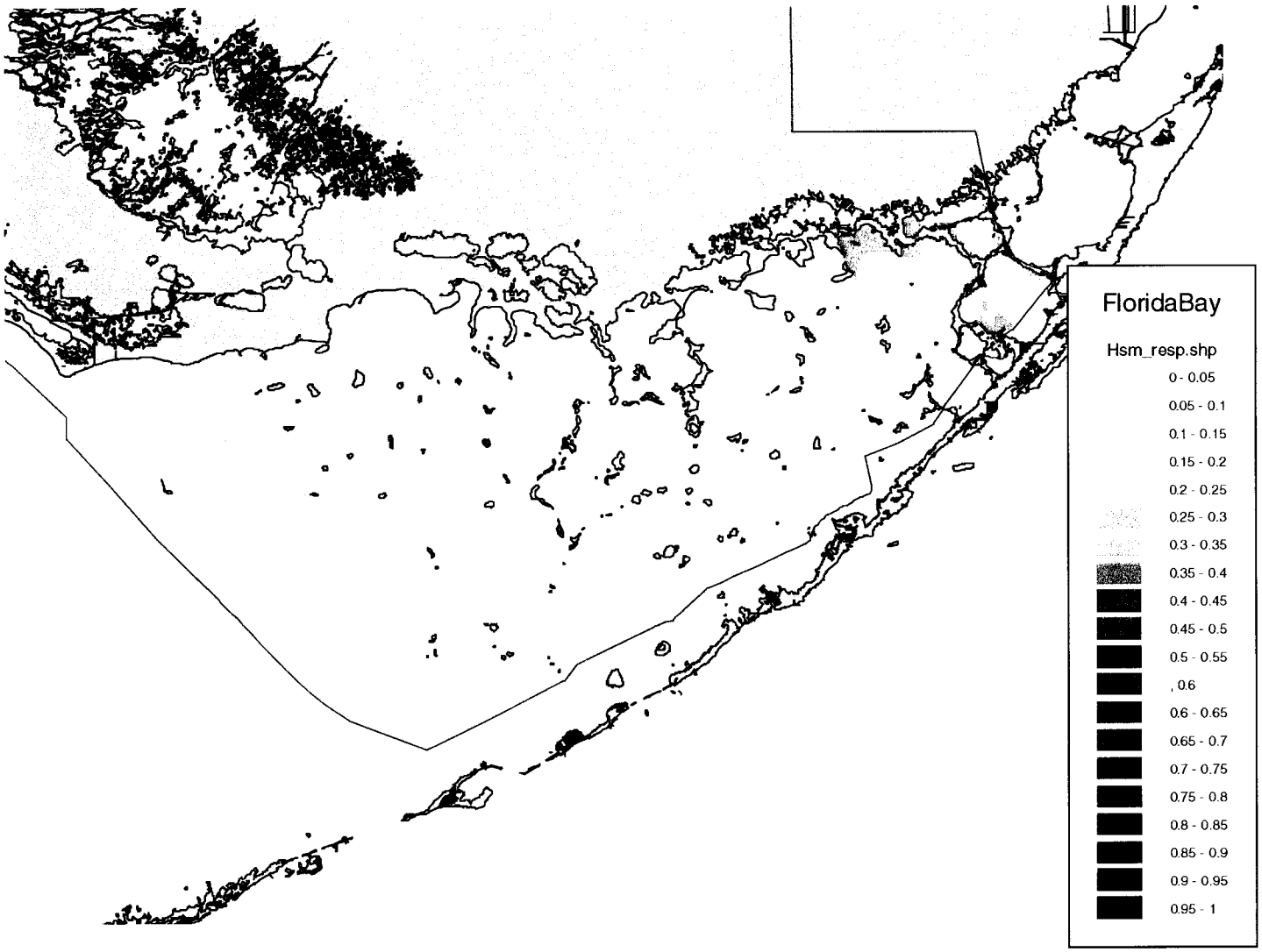


Figure 16. Model-predicted map of juvenile spotted seatrout habitat suitability (HSI) for September 2001.

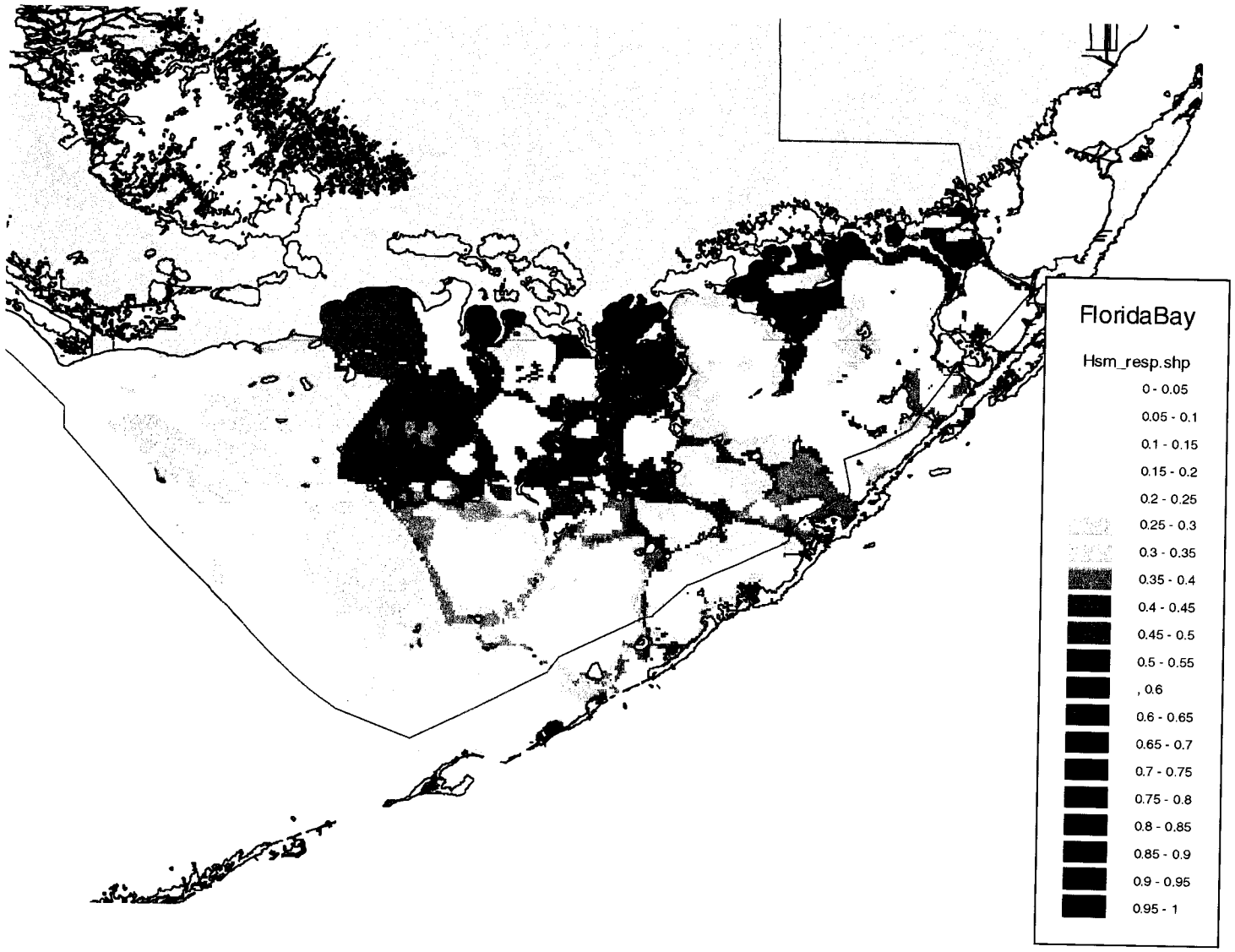
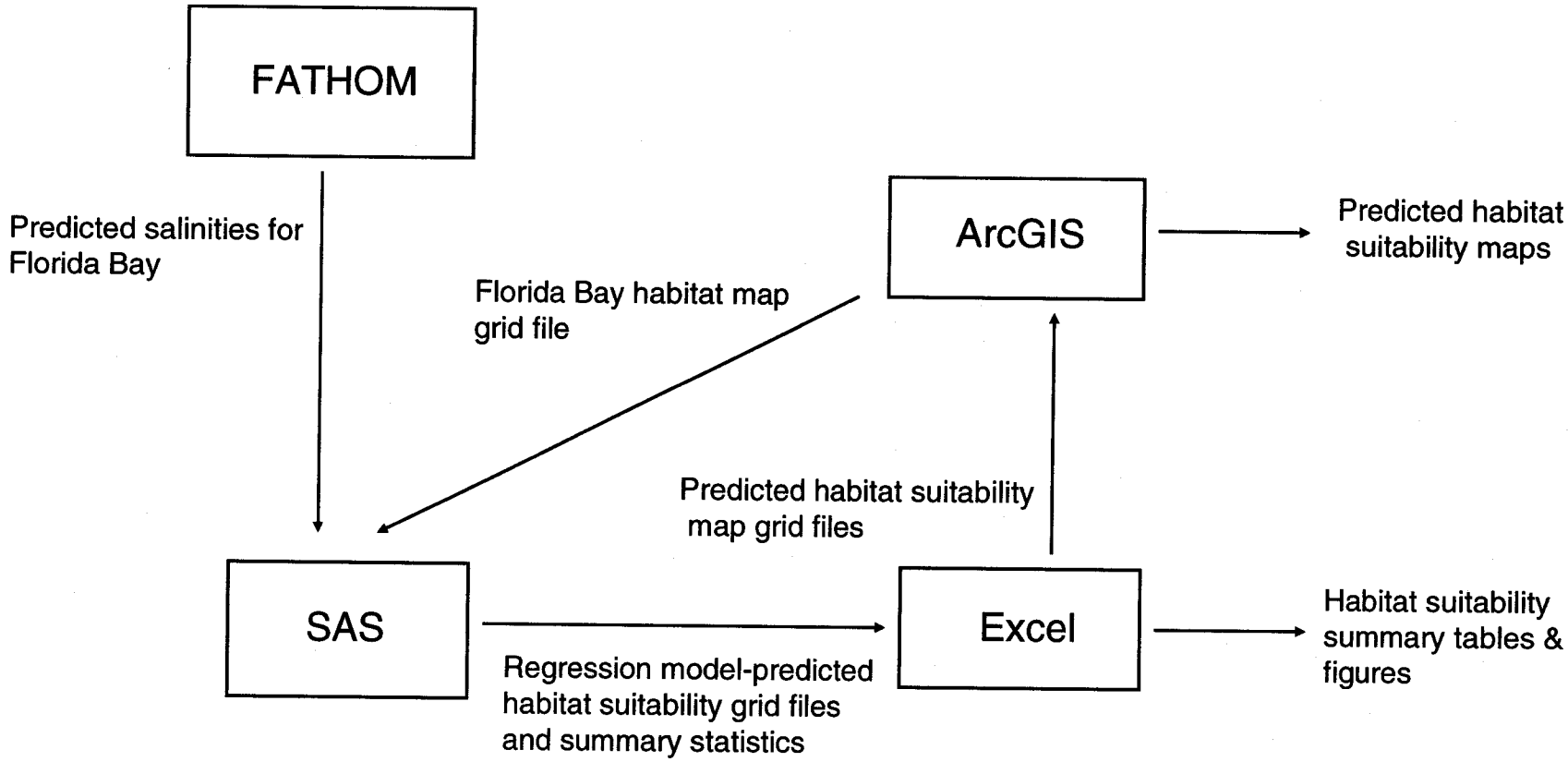


Figure 17. Flow diagram for the prototype decision support tool.



Appendix A-1. SAS program code for computing design-based probability of use of habitat strata.

```
/*program bbtrawl_habuse1.sas*/
/*stratum-specific StRS estimation*/
/*composite seasonal estimates*/
/*p (prob.)*/
options nonumber nodate;
data s1;
  infile 'c:\sgs\bbparrot\bbtrawl_ocychry_fdat2.txt';
  input specode$ 1-7 yrmo 9-14 stn 16-18 @20 tarea @28 lon @38 lat @48
dep
     @54 temp @60 sal @65 oxy hab9 71 hab5 73 hab3 75 len 77-80 @82
num;
run;
data s2;
  set s1;
  if yrmo=199604 or yrmo=199703 or yrmo=200003 then season='SP';
  else if yrmo=199608 or yrmo=199709 then season='SU';
  else if yrmo=199611 or yrmo=199711 or yrmo=199911 then season='FA';
  else season='-9';
  strat=hab9;
  if hab9=3 and hab5=1 then strat=2;
  else if strat=6 then strat=5;
  else if strat=7 then strat=8;
  else strat=strat;
run;
/*proc print;
quit;*/
/*lifestage specification*/
/*data ls1;
  set s2;
  if len=0 then delete;
run;
proc sort;
  by season;
quit;
proc univariate plot;
  by season;
  var len;
quit;*/
data s3;
  set s2;
  if len<150 then jnum=num;
  else jnum=0;
run;
proc means nway noprint;
  class yrmo stn;
  var jnum;
  id tarea strat season specode;
  output out=s4 (drop=_type_ _freq_) sum=abund;
quit;
/*proc print;
quit;*/
data s5;
  set s4;
```

```
  if abund>0 then pres=1;
  else pres=0;
  dns=abund/tarea;
run;
/*pres computations*/
/*stratum estimates by survey*/
proc means data=s5 nway noprint;
  class yrmo strat;
  var pres tarea;
  id season specode;
  output out=p1(drop=_type_ _freq_)n=n mean=av1 avtarea sum=smpres
sum2;
quit;
data d1;
  set p1;
  avprp=smpres/n;
  varprp=(avprp*(1-avprp))/(n-1);
run;
/*proc print;
quit;*/
proc sort;
  by season strat;
quit;
/*seasonal stratum estimates*/
proc means nway noprint;
  class season strat;
  var n;
  output out=d2 (drop=_type_ _freq_) sum=sn_n;
quit;
data d3;
  merge d1 d2;
  by season strat;
  sn_wh=n/sn_n;
run;
data d4;
  set d3;
  wavprp=sn_wh*avprp;
  wvarprp=sn_wh*varprp;
  wavtarea=sn_wh*avtarea;
run;
/*proc print;
quit;*/
proc means nway noprint;
  class season strat;
  var n wavprp wvarprp wavtarea;
  id specode;
  output out=d5 (drop=_type_ _freq_)mean=n av1 av2 av3 sum=sm1 avprp
varprp avtarea;
quit;
data d6;
  set d5;
  keep specode season strat n avprp varprp avtarea;
run;
/*proc print;
quit;*/
proc sort;
  by strat;
```

```
quit;
/*stratum weighting factor*/
data nt1;
  infile 'c:\sgs\bbparrot\areas9.txt';
  input strat area;
run;
data nt2;
  set nt1;
  if strat=6 then strat=5;
  else if strat=7 then strat=8;
  else strat=strat;
run;
proc means nway noprint;
  class strat;
  var area;
  output out=nt3 (drop=_type_ _freq_) sum=area;
quit;
/*proc print;
quit;*/
data d7;
  merge d6 nt3;
  by strat;
run;
data d8;
  set d7;
  ntot=area/avtarea;
run;
proc sort;
  by season;
quit;
proc means nway noprint;
  class season;
  var ntot;
  output out=nt4 (drop=_type_ _freq_) sum=ngrtot;
quit;
data d9;
  merge d8 nt4;
  by season;
  wh=ntot/ngrtot;
  drop avtarea area ngrtot;
run;
/*proc print;
quit;*/
data d10;
  set d9;
  wavprp=wh*avprp;
  f=n/ntot;
  vbar_prp=(1-f)*(varprp/n);
  wvbar=(wh**2)*vbar_prp;
  se_prp=sqrt(vbar_prp);
run;
/*proc print;
quit;*/
proc means nway noprint;
  class season;
  var n wavprp wvbar;
  id specode;
```

```
  output out=d11 (drop=_type_ _freq_) sum=n_st avprp_st vbar_st;
quit;
data d12;
  merge d10 d11;
  by season;
  seprp_st=sqrt(vbar_st);
  format n 3.0 n_st 3.0;
run;
/*proc print;
quit;*/
proc print noobs;
  var specode season strat n avprp se_prp n_st avprp_st seprp_st;
  title ' ';
quit;
```

Appendix A-2. SAS program code for computing design-based per unit and population amount of use of habitat strata.

```
/*program bbtrawl_habuse2.sas*/
/*stratum-specific StRS estimation*/
/*composite seasonal estimates*/
/*dens. (per unit) & abund. pop.) habitat use*/
/*tests for resource selection*/
options nonumber nodate;
data s1;
  infile 'c:\sgs\bbparrot\bbtrawl_lutgris_fdat2.txt';
  input specode$ 1-7 yrmo 9-14 stn 16-18 @20 tarea @28 lon @38 lat @48
dep
     @54 temp @60 sal @65 oxy hab9 71 hab5 73 hab3 75 len 77-80 @82
num;
run;
data s2;
  set s1;
  if yrmo=199604 or yrmo=199703 or yrmo=200003 then season='SP';
  else if yrmo=199608 or yrmo=199709 then season='SU';
  else if yrmo=199611 or yrmo=199711 or yrmo=199911 then season='FA';
  else season='-9';
  strat=hab9;
  if hab9=3 and hab5=1 then strat=2;
  else if strat=6 then strat=5;
  else if strat=7 then strat=8;
  else strat=strat;
run;
/*proc print;
quit;*/
/*lifestage specification*/
/*data ls1;
  set s2;
  if len=0 then delete;
run;
proc sort;
  by season;
quit;
proc univariate plot;
  by season;
  var len;
quit;*/
data s3;
  set s2;
  if len<165 then jnum=num;
  else jnum=0;
run;
proc means nway noprint;
  class yrmo stn;
  var jnum;
  id tarea strat season specode;
  output out=s4 (drop=_type_ _freq_) sum=abund;
quit;
/*proc print;
quit;*/
data s5;
```

```
  set s4;
  dns=abund/tarea;
run;
/*density computations*/
/*stratum estimates by survey*/
proc means data=s5 nway noprint;
  class yrmo strat;
  var dns tarea;
  id season specode;
  output out=d1 (drop=_type_ _freq_)n=n mean=avdns avtarea var=vardns
var2;
quit;
/*proc print;
quit;*/
proc sort;
  by season strat;
quit;
/*seasonal stratum estimates*/
proc means nway noprint;
  class season strat;
  var n;
  output out=d2 (drop=_type_ _freq_) sum=sn_n;
quit;
data d3;
  merge d1 d2;
  by season strat;
  sn_wh=n/sn_n;
run;
data d4;
  set d3;
  wavdns=sn_wh*avdns;
  wvardns=sn_wh*vardns;
  wavtarea=sn_wh*avtarea;
run;
/*proc print;
quit;*/
proc means nway noprint;
  class season strat;
  var n wavdns wvardns wavtarea;
  id specode;
  output out=d5 (drop=_type_ _freq_)mean=n av1 av2 av3 sum=sm1 avdns
vardns avtarea;
quit;
data d6;
  set d5;
  keep specode season strat n avdns vardns avtarea;
run;
/*proc print;
quit;*/
proc sort;
  by strat;
quit;
/*stratum weighting factor*/
data nt1;
  infile 'c:\sgs\bbparrot\areas9.txt';
  input strat area;
run;
```

```
data nt2;
  set nt1;
  if strat=6 then strat=5;
  else if strat=7 then strat=8;
  else strat=strat;
run;
proc means nway noprint;
  class strat;
  var area;
  output out=nt3 (drop=_type_ _freq_) sum=area;
quit;
/*proc print;
quit;*/
data d7;
  merge d6 nt3;
  by strat;
run;
data d8;
  set d7;
  ntot=area/avtarea;
  avdns=avdns*avtarea;
  vardns=vardns*(avtarea**2);
run;
proc sort;
  by season;
quit;
proc means nway noprint;
  class season;
  var ntot;
  output out=nt4 (drop=_type_ _freq_) sum=ngrtot;
quit;
data d9;
  merge d8 nt4;
  by season;
  wh=ntot/ngrtot;
  drop avtarea area ngrtot;
run;
/*proc print;
quit;*/
data d10;
  set d9;
  wavdns=wh*avdns;
  f=n/ntot;
  vbar_dns=(1-f)*(vardns/n);
  wvbar=(wh**2)*vbar_dns;
  se_dns=sqrt(vbar_dns);
run;
/*proc print;
quit;*/
proc means nway noprint;
  class season;
  var n wavdns wvbar;
  id specode;
  output out=d11 (drop=_type_ _freq_) sum=n_st avdns_st vbar_st;
quit;
data d12;
  merge d10 d11;
```

```
  by season;
  sedns_st=sqrt(vbar_st);
  cv_st=(sedns_st/avdns_st)*100;
  format n 3.0 n_st 3.0 cv_st 6.2;
run;
/*proc print;
quit;*/
/*proc print noobs;
  var specode season strat n avdns se_dns n_st avdns_st sedns_st cv_st;
  title ' ';
quit;*/
/*abundance computations*/
data y1;
  set d10;
  yhat=ntot*avdns;
  vbar_yhat=(ntot**2)*vbar_dns;
  se_yhat=sqrt(vbar_yhat);
run;
/*proc print;
quit;*/
proc means nway noprint;
  class season;
  var yhat;
  output out=y2 (drop=_type_ _freq_) sum=y_tot;
quit;
data y3;
  merge y1 y2;
  by season;
run;
data u1;
  set y3;
  p_A=wh;
  prb=0.025;
  df=n-1;
  t_05=abs(tinv(prb,df));
  LCI_yhat=yhat-(t_05*se_yhat);
  UCI_yhat=yhat+(t_05*se_yhat);
  p_yhat=yhat/y_tot;
  LCI_py=LCI_yhat/y_tot;
  UCI_py=UCI_yhat/y_tot;
  if p_A<LCI_py then select='positive';
  else if LCI_py<=p_A<=UCI_py then select='neutral';
  else if p_A>UCI_py then select='negative';
  format n 3.0;
run;
/*proc print;
quit;*/
proc print noobs;
  var specode season strat n p_A p_yhat LCI_py UCI_py select;
  title ' ';
quit;
```

Appendix A-3. SAS program code for logistic habitat use regression modeling.

```
/*program glim4.sas*/
/*logistic regression*/
/*multiple explanatory variables*/
/*single species-lifestage*/
options nonumber nodate ls=70;
data s1;
  infile 'c:\sgs\flmr2\grstd\abd_sdat_1720A.dat';
  input flmno 1-4 bay$ 6-7 stnymd 9-16 station$ 18-27 gear 29-32 @34
lat
    @44 long @54 depth @60 catch @73 effort @85 gcf_p @94 gcf_u
    fimstrat$ 103-105 bveg$ 107 @109 oxy @115 ph @121 sal @127 temp
    gz 133 yr 135-138 season 140;
run;
data s2;
  set s1;
  if catch>0 then pres=1;
  else pres=0;
  if pres=1 then gcf_pw=(1/gcf_p);
  else if pres=0 then gcf_pw=1;
  if season=3;
  if bay='CH';
  if bveg='V' then bvnum=1;
  else bvnum=2;
run;
/*create design matrix*/
%macro dsnmat;
  %do i=1989 %to 2000;
      if yr=&i then y&i=1;
      else if yr=2000 then y&i=-1;
      else y&i=0;
  %end;
  %do i=1 %to 2;
      if bvnum=&i then bv&i=1;
      else bv&i=-1;
  %end;
%mend dsnmat;
data m1;
  set s2;
  %dsnmat
run;
/*proc print;
quit;*/
data m2;
  set m1;
  if depth>4.0 then delete;
  depsq=depth*depth;
  depcb=depsq*depth;
  if sal<1.0 or sal>36.5 then delete;
  salsq=sal*sal;
  if temp<15.5 or temp>33.0 then delete;
  tempsq=temp*temp;
run;
/*presence-absence logistic regression*/
proc logistic descending;
```

```
  model pres= y1989-y1999 bv1 depth depsq
          sal salsq temp/ link=logit;
  weight gcf_pw;
quit;
```

Appendix A-4. SAS program code for positive CPUE (or density) habitat use regression modeling.

```
/*program glim3.sas*/
/*pos cpue regression model*/
/*multiple explanatory variables*/
/*single species-lifestage*/
options nonumber nodate ls=70;
data s1;
  infile 'c:\sgs\flmr2\grstd\abd_sdat_1720A.dat';
  input flmno 1-4 bay$ 6-7 stnymd 9-16 station$ 18-27 gear 29-32 @34
lat
    @44 long @54 depth @60 catch @73 effort @85 gcf_p @94 gcf_u
    fimstrat$ 103-105 bveg$ 107 @109 oxy @115 ph @121 sal @127 temp
    gz 133 yr 135-138 season 140;
run;
/*proc print;
quit;*/
data s2;
  set s1;
  if catch=0 then delete;
  catch=catch/gcf_u;
  cpue=catch/effort;
  u=cpue*153;
  logu=log(u);
  if season=3;
  if bay='CH';
  if bveg='V' then bvnum=1;
  else bvnum=2;
run;
/*create design matrix*/
%macro dsnmat;
  %do i=1989 %to 2000;
      if yr=&i then y&i=1;
      else if yr=2000 then y&i=-1;
      else y&i=0;
  %end;
  %do i=1 %to 2;
      if bvnum=&i then bv&i=1;
      else bv&i=-1;
  %end;
%mend dsnmat;
data m1;
  set s2;
  %dsnmat
run;
/*proc print;
quit;*/
data m2;
  set m1;
  if depth>3.0 then delete;
  depsq=depth*depth;
  if sal=-9 or sal>36.5 then delete;
  salsq=sal*sal;
  if temp=-9 then delete;
  if temp<15.5 or temp>33.0 then delete;
```

```
run;
/*pos cpue reg model*/
/*OLS normal pdf*/
proc reg data=m2;
  model logu= y1989-y1999 bv1 sal salsq
          temp;
  output out=u1 residual=resid;
quit;
/*proc univariate data=u1 normal plot;
  var resid;
quit;*/
/*proc chart data=u1;
  hbar resid/midpoints=-3.5 to 3.5 by 0.5;
quit;*/
/*proc print data=u1 noobs;
  var flmno bay season oxy resid;
quit;*/
/*MLE gamma pdf*/
/*proc genmod data=m2;
    model logu= y1989-y1999 depth depsq depcb/
                dist=gamma link=identity
                scale=2.0 intercept=1.2
                itprint;
quit;*/
```

Appendix A-5. SAS program code for computing regression model-predicted habitat suitability map grid datafiles and summary statistics for Florida Bay.

```
/*program modmap_ch-fb.sas*/
/*computes Charlotte Harbor regression model-predicted p & CPUE for
Florida Bay*/
/*computes Habitat Suitability Indices for mapping and summary
comparisons*/
/*spotted seatrout, early juv*/
options nonumber nodate;
/*                                                    */
/*Read-in and process GIS map grid datafile*/
/*                                                    */
proc import datafile="c:\sgs\enp_hab\seatrout\grid_flbay2.dbf"
    out=fb1 replace;
quit;
/*proc contents data=fb1;
quit;*/
data fb2;
  set fb1;
  if benthclass='Hardbottom' or benthclass='No veg' then bveg='N';
  else if benthclass='Veg' then bveg='V';
  else bveg='U';
  if gridcode=0 then depth=0.5;
  else if gridcode=-1 then depth=1.0;
  else if gridcode=-2 then depth=1.5;
  else if gridcode=-3 then depth=2.0;
  else depth=-9;
  temp=25;
  keep bveg depth temp fathom_id grid_ grid_id;
run;
proc sort;
  by fathom_id;
quit;
/*proc freq data=fb2;
  tables bveg depth;
quit;*/
/*                                  */
/*Read-in FATHOM model output       */
/*Select time periods for analysis*/
/*                                  */
proc import datafile="c:\sgs\enp_hab\seatrout\sal2.dbf"
    out=fb3 replace;
quit;
/*proc contents data=fb3;
quit;*/
data fb4;
  set fb3;
  keep fathom_id Z001_6 Z001_7 Z001_8 Z001_9 Z001_10 Z001_11;
run;
proc sort;
  by fathom_id;
quit;
/*proc print;
quit;*/
/*                                    */
```

```
/*Merge map grid and FATHOM datasets*/
/*                                   */
data fb5;
  merge fb2 fb4;
  by fathom_id;
  if bveg='U' or depth=-9 then delete;
  if grid_id=. then delete;
run;
proc sort;
  by grid_id;
quit;
/*proc print;
quit;*/
/*proc univariate plot;
  var Z001_6 Z001_7 Z001_8 Z001_9 Z001_10 Z001_11;
quit;*/
/*                                                                  */
/*Compute grid cell values of HS Abundance Index                    */
/*one data step for each selected FATHOM time period, year-month*/
/*                                                                  */
data m1a;
  set fb5;
  maxcp=2.121870905;
  sal=Z001_6;
  depsq=depth*depth;
  salsq=sal*sal;
  if sal<1.0 and bveg='V' then
    y=-3.7594-1.1248+0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
  else if sal<1.0 and bveg='N' then
    y=-3.7594-1.1248-0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
  else if 1.0<=sal<44.0 and bveg='V' then
    y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
          -0.0036*salsq+0.0998*temp;
  else if 1.0<=sal<44.0 and bveg='N' then
    y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
          -0.0036*salsq+0.0998*temp;
  else if sal>=44.0 and bveg='V' then
    y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
          -0.0036*(44.0**2)+0.0998*temp;
  else if sal>=44.0 and bveg='N' then
    y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
          -0.0036*(44.0**2)+0.0998*temp;
  p=exp(y)/(1+exp(y));
  if sal<44.0 and bveg='V' then
    logu=-0.50027+0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
  else if sal<44.0 and bveg='N' then
    logu=-0.50027-0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
  else if sal>=44.0 and bveg='V' then
    logu=-0.50027+0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
  else if sal>=44.0 and bveg='N' then
    logu=-0.50027-0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
  u=exp(logu);
  HA2001_6=(p*u)/maxcp;
  keep grid_id HA2001_6;
run;
data m1b;
  set fb5;
```

```
    maxcp=2.121870905;
    sal=Z001_7;
    depsq=depth*depth;
    salsq=sal*sal;
    if sal<1.0 and bveg='V' then
      y=-3.7594-1.1248+0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
    else if sal<1.0 and bveg='N' then
      y=-3.7594-1.1248-0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
    else if 1.0<=sal<44.0 and bveg='V' then
      y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
            -0.0036*salsq+0.0998*temp;
    else if 1.0<=sal<44.0 and bveg='N' then
      y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
            -0.0036*salsq+0.0998*temp;
    else if sal>=44.0 and bveg='V' then
      y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
            -0.0036*(44.0**2)+0.0998*temp;
    else if sal>=44.0 and bveg='N' then
      y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
            -0.0036*(44.0**2)+0.0998*temp;
    p=exp(y)/(1+exp(y));
    if sal<44.0 and bveg='V' then
      logu=-0.50027+0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
    else if sal<44.0 and bveg='N' then
      logu=-0.50027-0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
    else if sal>=44.0 and bveg='V' then
      logu=-0.50027+0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
    else if sal>=44.0 and bveg='N' then
      logu=-0.50027-0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
    u=exp(logu);
    HA2001_7=(p*u)/maxcp;
    keep grid_id HA2001_7;
  run;
  data m1c;
    set fb5;
    maxcp=2.121870905;
    sal=Z001_8;
    depsq=depth*depth;
    salsq=sal*sal;
    if sal<1.0 and bveg='V' then
      y=-3.7594-1.1248+0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
    else if sal<1.0 and bveg='N' then
      y=-3.7594-1.1248-0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
    else if 1.0<=sal<44.0 and bveg='V' then
      y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
            -0.0036*salsq+0.0998*temp;
    else if 1.0<=sal<44.0 and bveg='N' then
      y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
            -0.0036*salsq+0.0998*temp;
    else if sal>=44.0 and bveg='V' then
      y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
            -0.0036*(44.0**2)+0.0998*temp;
    else if sal>=44.0 and bveg='N' then
      y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
            -0.0036*(44.0**2)+0.0998*temp;
    p=exp(y)/(1+exp(y));
    if sal<44.0 and bveg='V' then
```

```
    logu=-0.50027+0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
  else if sal<44.0 and bveg='N' then
    logu=-0.50027-0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
  else if sal>=44.0 and bveg='V' then
    logu=-0.50027+0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
  else if sal>=44.0 and bveg='N' then
    logu=-0.50027-0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
  u=exp(logu);
  HA2001_8=(p*u)/maxcp;
  keep grid_id HA2001_8;
run;
data m1d;
  set fb5;
  maxcp=2.121870905;
  sal=Z001_9;
  depsq=depth*depth;
  salsq=sal*sal;
  if sal<1.0 and bveg='V' then
    y=-3.7594-1.1248+0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
  else if sal<1.0 and bveg='N' then
    y=-3.7594-1.1248-0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
  else if 1.0<=sal<44.0 and bveg='V' then
    y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
          -0.0036*salsq+0.0998*temp;
  else if 1.0<=sal<44.0 and bveg='N' then
    y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
          -0.0036*salsq+0.0998*temp;
  else if sal>=44.0 and bveg='V' then
    y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
          -0.0036*(44.0**2)+0.0998*temp;
  else if sal>=44.0 and bveg='N' then
    y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
          -0.0036*(44.0**2)+0.0998*temp;
  p=exp(y)/(1+exp(y));
  if sal<44.0 and bveg='V' then
    logu=-0.50027+0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
  else if sal<44.0 and bveg='N' then
    logu=-0.50027-0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
  else if sal>=44.0 and bveg='V' then
    logu=-0.50027+0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
  else if sal>=44.0 and bveg='N' then
    logu=-0.50027-0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
  u=exp(logu);
  HA2001_9=(p*u)/maxcp;
  keep grid_id HA2001_9;
run;
data m1e;
  set fb5;
  maxcp=2.121870905;
  sal=Z001_10;
  depsq=depth*depth;
  salsq=sal*sal;
  if sal<1.0 and bveg='V' then
    y=-3.7594-1.1248+0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
  else if sal<1.0 and bveg='N' then
    y=-3.7594-1.1248-0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
  else if 1.0<=sal<44.0 and bveg='V' then
```

```
      y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
            -0.0036*salsq+0.0998*temp;
    else if 1.0<=sal<44.0 and bveg='N' then
      y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
            -0.0036*salsq+0.0998*temp;
    else if sal>=44.0 and bveg='V' then
      y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
            -0.0036*(44.0**2)+0.0998*temp;
    else if sal>=44.0 and bveg='N' then
      y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
            -0.0036*(44.0**2)+0.0998*temp;
    p=exp(y)/(1+exp(y));
    if sal<44.0 and bveg='V' then
      logu=-0.50027+0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
    else if sal<44.0 and bveg='N' then
      logu=-0.50027-0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
    else if sal>=44.0 and bveg='V' then
      logu=-0.50027+0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
    else if sal>=44.0 and bveg='N' then
      logu=-0.50027-0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
    u=exp(logu);
    HA2001_10=(p*u)/maxcp;
    keep grid_id HA2001_10;
  run;
  data m1f;
    set fb5;
    maxcp=2.121870905;
    sal=Z001_11;
    depsq=depth*depth;
    salsq=sal*sal;
    if sal<1.0 and bveg='V' then
      y=-3.7594-1.1248+0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
    else if sal<1.0 and bveg='N' then
      y=-3.7594-1.1248-0.7116+0.7633*depth-0.6166*depsq+0.0998*temp;
    else if 1.0<=sal<44.0 and bveg='V' then
      y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
            -0.0036*salsq+0.0998*temp;
    else if 1.0<=sal<44.0 and bveg='N' then
      y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*sal
            -0.0036*salsq+0.0998*temp;
    else if sal>=44.0 and bveg='V' then
      y=-3.7594+0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
            -0.0036*(44.0**2)+0.0998*temp;
    else if sal>=44.0 and bveg='N' then
      y=-3.7594-0.7116+0.7633*depth-0.6166*depsq+0.1297*44.0
            -0.0036*(44.0**2)+0.0998*temp;
    p=exp(y)/(1+exp(y));
    if sal<44.0 and bveg='V' then
      logu=-0.50027+0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
    else if sal<44.0 and bveg='N' then
      logu=-0.50027-0.14887+0.04648*sal-0.00146*salsq+0.04378*temp;
    else if sal>=44.0 and bveg='V' then
      logu=-0.50027+0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
    else if sal>=44.0 and bveg='N' then
      logu=-0.50027-0.14887+0.04648*44.0-0.00146*(44.0**2)+0.04378*temp;
    u=exp(logu);
    HA2001_11=(p*u)/maxcp;
```

```
  keep grid_id HA2001_11;
run;
/*                                                          */
/*Merge HSAI datasets for all selected time periods*/
/*                                                          */
data m2;
  merge fb5 m1a m1b m1c m1d m1e m1f;
  by grid_id;
run;
/*proc print;
quit;*/
/*                                                                  */
/*Compute HS Composite Index for lifestage time intervals*/
/*                                                                  */
data m3;
  set m2;
  HSCI_E_2001=HA2001_6*HA2001_7*HA2001_8*HA2001_9;
  HSCI_M_2001=HA2001_7*HA2001_8*HA2001_9*HA2001_10;
  HSCI_L_2001=HA2001_8*HA2001_9*HA2001_10*HA2001_11;
  format HA2001_6 HA2001_7 HA2001_8 HA2001_9 HA2001_10 HA2001_11 5.3;
  format HSCI_E_2001 HSCI_M_2001 HSCI_L_2001 e8.;
run;
/*proc print;
quit;*/
/*                                  */
/*Export HS map grid to excel file*/
/*                                  */
proc export data=m3
   outfile="c:\sgs\enp_hab\seatrout\seatrout_regmap2001.xls"
   replace;
quit;
/*                                          */
/*Compute domain-wide summary HS indices*/
/*                                          */
proc means nway noprint;
  var HA2001_6 HA2001_7 HA2001_8 HA2001_9 HA2001_10 HA2001_11
     HSCI_E_2001 HSCI_M_2001 HSCI_L_2001;
  output out=m4 (drop=_type_ _freq_) sum= HA2001_6 HA2001_7 HA2001_8
     HA2001_9 HA2001_10 HA2001_11 HSCI_E_2001 HSCI_M_2001 HSCI_L_2001;
quit;
/*proc print;
quit;*/
/*                                          */
/*Export HS summary indices to excel file*/
/*                                          */
proc export data=m4
     outfile="c:\sgs\enp_hab\seatrout\seatrout_domain2001.xls"
   replace;
quit;
```