Florida Freshwater and Tidal Stream Fish Distribution Mapping: Phase I - Panhandle

FINAL REPORT

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ABSTRACT

North America contains the greatest temperate freshwater biodiversity on Earth. The United States in particular is home to 10% of all freshwater fish species, 30% of all freshwater mussels, and 61% of all freshwater crayfish that have been described worldwide. However, this diversity is disappearing at an alarming rate (Sowa et al. 1994, Jelks et al. 2008). The objectives of this project were to create predictive species distribution models for at least 25 species of fish documented to occur in the freshwater streams of Florida's Panhandle. Modeling potential species habitat is an increasingly important tool for ecology, conservation, invasive species management, and climate change research (Pearson 2007).

DesktopGARP was used to search for non-random associations between 20 environmental characteristics of localities of known occurrence versus those of the overall study region. The potential habitat ranges of 55 species of fish known to occur in Florida's panhandle region were mapped. Overall, GARP was able to predict the location of the validation points with acceptable accuracy (80% or better). This research can be used as a guide for mapping all of the freshwater fish occurring throughout Florida, as well as freshwater invertebrates such as mussels and crayfish. These maps will be valuable in increasing the long-term capacity for conservation and management of multiple freshwater fish and invertebrate species, aid in decision making regarding water and surrounding land acquisitions, aid in monitoring species and habitats, and aid in the coordination and integration of conservation efforts at the stream segment, landscape and regional levels.

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INTRODUCTION

Freshwater rivers and lakes comprise about .009% of the Earth's water, yet supports 43% (12,000 species) of total fish biodiversity. North America possesses the greatest temperate freshwater diversity on Earth, with the United States home to 10% of all freshwater fish species, 30% of all freshwater mussels, and 61% of all freshwater crayfish that have been described worldwide. Unfortunately however, this diversity is disappearing at an alarming rate (Sowa et al. 1994, Jelks et al. 2008). In the past century, 123 species of freshwater organisms have been recorded as extinct in North America (Ricciardi and Rasmussen 1999). Of the organisms found in the United States, 71% of the freshwater mussels, 51% of the crayfish, and 37% of the freshwater fish are considered vulnerable to extinction (Sowa et al. 1994). Ricciardi and Rasmussen (1999) used extinction records and an exponential decay model to derive recent and future extinction rates for North American freshwater fauna. These rates are 5 times higher than those for terrestrial fauna, and suggest that North America's temperate freshwater ecosystems are losing species at a rate similar to that of tropical rainforests.

Florida's freshwater streams are home to 126 native fish species, of which 50 are limited to freshwater. The remaining species are able to tolerate a wide range of salinities. Many streams originating in peninsular Florida are relatively young, having been completely covered by the ocean within the last 2 million years. However, streams flowing out of the highlands are much older, and their upper reaches in the Appalachian Mountains have been above sea level for up to 70 million years. This may have provided a refuge for freshwater species during periods of high sea levels, as well as providing a source of colonists once sea levels sank. Additionally, the age and isolation of some of

these ancient stream systems have allowed speciation to occur. All of Florida's freshwater fish species occur in these old stream systems, which by definition must flow through northern Florida. West Florida streams contain more species of fish than streams throughout the rest of the state, perhaps due to their proximity to the large Mississippian fauna to the west (Myers and Ewel 1990). Based on this, the streams of the Florida panhandle should contain the most diverse freshwater fish communities in the state.

Potential species habitat maps can contribute to the management and conservation of freshwater resources. These maps can be used to direct sampling efforts, identify areas suitable for species reintroduction, and to identify areas of high biodiversity and conservation value (Olden et al. 2002).

The objective of this project was to create predictive species distribution models for 25-50 species of fish documented to occur in the freshwater streams of Florida's Panhandle. For this project, the panhandle was defined as those portions of the National Hydrography Dataset's (NHD) subregions 0314 (Choctawhatchee-Escambia), 0313 (Apalachicola), and 0312 (Ochlockonee) that fall within the state boundaries of Florida (Figure 1).

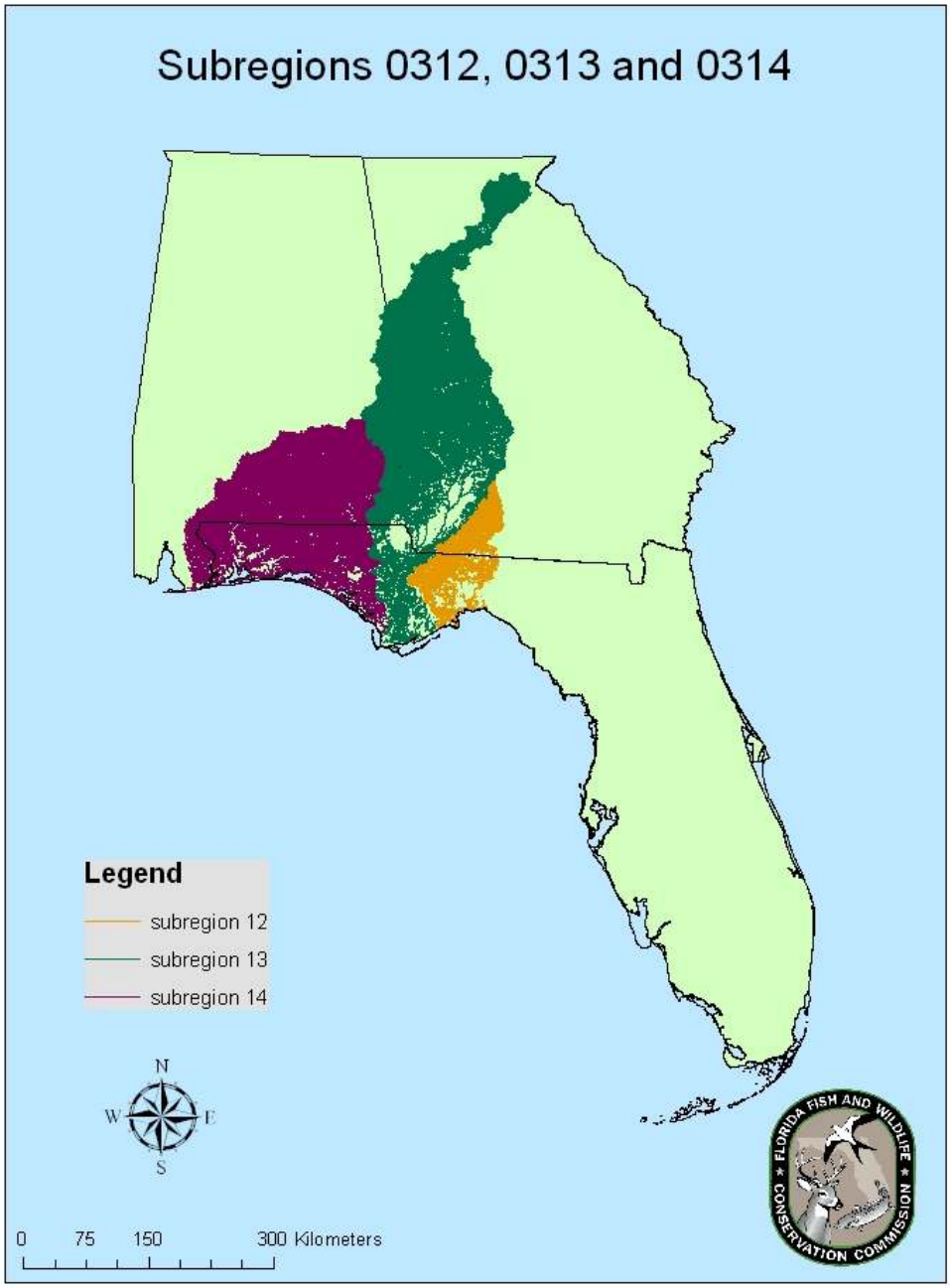


Figure 1. National Hydrography Dataset subregions 0312, 0313, and 0314.

DATA AND METHODS

Dataset Development

The development of the database occurred in 2 steps: (a) the creation of a spatial database containing species occurrences and (b) the development of the data layers representing stream attributes to be used in the modeling process. All spatial manipulations were performed using ArcGIS 9.2.

Species occurrence records.--The species occurrence records used for predictive habitat modeling were acquired from 2 sources (Figure 2). The fist set consists of survey data collected by John Knight (Florida Fish and Wildlife Conservation Commission - FWCC). His surveys were conducted from April 2005 to April 2008. During this interval 418 unique sites were sampled and a total of 12,401 records representing 116 species were collected. The second set is an existing FWCC database (fwc_fish). Although this database covers the entire state and includes lakes as well as streams, only those occurences within streams in the Florida panhandle were included in this study. These reords covered the period from Jan.1957 to Oct. 1994. They include 238 unique sites and a total of 14,218 records representing 160 species. In all, 656 unique sample sites and 26,619 records were included in the analysis. All occurrences were snapped (moved to stream segment closest to the occurence) to the Florida Stream Dataset (FSD) and checked against the recorded stream name for positional accuracy.

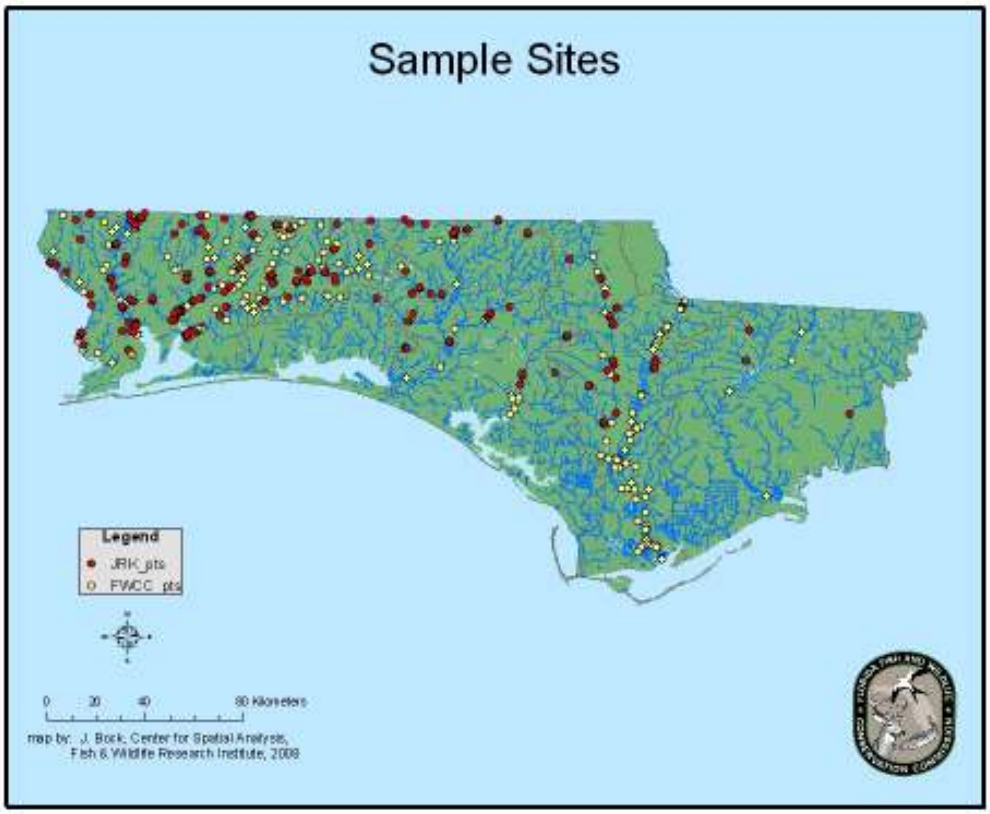


Figure 2. Map of the Florida panhandle showing sampling sites used in the analysis. Red dots represent sites surveyed by John Knight between April 2005 and April 2008. Yellow dots represent sites contained in the FWC database fwc_fish, which were surveyed between Jan. 1957 and Oct. 1994.

Stream Attribute Layers. --Data layers representing physical characteristics known to influence habitat selection in freshwater fish species were created individually. Attributes were assigned by stream segment unless otherwise noted.

Base layer.--The base layer for this project was the 1:24,000 Florida Stream Dataset (FSD). The FSD is a modified version of the Feb. 2007, USGS National Hydrography Dataset (NHD). The FSD covers the entire state, so those streams occurring beyond the boundaries of the panhandle region were removed from the layer. The FSD contains

some, but not all, of the characteristics necessary for predictive fish habitat modeling, so it was necessary to create additional layers.

Habitat characteristic layers.—Twenty habitat characteristics were used, including measures of: land use/land cover, stream size, Strahler order, location within the drainage network, flow, relative gradient, and sinuosity. Several of the layers were taken directly from the FSD, while others were derived using various methods described below.

a. Landuse/landcover

Eleven landuse/landcover categories were used to model potential habitat distributions (Table 1). Multiple studies have found that the correlation between land use and habitat quality is stronger for the whole catchment than for a buffer region (Roth et al.1996, Morely and Karr 2002), so landuse/landcover was determined for the entire HUC 12 (a 12 digit hydrologic unit code signifying a subwatershed), rather than for a buffer area. These categories represent the percentage of land in each HUC 12 containing: any type of natural land cover, forest, natural barrens, shrubland, wetlands, any type of agriculture, crops, pasture, urban areas, manmade barrens, and any type of manmade landscape. The HUC 12_landscape_2003 layer, a HUC 12 level assessment of land cover based on the FWCC's Florida Vegetation and Land Cover 2003 classification, was used to assign landuse/landcover characteristics for each stream segment in the base layer. The percentages were then reclassified into categories spanning ranges of 10% (i.e... 0-10%, greater than 10-20%, etc).

Table 1: Attribute names and definitions for the 11 landuse/landcover variables used in the modeling process.

Attribute	Definition
N_INDEX	Percentage of entire HUC 12 that consists of all natural land cover types
U_INDEX	percentage of entire HUC 12 that consists of all human-based land cover types
P_FOR	percentage of entire HUC 12 that consists of all forest land cover
PAGC	percentage of entire HUC 12 that consists of all cropland land cover
PAGP	percentage of entire HUC 12 that consists of all pasture land cover
PAGT	percentage of entire HUC 12 that consists of all agricultural land cover
P_MBAR	percentage of entire HUC 12 that consists of all manmade barren land cover
P_SHRB	percentage of entire HUC 12 that consists of all shrub lands land cover
P_URB	percentage of entire HUC 12 that consists of all urban land cover
P_WETL	percentage of entire HUC 12 that consists of all wetland land cover
P_NBAR	percentage of entire HUC 12 that consists of all natural barren land cover

b. Size

Size classification was based on catchment area. Catchment area was determined using ArcHydro 1.2 and 10m DEMs for subregions 12, 13, and 14 to create a stream network for all streams with a catchment area larger than 1 Km. The steps involved in this process were:

1. Trim DEM by HUC 8 to create a small enough area for ArcHydro.

2. Run DEM Reconditioning (Terrain Preprocessing) on the DEM to enforce the FSD stream lines. This step caused the stream network created by ArcHydro to match the FSD stream network.

3. Run Fill Sinks (Terrain Preprocessing)

4. Run Flow Direction (Terrain Preprocessing)

5. Run Flow Accumulation (Terrain Preprocessing)

6. Run Stream Definition (Terrain Preprocessing) - This step creates a stream link gird with cells from a flow accumulation grid that exceed a user defined threshold, in this case 1 Km.

7. Run Stream Segmentation (Terrain Preprocessing)

8. Run Catchment Grid Delineation (Terrain Preprocessing)

9. Run Catchment Polygon Processing (Terrain Preprocessing)

10. Run Drainage Line Processing (Terrain Preprocessing)

11. Run Drainage Point Processing (Terrain Preprocessing)

12. Run Hydro Network Generation (Network Tools)

13. Run Node/Link Schema Generation (Network Tools)

14. Run Accumulate Attributes (Attribute Tools)

The accumulate attribute function determined the area draining into each junction in the network. In most cases, there was no connection between the streams in separate HUC 8s (an eight digit hydrologic unit code signifying a subwatershed). When there was a connection, the drainage area of the upstream junction was added to the first junction downstream of where the HUC 8 change occurred prior to running Accumulate Attributes. The resulting drainage areas were then transferred to a copy of the FSD which

had been clipped to the extent of the Panhandle and dissolved by segment, then classified using the Jenks natural breaks method with Log normalization (Table 2). Drainage area was not determined for canals, due to their artificial nature. Canals were classified as a separate size category.

Table 2. Drainage areas for the five size categories used in the modeling process. Drainage area was classified using the Jenks natural break method with log normalization.

Size Class	Drainage Area
Headwater	Less than 3.7460 km²
Creek	3.7490 km² - 17.1436 km²
Small River	17.4962 km² - 126.6900 km²
Large River	126.7711km² - 1674.1980 km²
Big River	Greater than 1677.6140 km²

c. Strahler order

Stream order is a means of classifying streams according to their pattern of branching. Headwater streams are first order streams, which converge to form second order streams. A third order stream is formed by the union of 2 second order streams and so on until the main river is reached. In most systems habitat diversity, stream size, turbidity, and temperatures increase with stream order; and gradient and environmental fluctuations decrease. The number of species in the fish community also tends to increase with stream order (Moyle and Cech 2004). Strahler order was determined from the attributes in the FSD.

d. Location within the drainage network – connectivity and size discrepancy

Connectivity and size discrepancy describe the spatial location of a segment within the drainage network. Connectivity simply describes the size of the next segment downstream from the segment of interest. The 2 size discrepancy classes were included

and coded following the protocol developed by MoRAP (Missouri Resource Assessment Partnership) (Annis 2002) (Table 3). For streams of similar size, tributaries to the main channel may have greater species richness than streams located in the headwaters of a basin. Large river species can migrate into the lower parts of tributaries, and larger streams could provide a pool of immigrants for recolonization following a disturbance (Collares-Pereira 2002).

Table 3. Size discrepancy between panhandle streams and the associated size discrepancy codes classified with 11 classes and with 2 classes

Size Discrepancy	Size Discrepancy 11	Size Discrepancy 2
None	0	0
Headwater - Creek	1	0
Headwater- Sm. River	2	1
Headwater - Lg. River	3	1
Headwater - Big River	4	1
Creek - Sm. River	5	1
Creek - Lg. River	6	1
Creek - Big River	7	1
Sm. River - Lg. River	8	0
Sm. River - Big River	9	1
Lg. River - Big River	10	0
Any Disconnects	-1	-1

e. Flow

Flow describes the constancy of stream water flow (i.e. perennial vs. intermittent) during normal low flow conditions or periods of no rainfall. Flow can exert a considerable influence on the community composition and abundance of riverine assemblages, and therefore must be considered when modeling distribution in aquatic systems (Loan-Wilsey et al. 2005). The FSD contained flow data for most segments; however, those reaches not included in the NHD did not have flow data. Flow for

unknown segments was determined following the procedure described by Annis (2002). The segments with known flow in each ecological drainage unit were queried to determine the average Shreve link at which flow generally changes from intermittent to perennial (Table 4). This information was then applied to all segments with unknown flow. Flow was determined for 680 out of 26,358 segments in this manner.

Table 4. Average shreve link at which flow becomes perennial for streams within each ecological drainage unit in the study area.

EDU	Average link at which flow becomes perennial
Big Bend	1
Chattahoochee	3
Choctawhatchee Bay	2
Flint - Apalachicola	2
Panama City	4
West Florida Panhandle	2

f. Relative gradient

Gradient, or the ratio of change in elevation in a stream per unit distance, has been found to influence many key environmental variables in aquatic habitats. The presence, nature, and diversity of riverine habitat types, such as number, size, and depth of pools; as well as mean annual discharge, drainage area, and median size of bed materials are all related to gradient. Gradient can also affect mean values and spatial patterns of stream temperatures and dissolved oxygen concentrations at local scales (Moyle and Cech 2004, Loan-Wilsey et al. 2005). Therefore, relative gradient was included as a predictive variable. The gradient of all segments classified as headwaters was calculated as the first step. Segments classified as headwaters were then removed prior to the calculation of

gradient for the larger stream classes. Gradient was calculated for segments between all confluences. This resulted in the gradient being taken over much longer distances than if the streams had been segmented by numerous headwater tributaries. This becomes important when considering the small drop in elevation experienced by a large stream over a set distance. Generating gradients between confluences with headwaters for the larger streams results in many of the segments getting a gradient of zero or even a negative gradient (from minor errors in the DEM and/or from the stream not laying on the exact grid cell it should). Gradient was relativized to both subregion and stream size class, and was classified following the procedure described in Annis (2002) (Table 5).

Table 5. Classification table for gradient after it has been relativized to both size class and subregion. Gradient was determied and classified following the procedure described in Annis (2002)

Size	Relative Gradient	SR12	SR13	SR14
Big River	Low	0-.1	0-.1	0-.1
	Medium	.2-.3	.2-.3	.2-.3
	High	≥ .4	≥ 4	≥ .4
Large River	Low	0-.2	0-.2	0-.4
	Medium	.3-.5	.3-.5	.5-.8
	High	≥ .6	≥ .6	≥ .9
Small River	Low	0-.7	0-.6	0-1
	Medium	.8-1.5	.7-1.3	1.1-1.9
	High	≥ 1.6	≥ 1.4	≥ 2
Creek	Low	0-2	0-1.8	0-2.3
	Medium	2.1-3.8	1.9-3.6	2.4-3.7
	High	≥ 3.9	≥ 3.7	≥ 3.8
Headwater	Low	0-5.2	0-5.1	0-6.9
	Medium	5.3-9.9	5.2-10.1	7-12.3
	High	≥ 10	≥ 10.2	≥ 12.4

g. Sinuosity

For this study, sinuosity was classified based on Rosgen's (1994) description of major stream types (Table 6). Sinuosity was determined using an ArcScript (Bull 2005).

Table 6. Classification values for sinuosity. Values are taken from Rosgen (1994)

Straight	1.0 -1.2
Low sinuosity	greater than 1.2 - 1.4
Meandering	greater than 1.4 – 1.5
Tortuosly meandering	greater than 1.5

h. Surficial geology

Surficial geology was included as a substitute for substrate data. Surficial geology was taken from the FSD, and segments were assigned the type of surficial geology through which the majority of the segment flowed. There were 15 possible categories of surficial geology in the Panhandle: alluvium, clay, sand and gravel; clay, sand, fossils; clayey sand, clay; clayey sand, clay, shell; clayey sand, clay, silt; fossiliferous sand, clay, calcareous; gravel, coarse sand, silt, clay; limestone; limestone, dolostone, clay; limestone, sand, clay, shell; med fine sand silt; sand; sand, peat, clay; and sand, silt, clay, limestone

Other habitat characteristic layers. Ecological drainage unit was considered for inclusion in the modeling process; however, due to the scarcity of sample sites in the Chattahoochee, Choctawhatchee Bay and Big Bend EDUs leading to unrealistic range restrictions for the majority of species, this layer was not used in the production of the final model.

Model Creation

Modeling Algorithm.--Many types of algorithms are able to classify the probability of a species presence as a function of a set of environmental variables. Selection of the best modeling algorithm requires careful consideration of various factors, such as ability to work with presence only data, ability to work well with small sample sizes and proven track record (Pearson 2007). DesktopGARP (Genetic Algorithm Rule-Set Prediction) was used to model potential species distribution. GARP is able to use presence only data, can produce accurate models from a small sample size, and has a history of successful use in predictive species modeling (Stockwell and Peters 2002, Peterson and Shaw 2003).

Explanation of Genetic Algorithms and GARP.-- Genetic algorithms mimic evolution by natural selection by operating on populations of competing solutions to a problem that evolve over time to converge to an optimal solution. The basic approach involves 4steps. First, random potential solutions (chromosomes) are developed. Second, the potential solutions are modified using the processes of reproduction, mutation, and crossover. Third, the fitness of the new solutions (i.e. how well they solve the problem) is evaluated. Fourth, the most fit or best solutions are selected. Steps 2 through 4, which can be seen as a generation, are repeated using the solutions selected in step 4 until a stopping criterion is reached. In this way, solutions to a problem evolve through the multiple iterations (Olden et al. 2008).

The program GARP searches for non-random associations between environmental characteristics of localities of recorded occurrence versus those of the overall study area. It works in an iterative process of rule selection, evaluation, testing and incorporation or rejection to produce a heterogeneous rule-set characterizing the species' ecological

requirements. First, an initial population of rules is developed with each rule based on one of 4 rule types: atomic, BIOCLIM, negated BIOCLIM and logit. An atomic rule is a conjunction of categories or single values of some variables. A BIOCLIM rule creates an envelope indicating where the habitat is suitable for a species by taking the range for all variables in which that species has been found to occur. A negated BIOCLIM rule is similar, except that some variables may be irrelevant. Logit rules are an adaptation of logistic regression models to rules. GARP then tests the population of rules against a randomly selected subset of the data and saves the best rules to a rule archive. GARP then selects a new population, using the rule archive and a randomized selection procedure. The new population is then modified by the application of 3 heuristic operators designed to mimic genetic recombination: join, crossover, and mutate. Join is simply the merging of 2 rules to create a longer rule. The crossover operation occurs when 2 rules exchange a part of their binary code, creating 2 new rules. The mutate operator changes a rule by randomly changing a single value. After the new rules are created GARP measures their fitness, and the more successful an operator is, the more it will be used in future generations. The change in predictive accuracy from one iteration to the next is used to evaluate whether a particular rule should be included in the model (rule-set). The model runs until the specified number of iterations or until convergence (addition of new rules has no appreciable effect on the intrinsic accuracy measure) (Stockwell and Peters 1999 and Anderson et al. 2003).

Preparation of Occurrence Points.--A separate layer of occurrence points was created for each species to be modeled. This layer was then cleaned to prevent areas that had been sampled more than once from being counted as multiple points. Species were

selected for modeling if they had 25 or more seperate occurence points. For each species, 25% of the occurrence points were randomly selected to be used to independently validate the models. These validation points were withheld completely from GARP's model- building and internal evaluation process, and were used only for evaluating the final model. Random selection was accomplished using an ESRI ArcScript (Lead 2008). The remaining 75 % of the species occurrence records, or model points, were entered into GARP for use in model calibration.

Dataset creation.--All habitat characteristic layers were converted into ASCII grids, the format required by GARP. Additionally, 1 ASCII layer was used as a mask to define the extent of the study area. For this study, ASCII cells were ste to 100m. These ASCIIs were all placed in the same folder and converted to a GARP dataset using GARP dataset manager.

Settings Used with GARP.--DesktopGARP was set to use 75% of the model points in model building and the remaining 25% of the model points for validation. A minimum of 1,000 runs was performed per species in order to ensure the creation of sufficient high-quality models. The number of runs was increased to 2,000 runs for more common species. The convergence limit was set to .01 and the maximum number of iterations was set to 1,000. In practice, the number of iterations never exceeded 130, meaning that the convergence limit was always reached.

Best Subset Selection.--Because of stochastic elements in the GARP algorithm, such as mutation and crossing over, GARP does not produce a single unique solution. In fact, the under-determination (the available data do not let us make a decision between 2 or more theories) of the system yields multiple solutions holding identical values for the

optimization criterion (Anderson et al. 2003). To optimize model performance, 1,000-2,000 replicate models of predicted distribution were created for each species. From these, all models achieving less than 10% extrinsic and intrinsic omission error were selected for further consideration. Covert et al. (2007) found that using less than 10% omission error offered the best compromise between omission and commission error values when mapping predicted species distributions for the Ohio Aquatic GAP. Of these, the 20 models having the lowest commission error were combined to create the predictive model for each species. Summing the 20 models for each species (value of 1 for a pixel of predicted presence; value of 0 for a predicted absence) produced a composite map with grid values ranging from 0-20, representing the number of models that predicted the species' presence in the pixel (Anderson et al. 2003). Lastly, the omission error of the final map was limited to 10% by finding the grid value at which 90% of the model points fell within an area predicted present. This grid value was then used to create the final map of the predicted species distribution (Covert et al. 2007). The final map was trimmed to the known range, unless there were occurrence points beyond the range cited in the literature.

Model Validation

The lack of absence data creates difficulties when validating predictive habitat models. Traditional confusion matrix based measures, such as accuracy and Kappa, are not possible when absence data is lacking. Additionally, validation methods which make use of commission error may be inappropriate when large areas of the study area have not been adequately sampled. Commission errors might represent true absences, or they might represent areas which have not been sampled, or in which the species was present

but not detected (Pearson 2007). The proportion of observed occurrences predicted correctly, or the sensitivity, is a common measure of a model's usefulness. The final predicted species distribution was tested against the validation points created by withholding 25% of the species occurrence records from the modeling process. A disadvantage to using sensitivity to evaluate a model's usefulness is that it is possible to achieve a very high sensitivity by simply predicting that the species is present at an excessively large proportion of the study area. To overcome this problem it is necessary to test the model for statistically. An exact one-tailed binomial test was used to test whether occurrence points fell into areas predicted present more often than expected under a random model (the product of proportional area and number of test occurrence points). The percentage of the study area predicted present for each species was determined using an ArcScript (O'Neal 2004). Sensitivity was calculated for model points, validation points and total occurrence points for each species. Significance was assessed for the sensitivity of validation points and total points. It was not calculated for model points because the sensitivity was forced to be at least 90% by the modeling procedure.

Testing the Effect of Using Only Three Broad Landuse/Landcover Characteristics

The models with validation sensitivities of less than 80% were rerun using only 3 broad categories of landuse/landcover: percent natural cover, percent human altered cover, and percent land used for any type of agriculture (as well as all other stream attributes used for the creation of the other models). This was to determine whether the inclusion of so many landuse/landcover characteristics was causing the model to overfit the data.

RESULTS

Models Created Using all Habitat Variables

The potential habitat ranges of 55 species of fish known to occur in Florida's panhandle region were mapped (Table 7) (Figures 3-57). The number of models required to achieve an omission rate of 10% or less ranged from 1 to 15. Commission errors for the models used in the mapping process ranged from 4.25% to 33.04%. The percentage of the study area classified as suitable habitat varied between 4% and 28% (Table 8). Sensitivity values, or the percentage of occurrence points correctly predicted as presence, ranged from 50% to 100% when only validation points were considered and from 83% to 100% when all points were considered. The p-values for these sensitivity values were never greater than .01 (Table 9).

Table 7. The scientific names, common names, and Integrated Taxonomic Information System codes of the 55 species of Panhandle fish modeled in this study.

Scientific Name	Common Name	IT IS code
Alosa alabamae	Alabama shad	161705
Alosa chrysochloris	Skipjack herring	161707
Ambloplites ariommus	Shadow bass	168099
Ameiurus natalis	Yellow Bullhead	164041
Amia calva	Bowfin	161104
Ammocrypta bifascia	Florida sand darter	168514
Anguilla rostrata	American eel	161127
Carpiodes cyprinus	Quillback	163917
Cyprinella venusta	Blacktail shiner	163809
Dorosoma cepedianum	Gizzard shad	161737
Dorosoma petenense	Threadfin shad	161738
Elassoma zonatum	Banded pygmy sunfish	168171
Erimyzon sucetta	Lake chubsucker	163922
Erimyzon tenuis	Sharpfin chubsucker	163926
Esox niger	Chain Pickerel	162143
Etheostoma davisoni	Choctawhatchee darter	168387
Etheostoma edwini	Brown Darter	168390
Etheostoma swaini	Gulf Darter	168439
Fundulus escambiae	Eastern starhead topminnow	165675
Fundulus olivaceous	Blackspotted topminnow	165655
Gambusia affinis	Mosquitofish	165878
Hybopsis sp. cf winchelli	Coastal chub	
Ichthyomyzon gagei	Southern brook lamprey	159727
Ictalurus punctatus	Channel catfish	163998
Labidesthes sicculus	Brook silverside	166016
Lepisosteus oculatus	Spotted gar	161095
Lepisosteus osseus	Longnose gar	161094
Lepomis auritus	Redbreast sunfish	168131
Lepomis cyanellus	Green sunfish	168132
Lepomis macrochirus	Bluegill	168141
Lepomis marginatus	Dollar sunfish	168152
Lepomis megalotis	Longear sunfish	168153
Lepomis microlophus	Redear sunfish	168154
Lepomis punctatus	Spotted sunfish	168155
Micropterus punctulatus	Spotted bass	168161
Micropterus salmoides	Largemouth bass	168160
Minytrema melanops	Spotted sucker	163959
Morone saxatilis	Striped bass	167680
Moxostoma poecilurum	Blacktail redhorse	163932
Mugil cephalus	Striped mullet	170335
Notemigonus crysoleucas	Golden shiner	163368
Notropis chalybaeus	Ironcolor shiner	163403

Scientific Name	Common Name	IT IS code
Notropis harperi	Redeye chub	163444
Notropis longirostris	Longnose shiner	163452
Notropis maculatus	Taillight shiner	163454
Notropis petersoni	Coastal shiner	163460
Notropis texanus	Weed shiner	163420
Noturus leptacanthus	Speckled madtom	164019
Opsopoeodus emiliae	Pugnose minnow	163876
Percina nigrofasciata	Blackbanded darter	168490
Pomoxis nigromaculatus	Black crappie	168167
Pteronotropis hypselopterus	Sailfin shiner	201941
Semotilus thoreauianus	Dixie chub	163379
Strongylura marina	Atlantic needlefish	165551
Trinectes maculatus	Hogchoker	172982

Table 8. Parameters of the 55 Panhandle fish species modeled in this study. Occurrence points describes: the total number of occurrence points for each species (a) the number of points input into GARP for modeling (b) and the number of points withheld for independent validation of the model (c). Range of commission error of the best 20 GARP models used to produce the final potential distributions (d). After the best 20 GARP models were combined, this value represents the minimum number of models that, when summed, agreed to produce a less than 10% omission error (e). The number of runs performed per species (f). The percent of the total study area predicted to be potential habitat by the final potential distribution model (g).

Scientific Name	Occurrence Points Total (a)	Model (b)	Val. (c)	Commission range of 20 models (%) (d)	Number of models used to achieve less than 10% omission error (out of 20) (e)	Runs (f)	%study area predicted (g)
Alosa alabamae	36	27	9	6.05-9.19	1	1000	5
Alosa chrysochloris	55	41	14	10.27-16.78	3	1000	9
Ambloplites ariommus	164	123	41	16.51-18.99	5	2000	6
Ameiurus natalis	159	119	40	25.93-28.78	3	2000	24
Amia calva	122	92	30	9.23-15.06	4	1000	8
Ammocrypta bifascia	61	46	15	8.22-11.14	4	1000	7
Anguilla rostrata	168	126	42	20.20-24.70	9	2000	21
Carpiodes cyprinus	60	45	15	5.39-7.51	5	1000	3
Cyprinella venusta	305	229	76	16.74-19.00	9	2000	15
Dorosoma cepedianum	75	56	19	8.01-11.64	5	2000	7
Dorosoma petenense	63	47	16	4.25-7.97	5	1000	4
Elassoma zonatum	30	23	7	22.34-33.04	2	1000	14
Erimyzon sucetta	72	54	18	26.70-29.91	4	1000	27
Erimyzon tenuis	77	58	19	13.31-16.41	1	1000	11
Esox niger	133	100	33	13.41-16.67	15	2000	18
Etheostoma davisoni	38	29	9	11.52-16.00	2	1000	09
Etheostoma edwini	151	113	38	18.59-20.70	1	2000	14
Etheostoma swaini	90	68	22	16.22-20.01	4	1000	15
Fundulus escambiae	40	30	10	15.22-22.81	2	1000	13
Fundulus olivaceous	224	168	56	21.95-24.99	3	2000	19
Gambusia affinis	71	53	18	20.20-26.00	4	1000	19
Hybopsis sp. cf winchelli	116	88	28	12.82-15.31	4	1000	12
Ichthyomyzon gagei	201	151	50	21.95-28.66	4	2000	2
Ictalurus punctatus	121	91	30	7.40-10.85	4	1000	8
Labidesthes sicculus	193	145	48	13.73-19.48	8	1000	15

Scientific Name	Occurrence Points Total (a)	Model (b)	Val. (c)	Commission range of 20 models (%) (d)	Number of models used to achieve less than 10% omission error (out of 20) (e)	Runs (f)	%study area predicted (g)
Lepisosteus oculatus	150	113	37	8.11-11.24	7	2000	11
Lepisosteus osseus	102	77	25	9.31-13.46	1	1000	6
Lepomis auritus	191	143	48	14.78-18.27	3	2000	11
Lepomis cyanellus	32	24	8	19.13-22.73	1	1000	13
Lepomis macrochirus	327	247	80	18.35-25.10	6	2000	19
Lepomis marginatus	124	93	31	20.93-23.78	8	2000	2
Lepomis megalotis	240	180	60	13.88-19.34	5	2000	13
Lepomis microlophus	208	156	52	12.75-16.94	8	2000	14
Lepomis punctatus	199	149	50	22.56-25.64	13	2000	26
Micropterus punctulatus	178	134	44	12.62-17.30	8	2000	12
Micropterus salmoides	286	215	71	15.62-18.92	14	2000	21
Minytrema melanops	265	199	66	14.40-19.16	8	2000	16
Morone saxatilis	31	23	8	7.24-10.52	1	1000	4
Moxostoma poecilurum	161	121	40	10.72-12.62	7	1000	11
Mugil cephalus	127	95	32	7.58-10.97	7	2000	7
Notemigonus crysoleucas	59	44	15	14.17-21.85	14	1000	23
Notropis chalybaeus	34	26	8	23.25-31.79	2	1000	6
Notropis harperi	74	56	18	13.01-17.01	2	1000	8
Notropis longirostris	128	96	32	9.04-10.23	2	2000	9
Notropis maculatus	42	32	10	6.58-13.36	2	1000	5
Notropis petersoni	182	137	45	15.04-18.40	9	2000	19
Notropis texanus	384	289	95	24.36-27.69	4	2000	22
Noturus leptacanthus	316	237	79	23.56-28.57	5	2000	26
Opsopoeodus emiliae	86	65	21	10.94-14.30	8	1000	7
Percina nigrofasciata	431	323	108	27.76-29.71	3	2000	28
Pomoxis nigromaculatus	89	67	22	8.71-12.31	8	1000	8
Pteronotropis hypselopterus	264	198	66	16.91-19.57	4	2000	16
Semotilus thoreauianus	47	35	12	15.09-20.61	1	1000	12
Strongylura marina	59	44	15	11.35-15.82	1	1000	7
Trinectes maculatus	129	97	32	11.34-15.38	8	2000	11

Table 9. Accuracy statistics for the potential distributions for the 55 fish modeled in the project. The ratio of total points falling in areas of predicted habitat to total points (a). Sensitivity, or percent correctly classified as present, for all of the points for a species (b) p-value for total sensitivity, or the chance that the number of points classified correctly could be the results of chance alone (c). The ratio of model points falling in areas of predicted habitat to total model points (d). Sensitivity, or percent correctly classified as present, for all of the model points for a species (e). The ratio of validation points falling in areas of predicted habitat to total validation points (f). Sensitivity, or percent correctly classified as present for all of the validation points for a species (g). P-value for validation sensitivity, or the chance that the number of validation points classified correctly could be the results of chance alone (h).

Scientific Name	Total points classified correctly (a)	sensitivity (b)	p-value (c)	Model points classified correctly (d)	sensitivity (e)	Validation points classified correctly (f)	sensitivity (g)	p-value (h)
Alosa alabamae	33/36	0.92	7.16E-40	27/27	1.00	6/9	0.67	1.15102E-06
Alosa chrysochloris	51/55	0.93	1.09E-48	37/41	0.90	14/14	1.00	2.29E-15
Ambloplites ariommus	144/164	0.88	1.89E-91	111/123	0.90	33/41	0.80	1.35E-19
Ameiurus natalis	144/159	0.91	3.85E-71	108/119	0.91	36/40	0.90	1.04E-24
Amia calva	108/122	0.89	9.20E-102	83/92	0.90	25/30	0.83	3.61E-23
Ammocrypta bifascia	42/46	0.91	3.84E-44	42/46	0.91	11/15	0.73	2.07E-10
Anguilla rostrata	151/168	0.90	6.97E-82	114/126	0.90	37/42	0.88	2.27E-20
Carpiodes cyprinus	53/60	0.88	6.07E-73	42/45	0.93	11/15	0.73	2.16E-14
Cyprinella venusta	272/305	0.89	6.92E-183	205/229	0.90	67/76	0.88	2.12E-45
Dorosoma cepedianum	69/75	0.92	2.69E-72	51/56	0.91	18/19	0.95	2.89E-20
Dorosoma petenense	57/63	0.90	3.47E-67	43/47	0.91	14/16	0.88	6.66E-17
Elassoma zonatum	28/30	0.93	4.02E-22	22/23	0.96	6/7	0.86	4.64E-05
Erimyzon sucetta	63/72	0.88	7.92E-27	49/54	0.91	14/18	0.78	1.05E-05
Erimyzon tenuis	68/77	0.88	3.75E-55	53/58	0.91	15/19	0.79	1.05E-11
Esox niger	121/133	0.91	2.80E-75	90/100	0.90	31/33	0.94	2.95E-21
Etheostoma davisoni	36/38	0.95	1.32E-35	27/29	0.93	9/9	1.00	3.87E-10
Etheostoma edwini	133/151	0.88	1.67E-92	102/113	0.90	31/38	0.82	1.54E-20
Etheostoma swaini	80/90	0.89	1.41E-54	62/68	0.91	18/22	0.82	5.86E-12
Fundulus escambiae	39/40	0.98	9.70E-34	29/30	0.97	1010	1.00	1.38E-09
Fundulus olivaceous	206/224	0.92	9.51E-125	151/168	0.90	55/56	0.98	9.77E-39
Gambusia affinis	61/71	0.86	5.89E-34	48/53	0.91	13/18	0.72	1.37E-06
Hybopsis sp. cf winchelli	104/116	0.90	2.59E-81	79/88	0.90	25/28	0.89	2.16E-20
Ichthyomyzon gagei	186/201	0.93	5.57E-110	139/151	0.92	47/50	0.94	1.43E-29
Ictalurus punctatus	109/121	0.90	1.19E-104	82/91	0.90	27/30	0.90	7.72E-27
Labidesthes sicculus	171/193	0.89	1.82E-114	130/145	0.90	41/48	0.85	4.03E-27
Lepisosteus oculatus	138/150	0.92	2.22E-116	102/113	0.90	36/37	0.97	1.02E-33
Lepisosteus osseus	91/102	0.89	2.22E-116	69/77	0.90	22/25	0.88	2.54E-24
Lepomis auritus	170/191	0.89	4.77E-137	128/143	0.90	42/48	0.88	3.40E-34
Lepomis cyanellus	28/32	0.88	2.74E-26	24/24	1.00	4/8	0.50	1.29E-02
Lepomis macrochirus	290/327	0.89	8.55E-137	224/247	0.91	66/80	0.83	2.07E-34
Lepomis marginatus	84/93	0.90	2.56E-48	84/93	0.90	25/31	0.81	6.87E-13
Lepomis megalotis	218/240	0.91	2.50E-164	163/180	0.91	55/60	0.92	5.10E-43

Scientific Name	Total points classified correctly (a)	sensitivity (b)	p-value (c)	Model points classified correctly (d)	sensitivity (e)	Validation points classified correctly (f)	sensitivity (g)	p-value (h)
Lepomis microlophus	182/208	0.88	7.22E-125	140/156	0.90	42/52	0.81	4.99E-27
Lepomis punctatus	179/199	0.90	6.98E-81	134/149	0.90	45/50	0.90	2.31E-21
Micropterus punctulatus	159/178	0.89	6.06E-123	120/134	0.90	39/44	0.89	7.14E-31
Micropterus salmoides	253/286	0.88	2.79E-132	194/215	0.90	59/71	0.83	8.19E-29
Minytrema melanops	242/265	0.91	3.62E-162	183/199	0.92	59/66	0.89	2.60E-39
Morone saxatilis	28/31	0.90	2.88E-36	22/23	0.96	6/8	0.75	1.07E-07
Moxostoma poecilurum	144/161	0.89	4.91E-117	110/121	0.91	34/40	0.85	4.98E-27
Mugil cephalus	115/127	0.91	1.39E-117	86/95	0.91	29/32	0.91	1.29E-30
Notemigonus crysoleucas	52/59	0.88	3.68E-26	40/44	0.91	12/15	0.80	4.88E-06
Notropis chalybaeus	32/34	0.94	3.96E-37	24/26	0.92	8/8	1.00	1.68E-10
Notropis harperi	65/74	0.88	2.65E-61	51/56	0.91	14/18	0.78	9.87E-13
Notropis longirostris	114/128	0.89	2.86E-102	86/96	0.90	28/32	0.88	1.31E-25
Notropis maculatus	35/42	0.83	5.54E-39	29/32	0.91	6/10	0.60	2.75458E-06
Notropis petersoni	158/182	0.87	4.19E-87	122/137	0.89	36/45	0.80	1.53E-18
Notropis texanus	345/384	0.90	3.58E-178	259/289	0.90	86/95	0.91	3.63E-46
Noturus leptacanthus	282/316	0.89	2.06E-124	214/237	0.90	68/79	0.86	5.76E-29
Opsopoeodus emiliae	80/86	0.93	1.24E-84	61/65	0.94	19/21	0.90	2.09E-20
Percina nigrofasciata	388/431	0.90	8.74E-162	291/323	0.90	97/108	0.90	2.30E-41
Pomoxis nigromaculatus	82/89	0.92	4.38E-81	62/67	0.93	20/22	0.91	2.27E-20
Pteronotropis hypselopterus	234/264	0.89	9.63E-150	180/198	0.91	54/66	0.82	6.67E-32
Semotilus thoreauianus	43/47	0.91	2.75E-35	33/35	0.94	10/12	0.83	3.24E-08
Strongylura marina	59/59	1.00	7.26E-69	44/44	1.00	15/15	1.00	4.75E-18
Trinectes maculatus	118/129	0.91	5.72E-99	87/97	0.90	31/32	0.97	5.49E-29

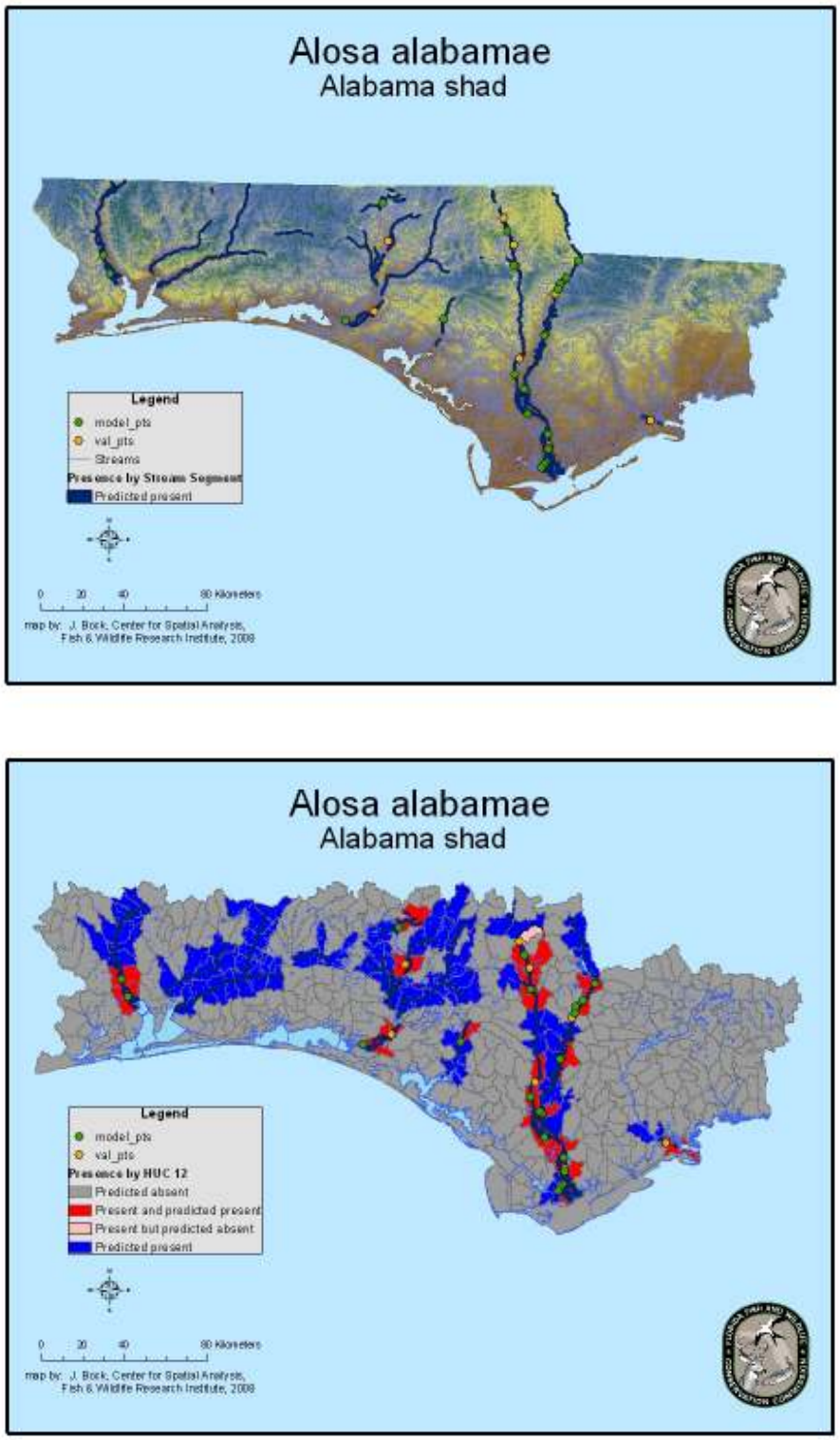
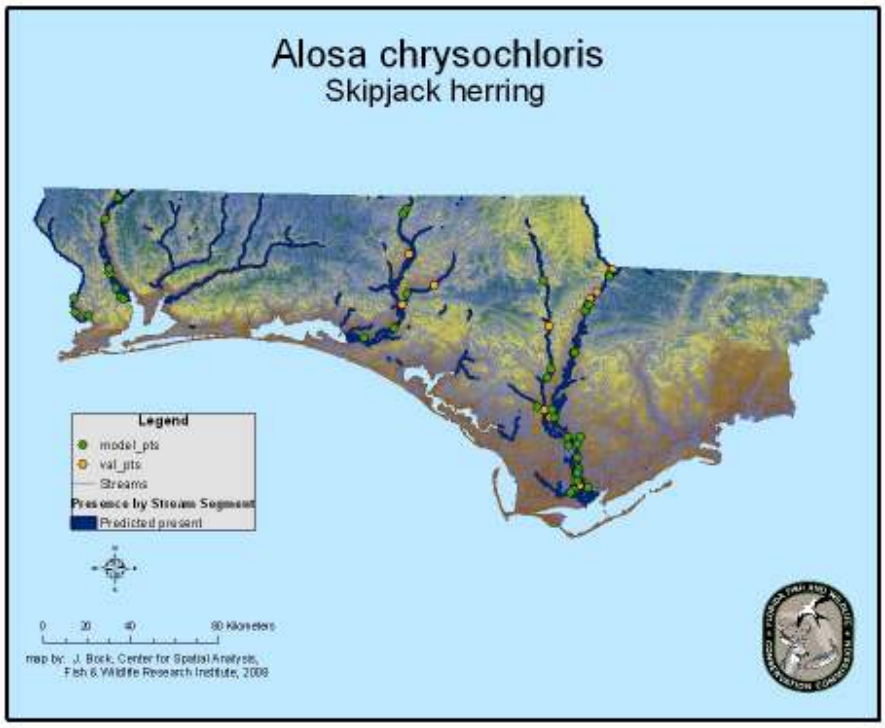


Figure 3. Potential habitat for *Alosa alabamae* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 27) represent the species occurrence points used in the modeling process while val_pts. (n =9) represent the species occurrence records withheld from the modeling process for independent validation.



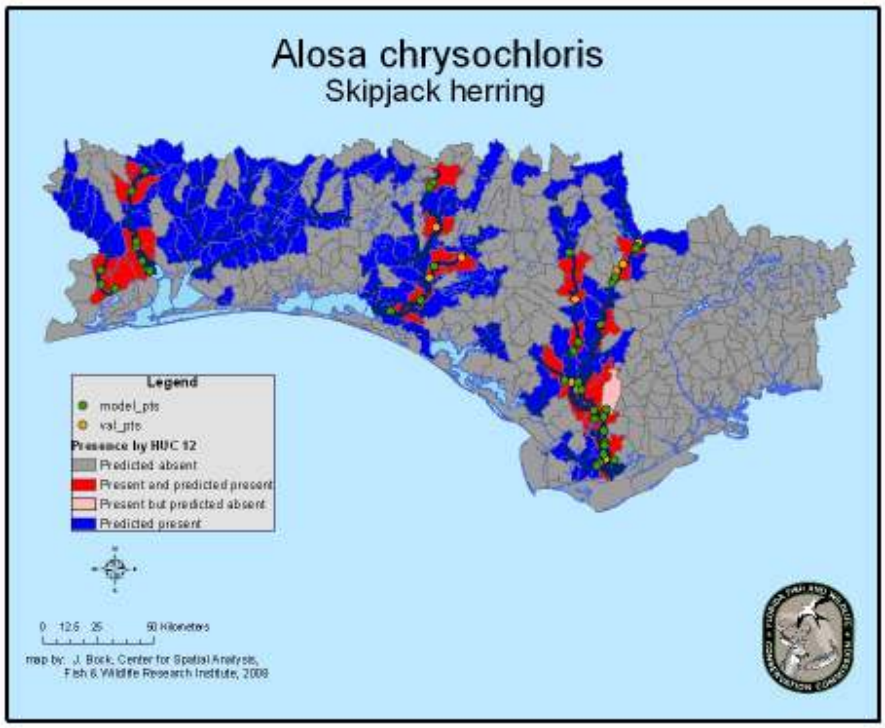
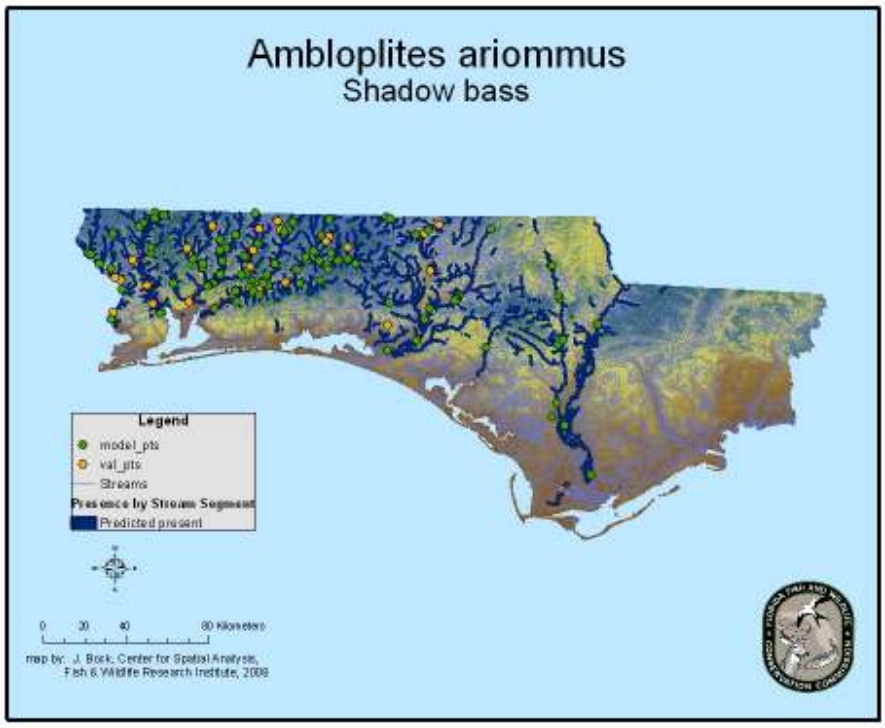


Figure 4. Potential habitat for *Alosa chrysochloris* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 41) represent the species occurrence points used in the modeling process while val_pts. (n =14) represent the species occurrence records withheld from the modeling process for independent validation.



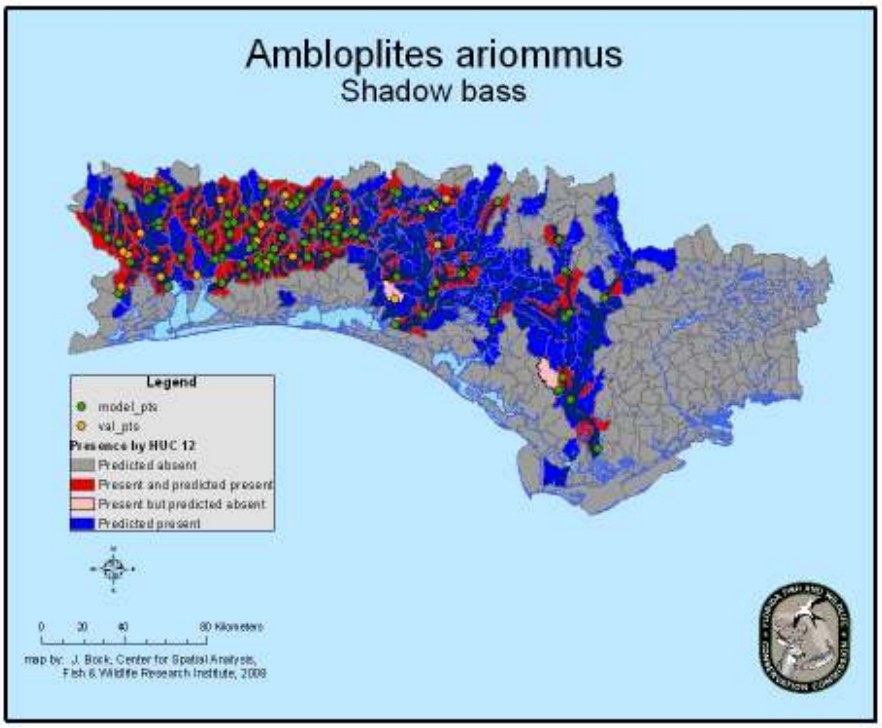
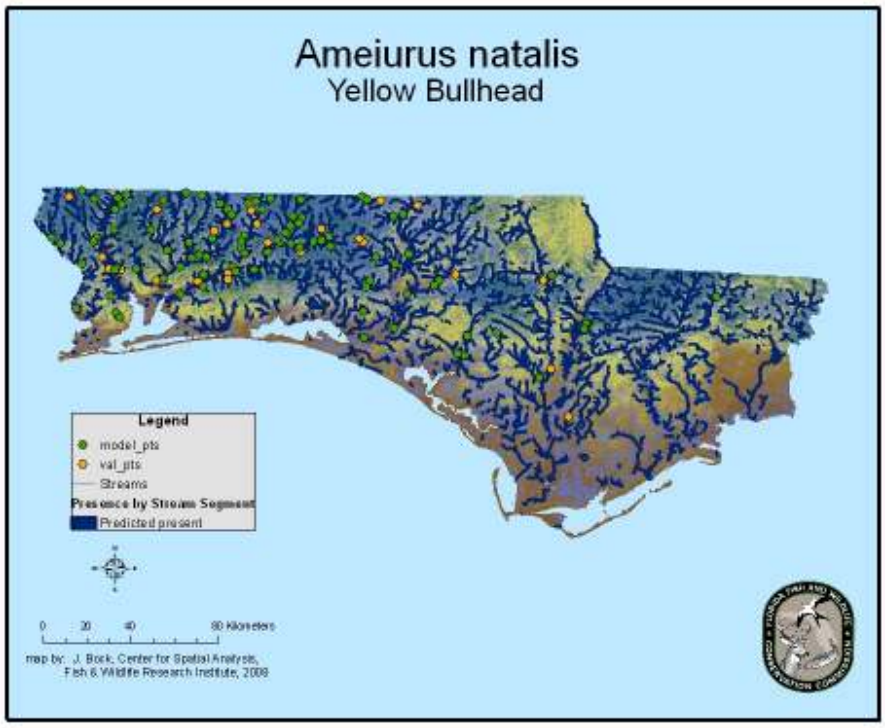


Figure 5. Potential habitat for *Ambloplites ariommus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 123) represent the species occurrence points used in the modeling process while val_pts. (n = 41) represent the species occurrence records withheld from the modeling process for independent validation.



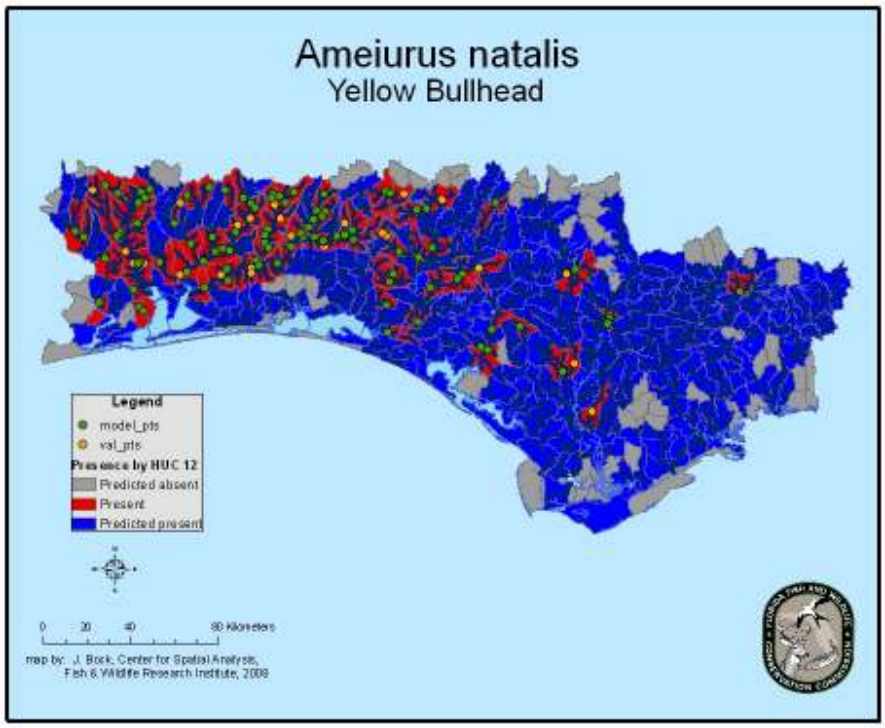


Figure 6. Potential habitat for *Ameiurus natalis* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 119) represent the species occurrence points used in the modeling process while val_pts. (n = 40) represent the species occurrence records withheld from the modeling process for independent validation.

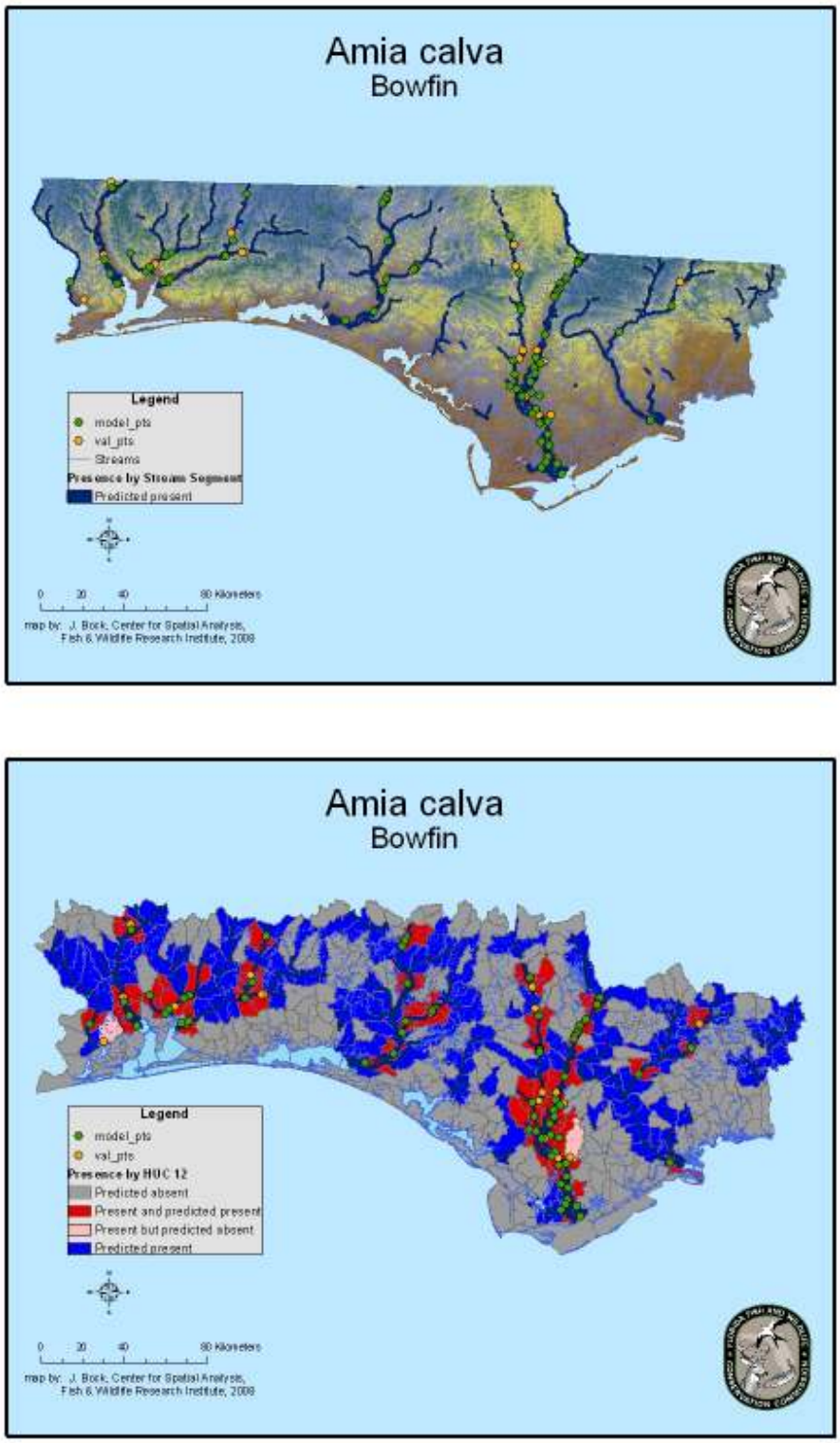
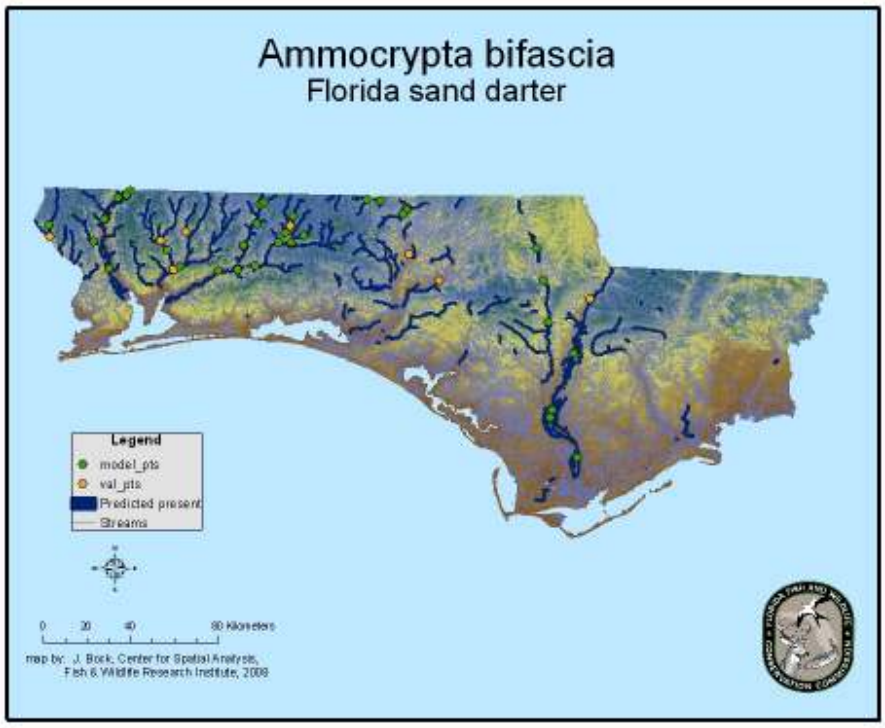


Figure 7. Potential habitat for *Amia calva* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 92) represent the species occurrence points used in the modeling process while val_pts. (n = 30) represent the species occurrence records withheld from the modeling process for independent validation.



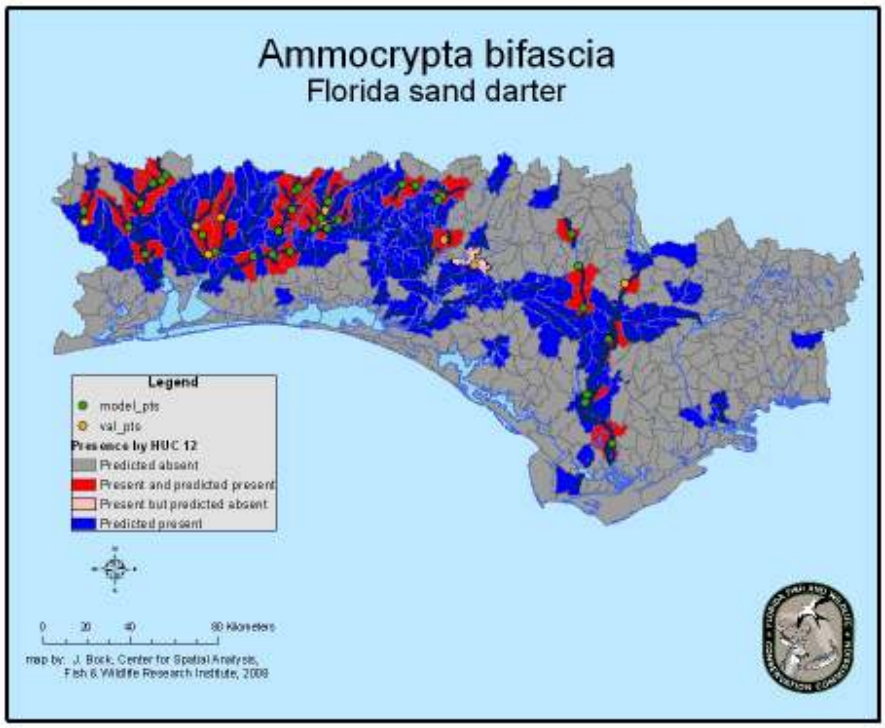
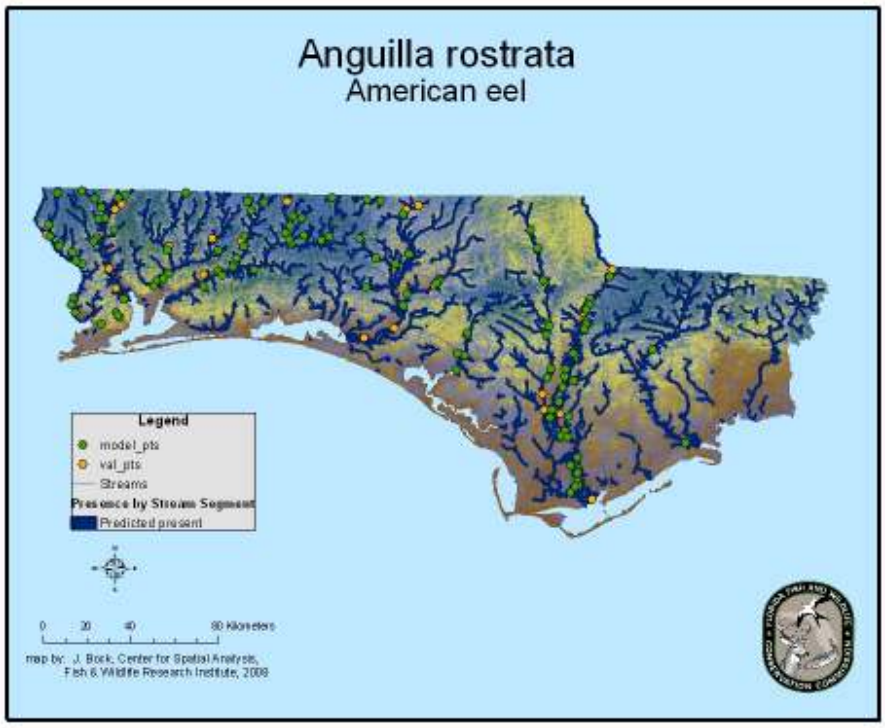


Figure 8. Potential habitat for *Ammocrypta bifascia* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 46) represent the species occurrence points used in the modeling process while val_pts. (n = 15) represent the species occurrence records withheld from the modeling process for independent validation.



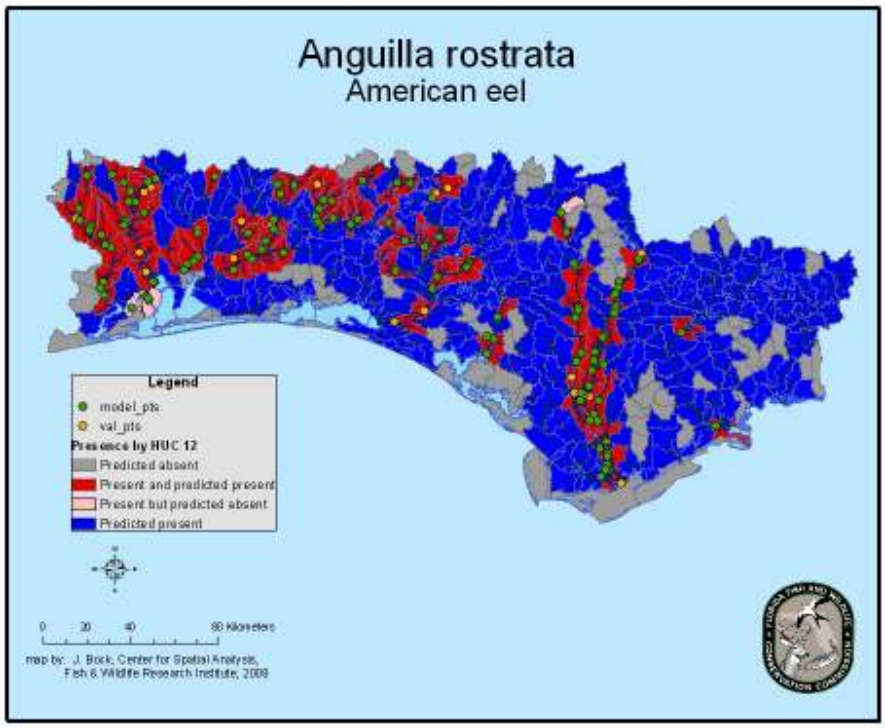
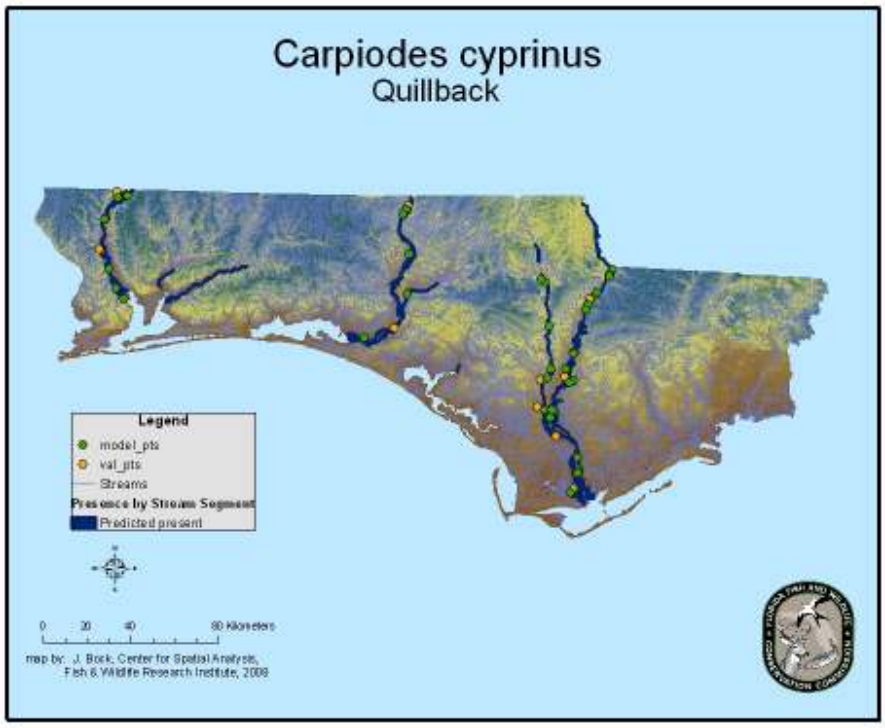


Figure 9. Potential habitat for *Anguilla rostrata* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 126) represent the species occurrence points used in the modeling process while val_pts. (n = 42) represent the species occurrence records withheld from the modeling process for independent validation.



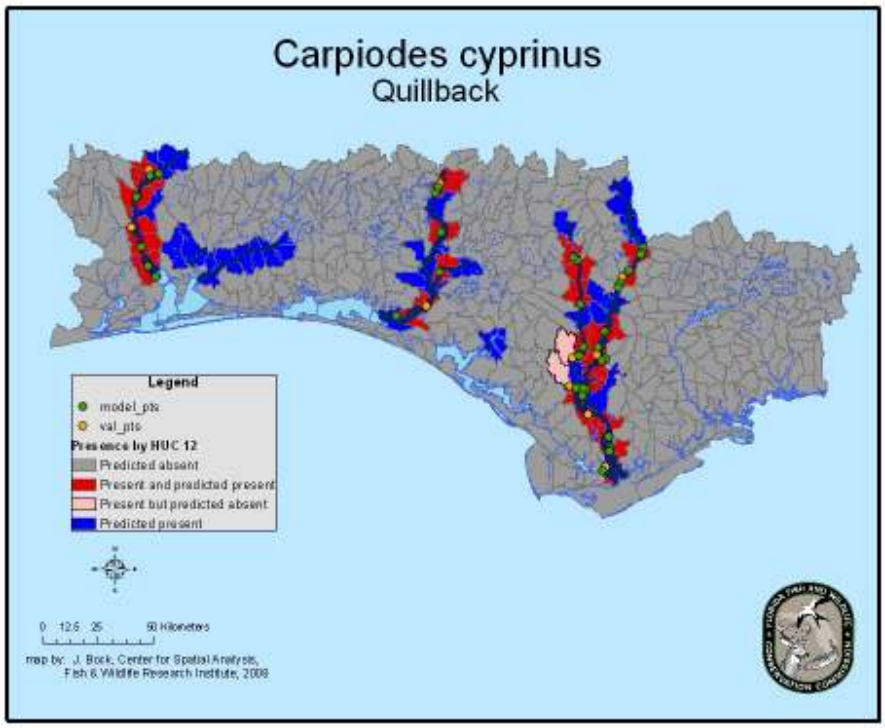
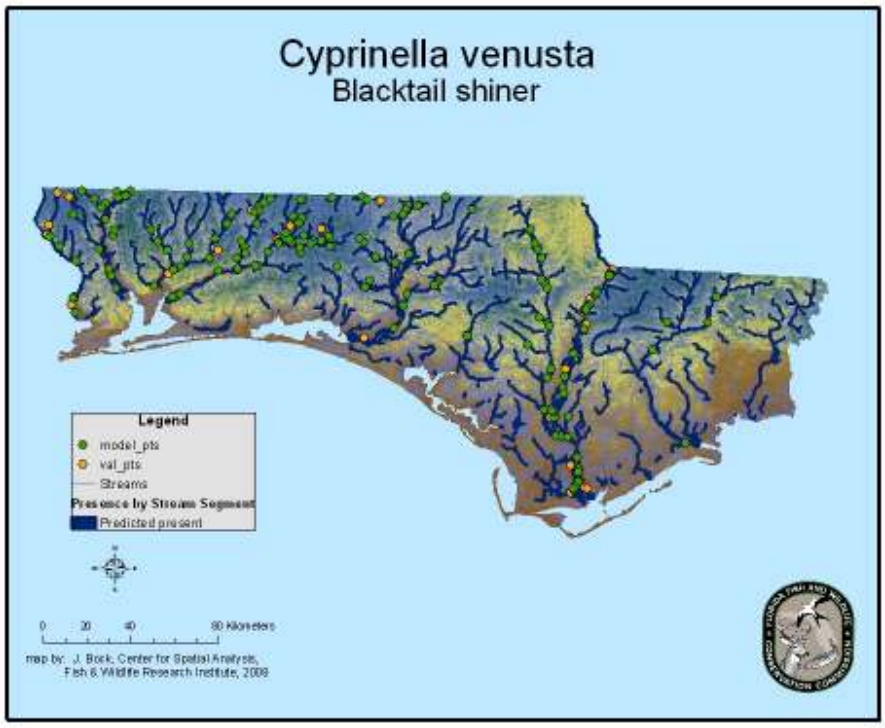


Figure 10. Potential habitat for *Carpiodes cyprinus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 45) represent the species occurrence points used in the modeling process while val_pts. (n = 15) represent the species occurrence records withheld from the modeling process for independent validation.



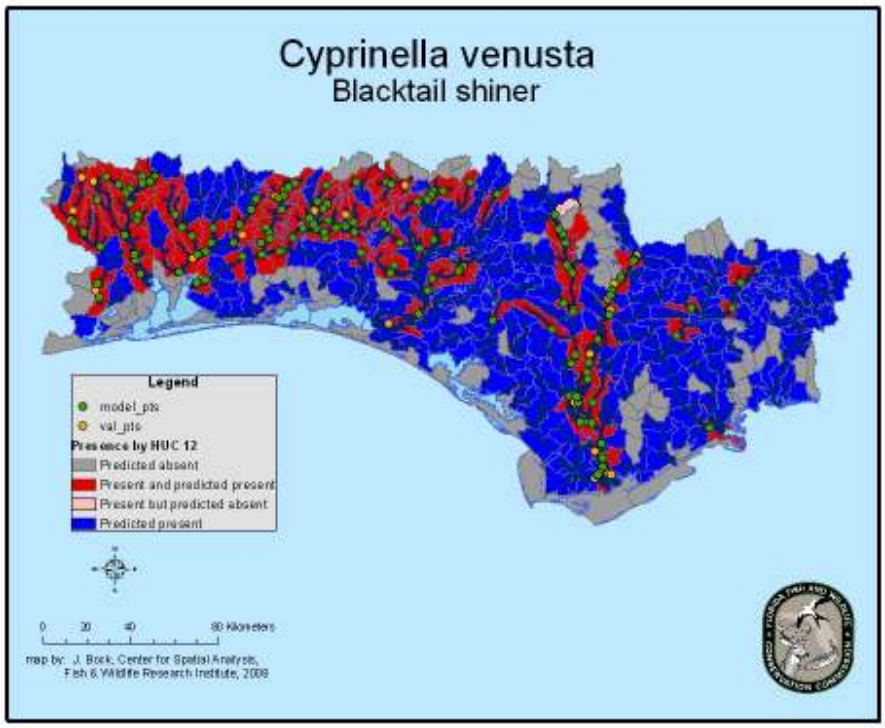


Figure 11. Potential habitat for *Cyprinella venusta* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 229) represent the species occurrence points used in the modeling process while val_pts. (n = 76) represent the species occurrence records withheld from the modeling process for independent validation.

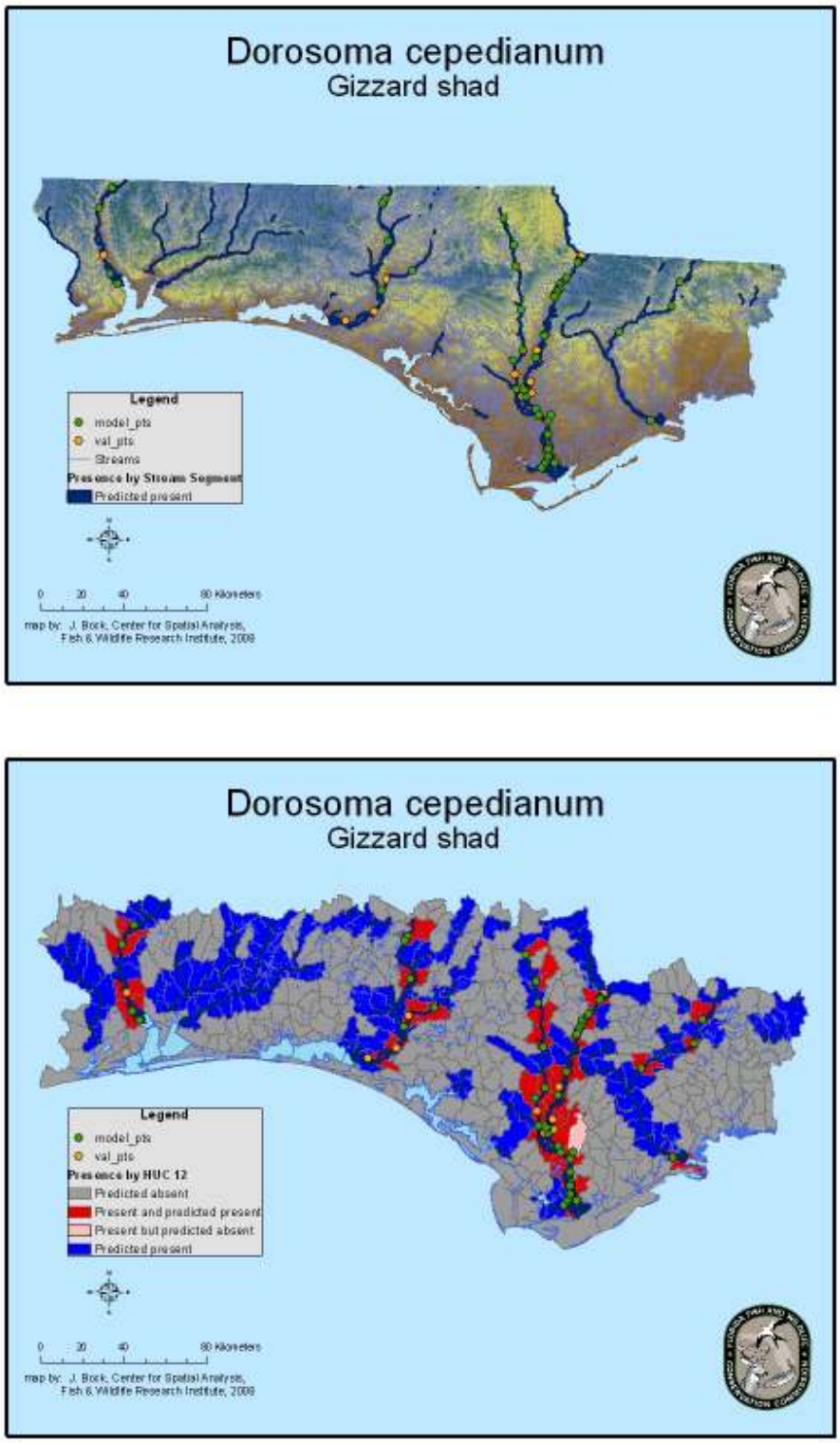
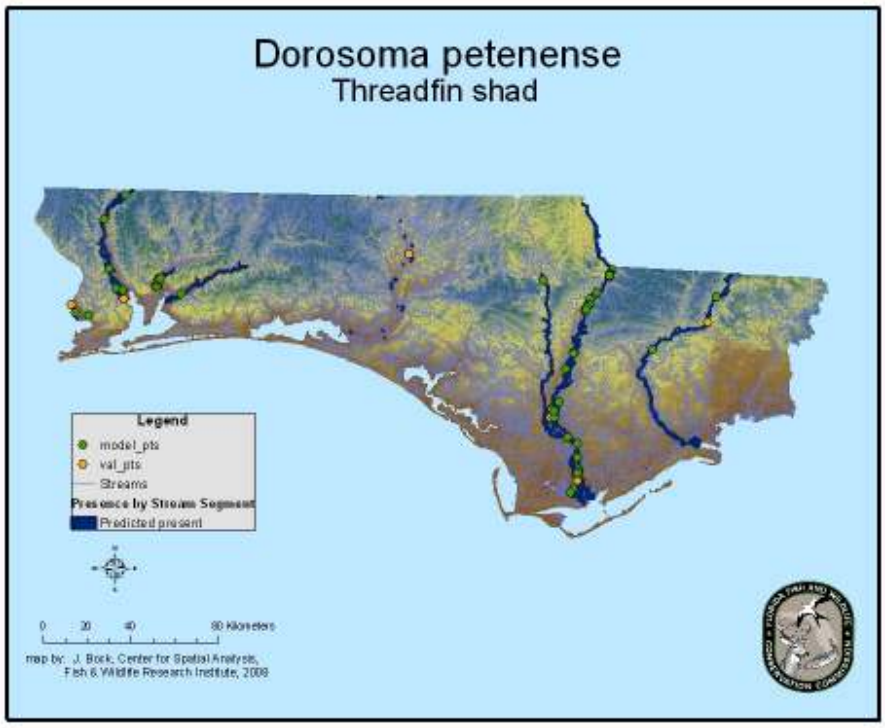


Figure 12. Potential habitat for *Dorosoma cepedianum* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 56) represent the species occurrence points used in the modeling process while val_pts. (n = 19) represent the species occurrence records withheld from the modeling process for independent validation.



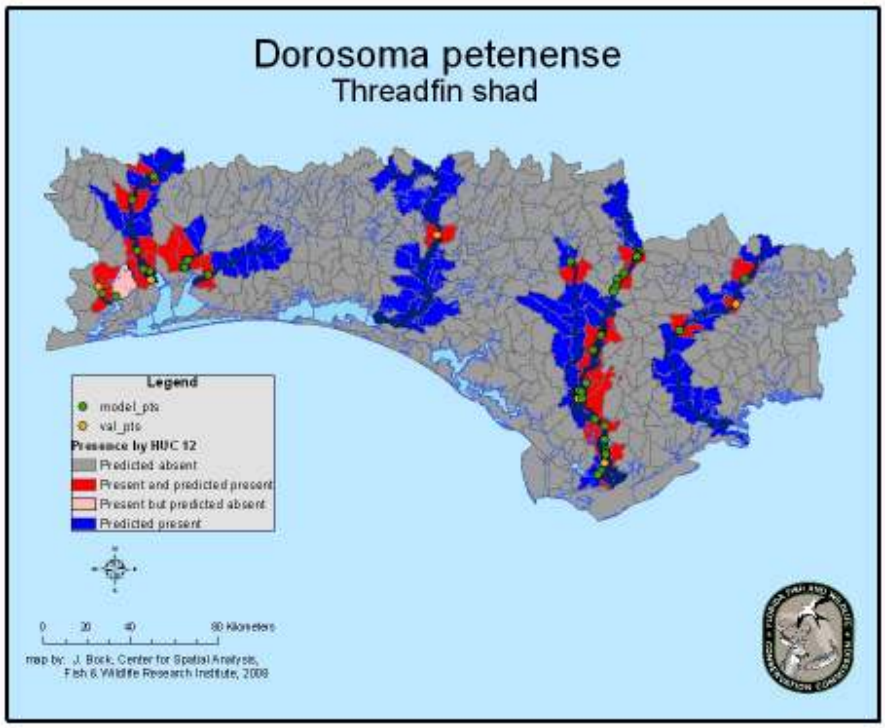
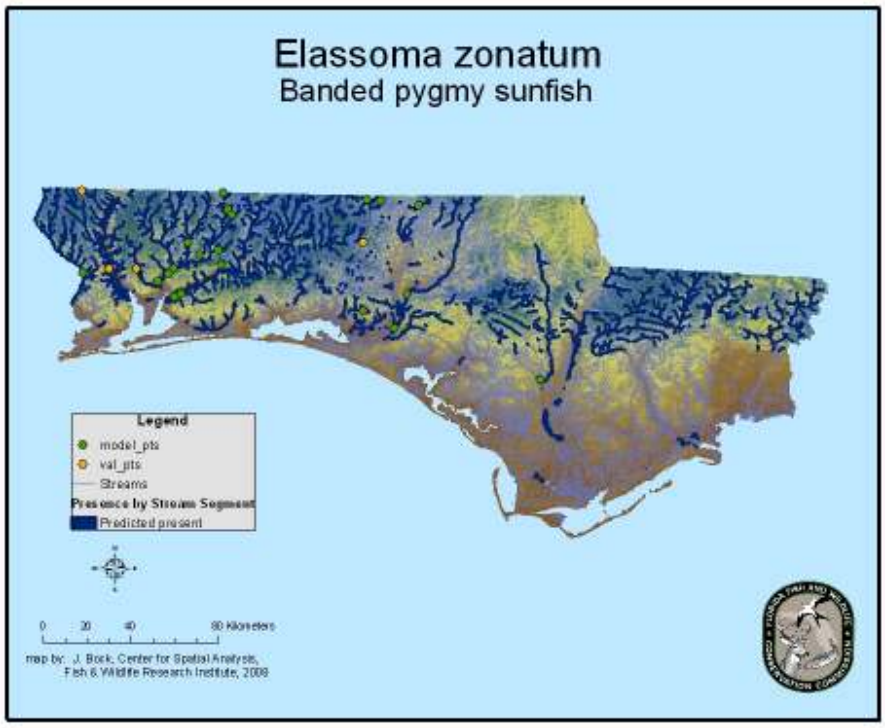


Figure 13. Potential habitat for *Dorosoma petenense* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 47) represent the species occurrence points used in the modeling process while val_pts. (n = 16) represent the species occurrence records withheld from the modeling process for independent validation.



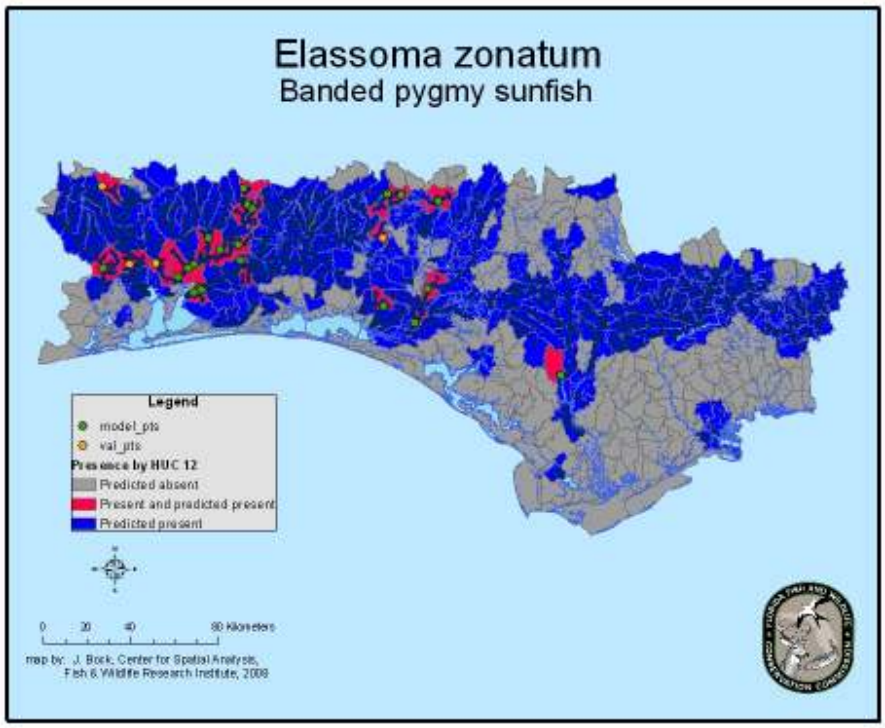
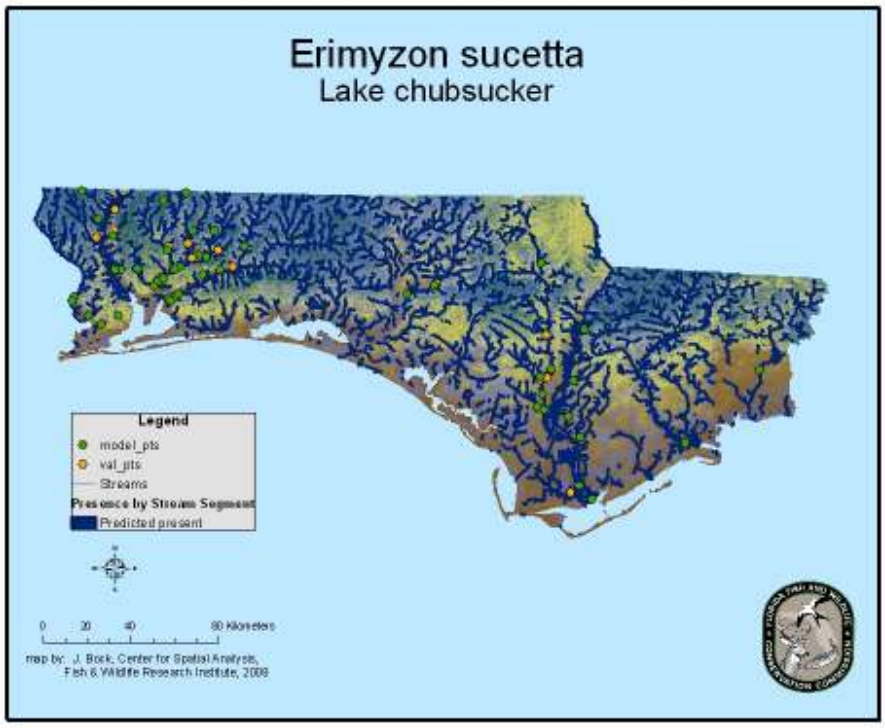


Figure 14. Potential habitat for *Elassoma zonatum* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 23) represent the species occurrence points used in the modeling process while val_pts. (n = 7) represent the species occurrence records withheld from the modeling process for independent validation.



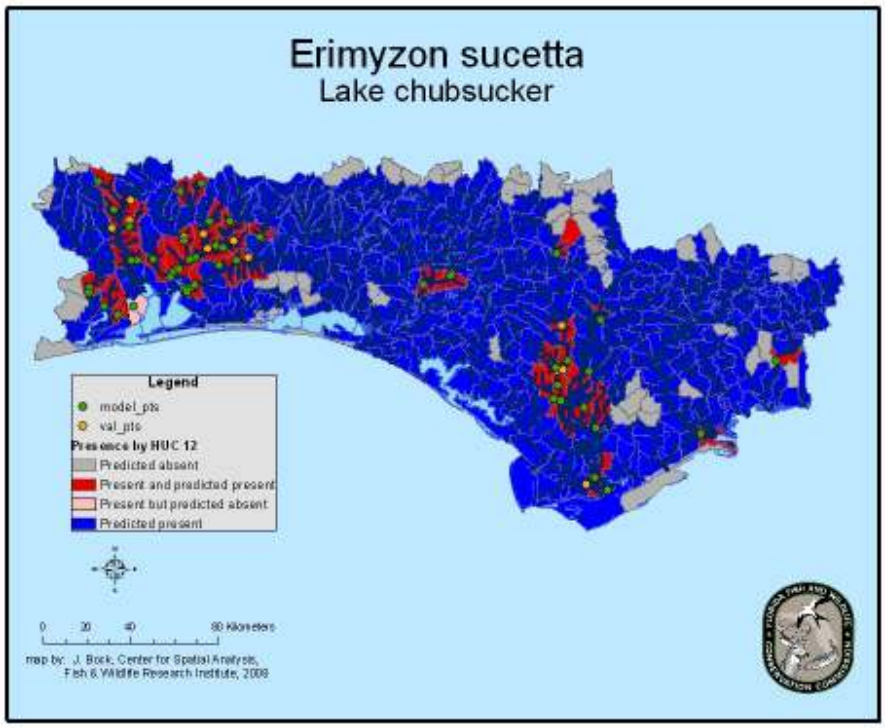
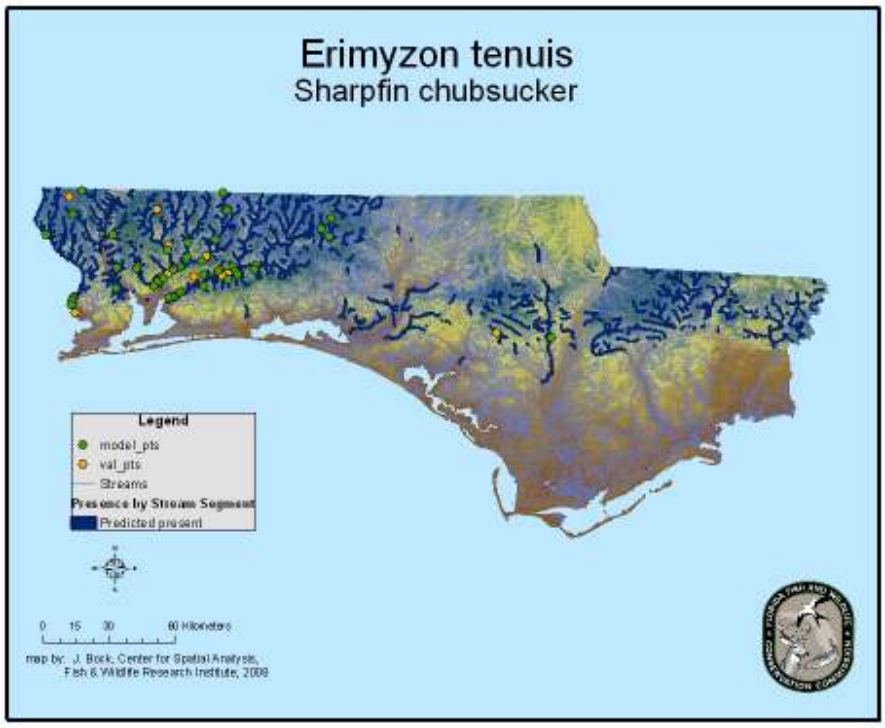


Figure 15. Potential habitat for *Erimyzon sucetta* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 54) represent the species occurrence points used in the modeling process while val_pts. (n = 18) represent the species occurrence records withheld from the modeling process for independent validation.



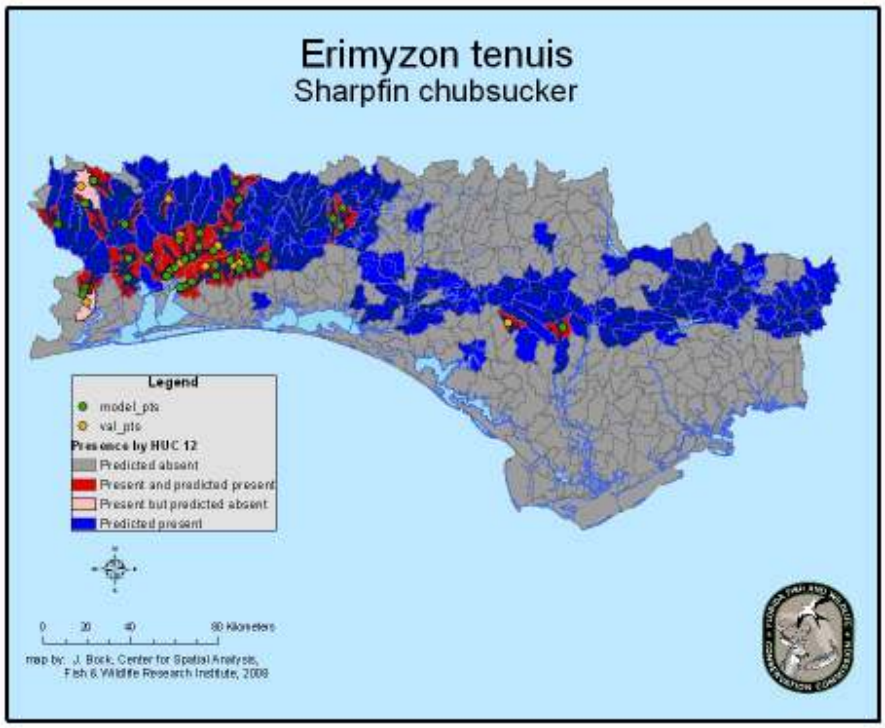
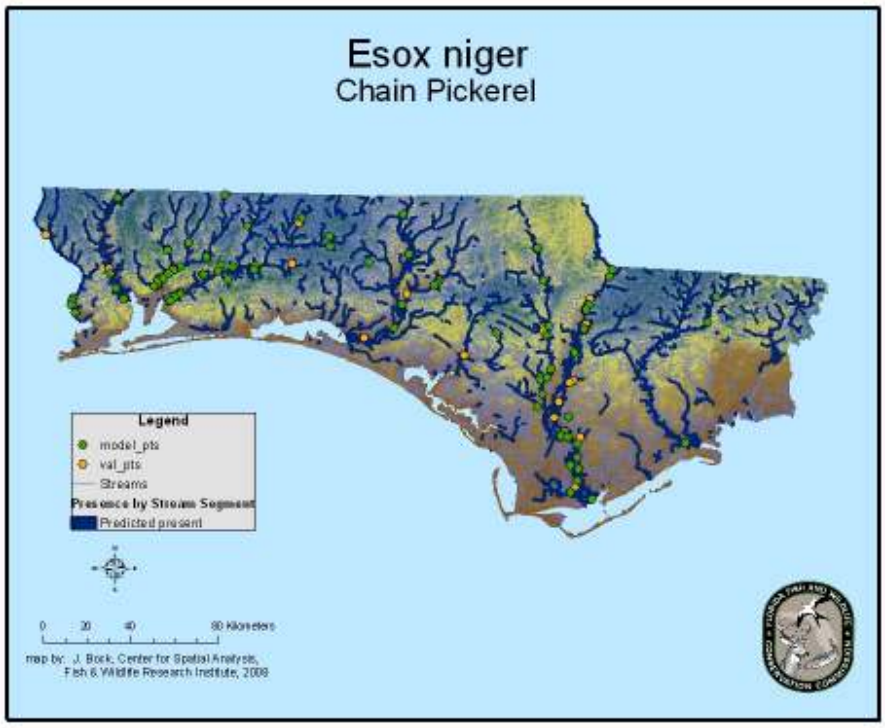


Figure 16. Potential habitat for *Erimyzon tenuis* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 58) represent the species occurrence points used in the modeling process while val_pts. (n = 19) represent the species occurrence records withheld from the modeling process for independent validation.



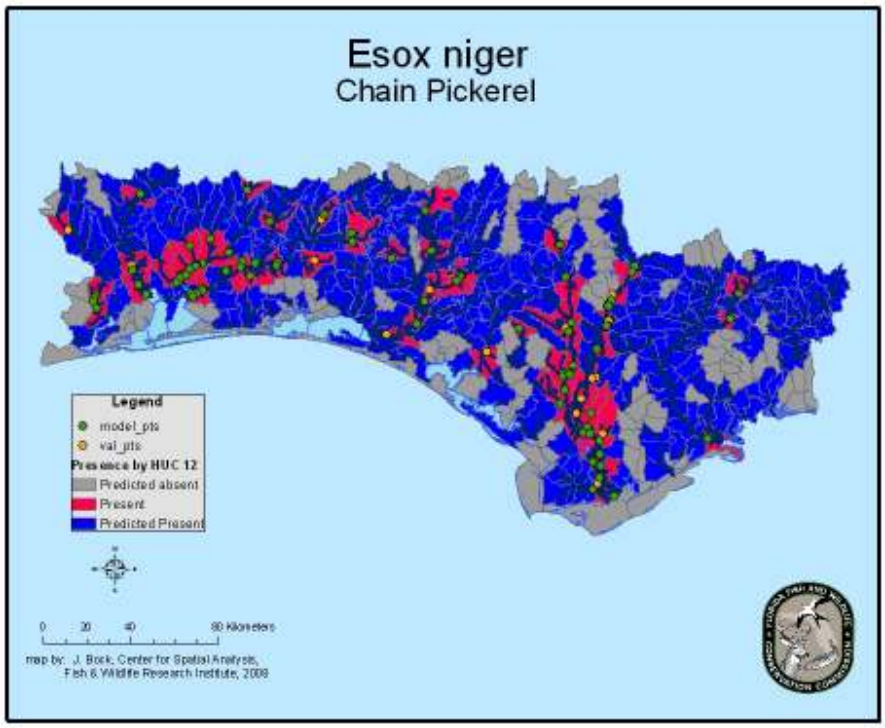
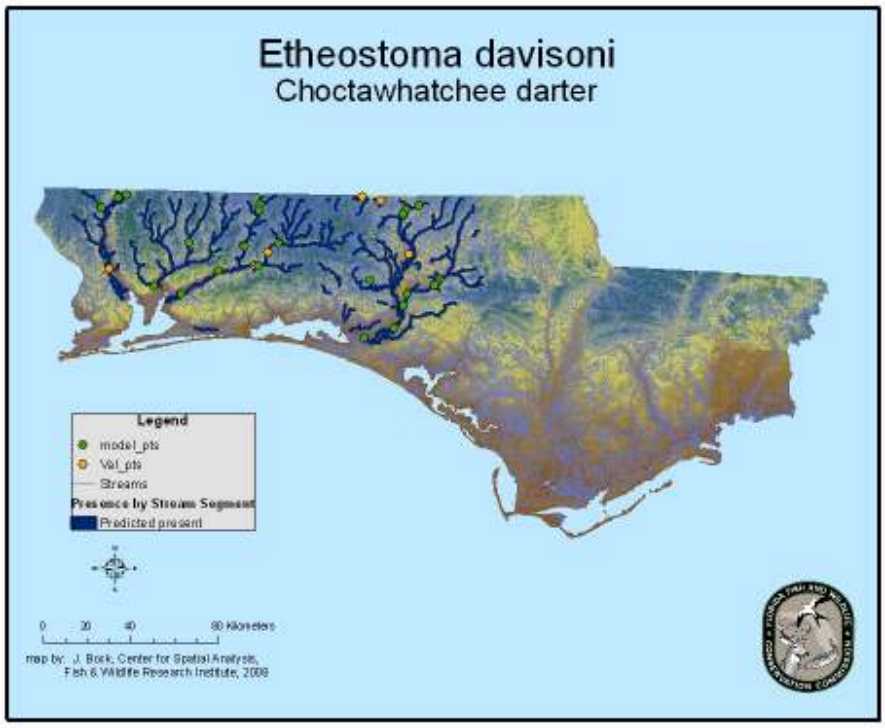


Figure 17. Potential habitat for *Esox niger* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 100) represent the species occurrence points used in the modeling process while val_pts. (n = 33) represent the species occurrence records withheld from the modeling process for independent validation.



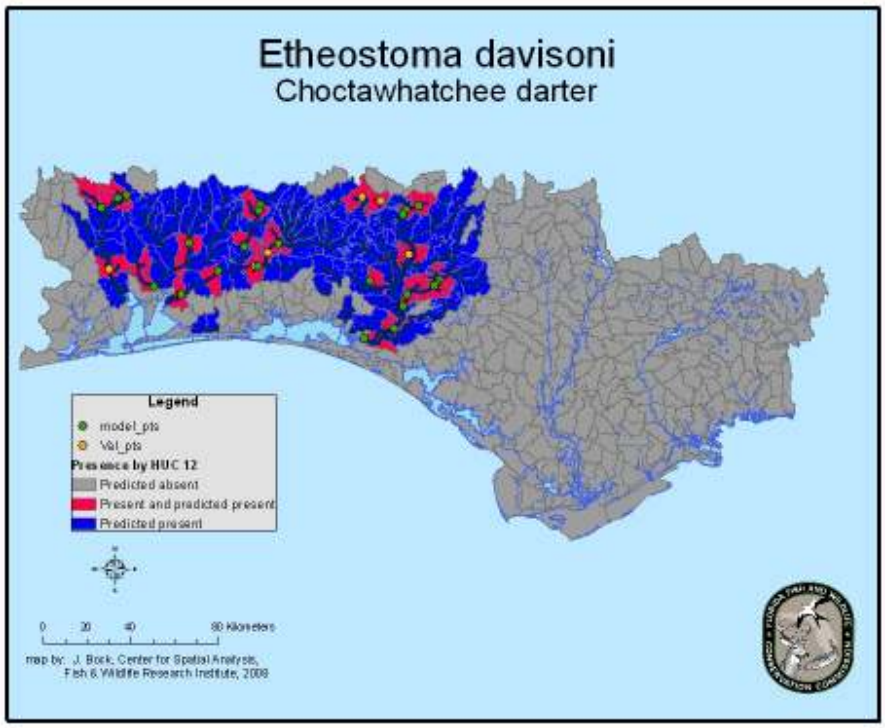
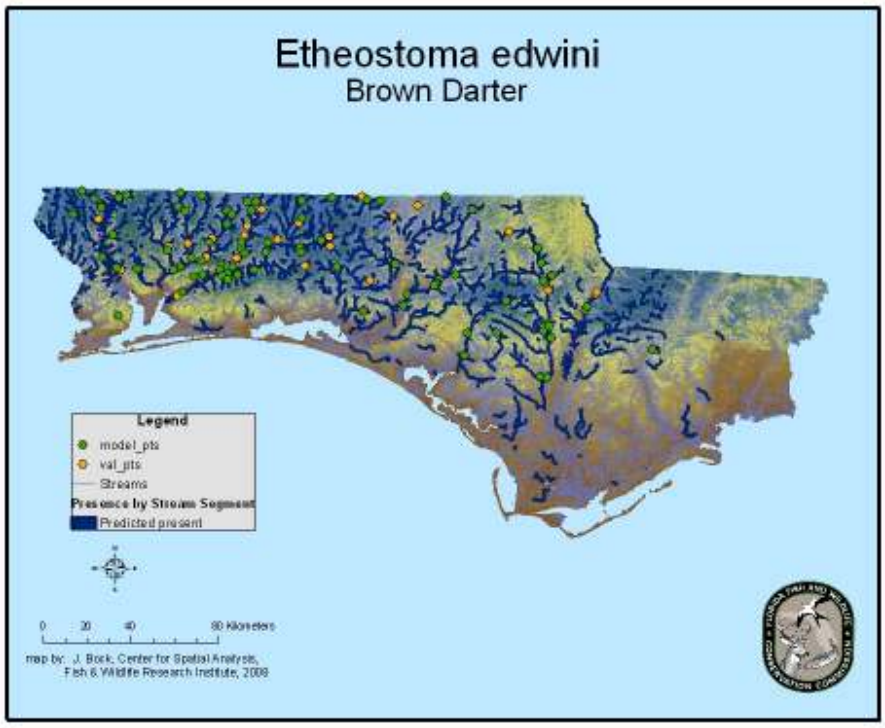


Figure 18. Potential habitat for *Etheostoma davisoni* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 29) represent the species occurrence points used in the modeling process while val_pts. (n = 9) represent the species occurrence records withheld from the modeling process for independent validation.



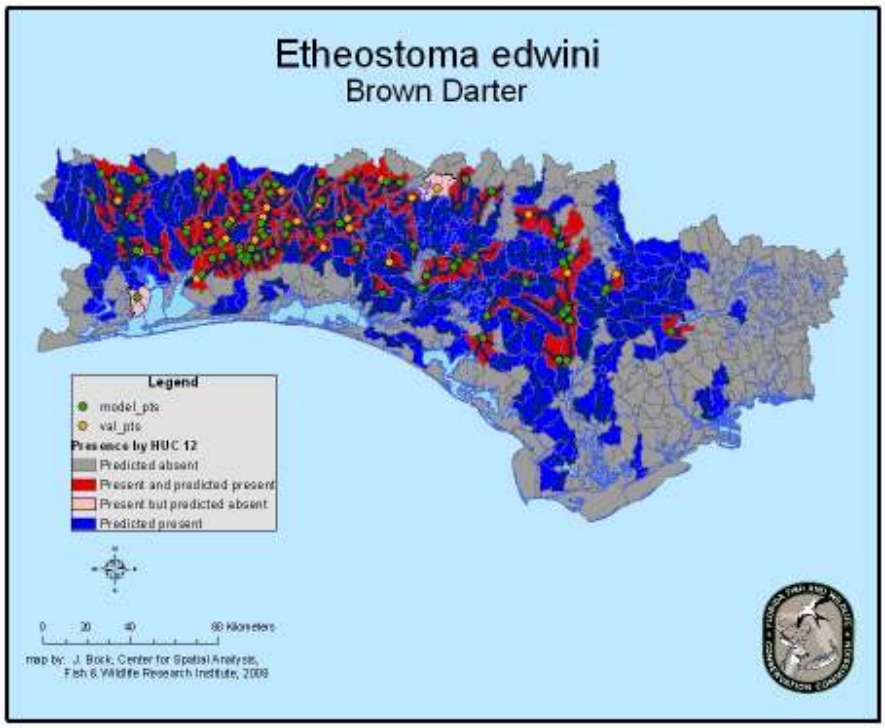
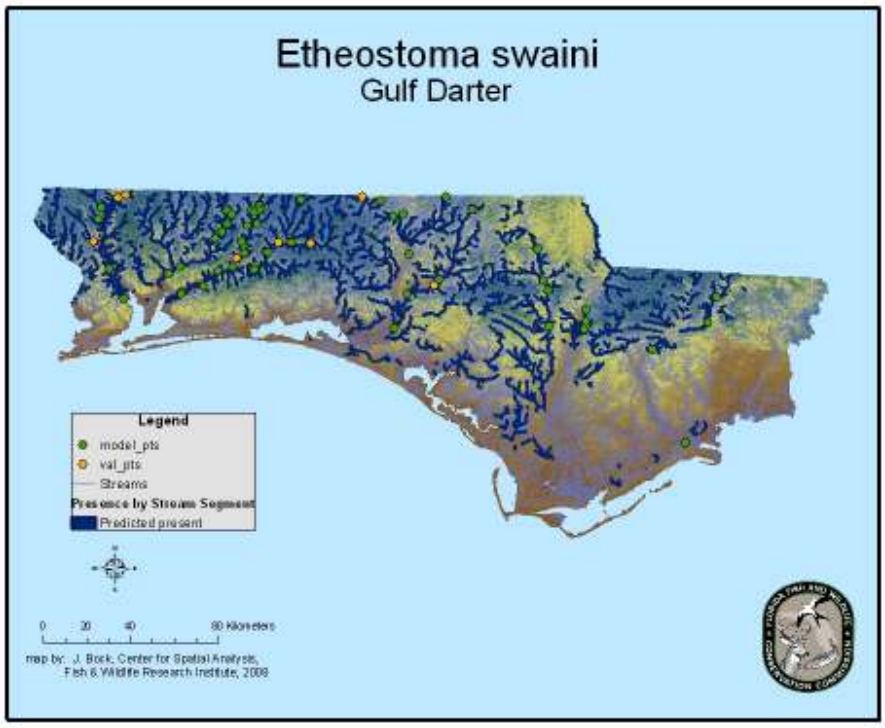


Figure 19. Potential habitat for *Etheostoma edwini* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 113) represent the species occurrence points used in the modeling process while val_pts. (n = 38) represent the species occurrence records withheld from the modeling process for independent validation.



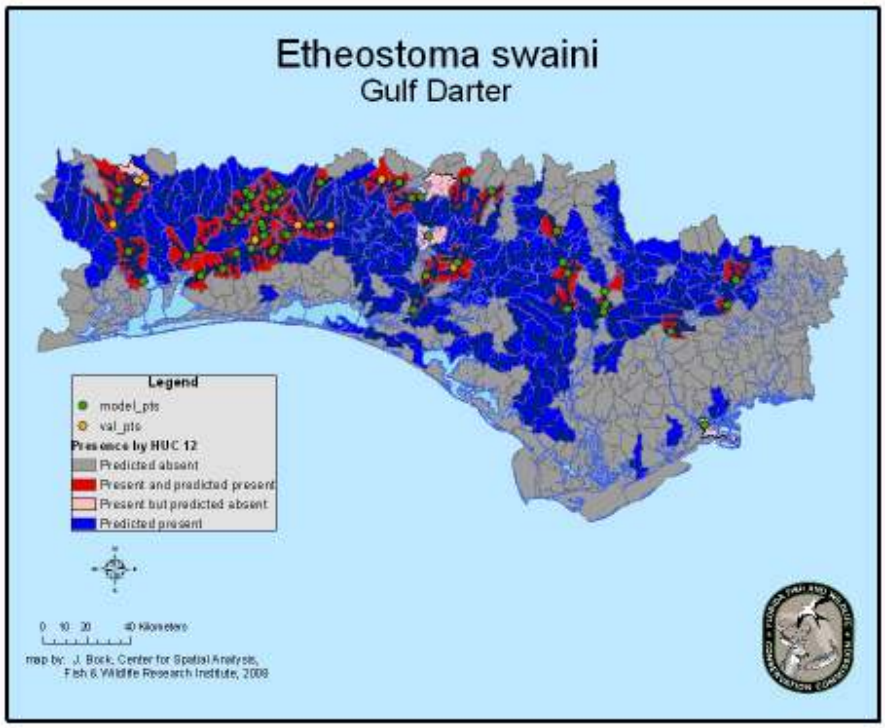
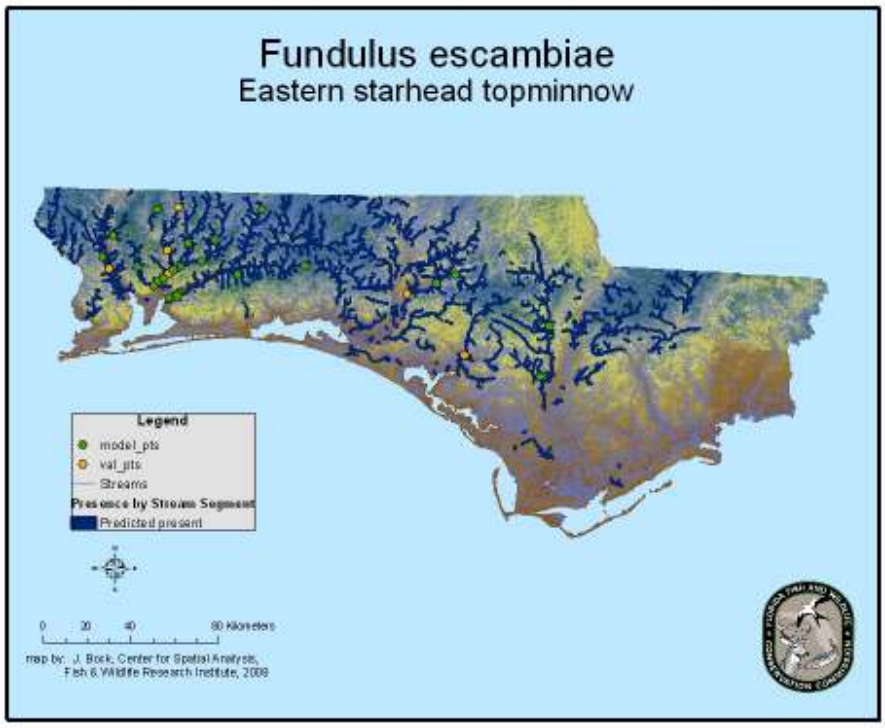


Figure 20. Potential habitat for *Etheostoma swaini* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 68) represent the species occurrence points used in the modeling process while val_pts. (n = 22) represent the species occurrence records withheld from the modeling process for independent validation.



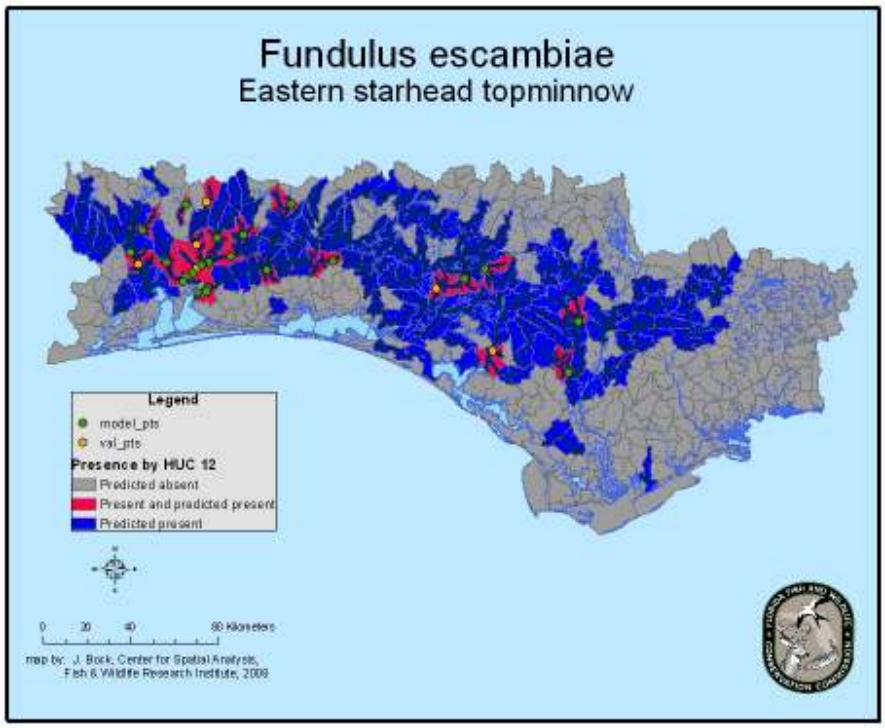
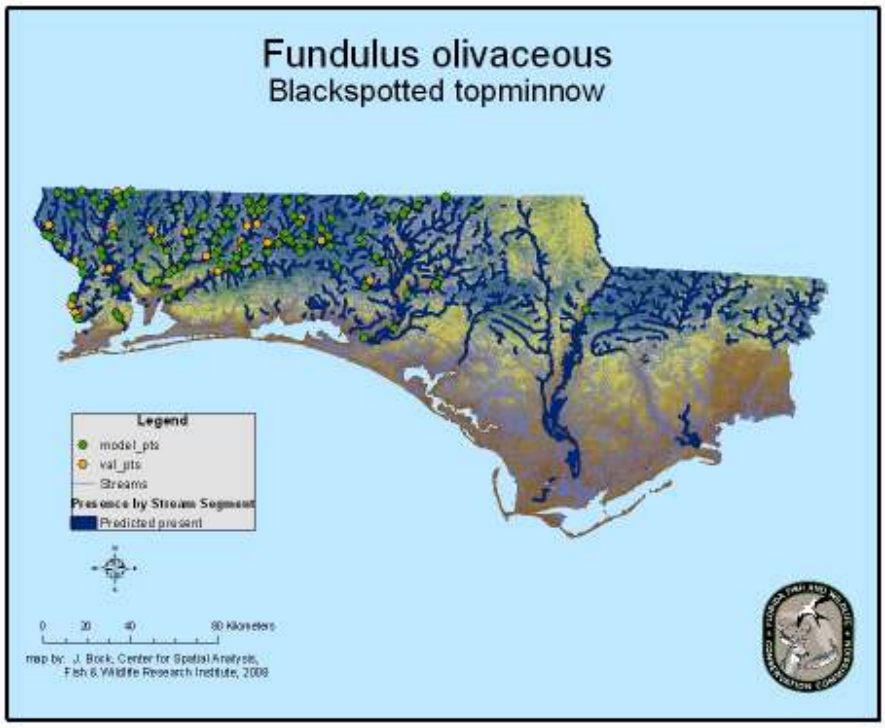


Figure 21. Potential habitat for *Fundulus escambiae* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 30) represent the species occurrence points used in the modeling process while val_pts. (n = 10) represent the species occurrence records withheld from the modeling process for independent validation.



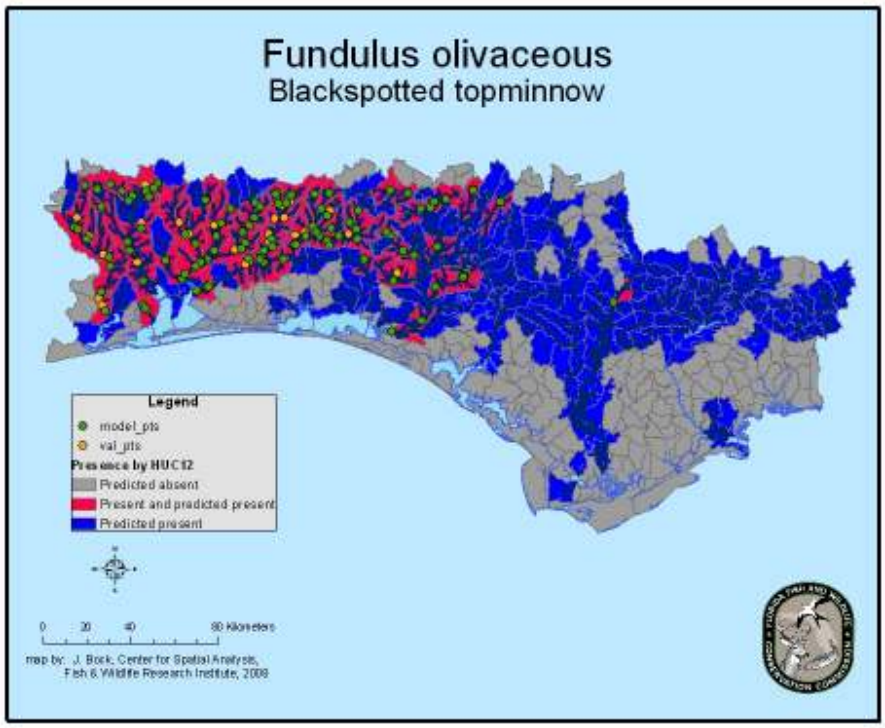
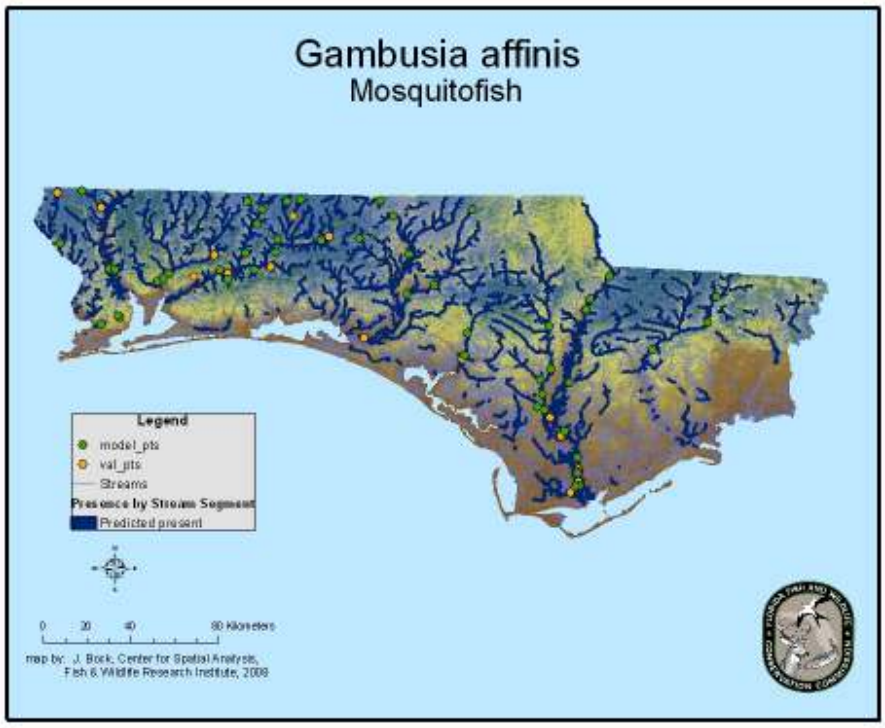


Figure 22. Potential habitat for *Fundulus olivaceous* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 168) represent the species occurrence points used in the modeling process while val_pts. (n = 56) represent the species occurrence records withheld from the modeling process for independent validation.



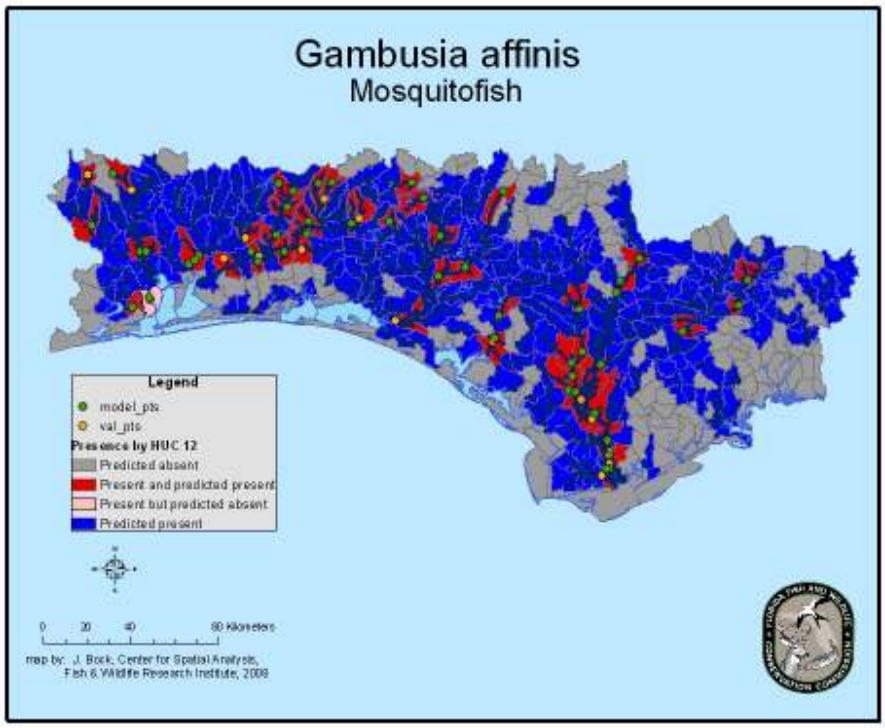
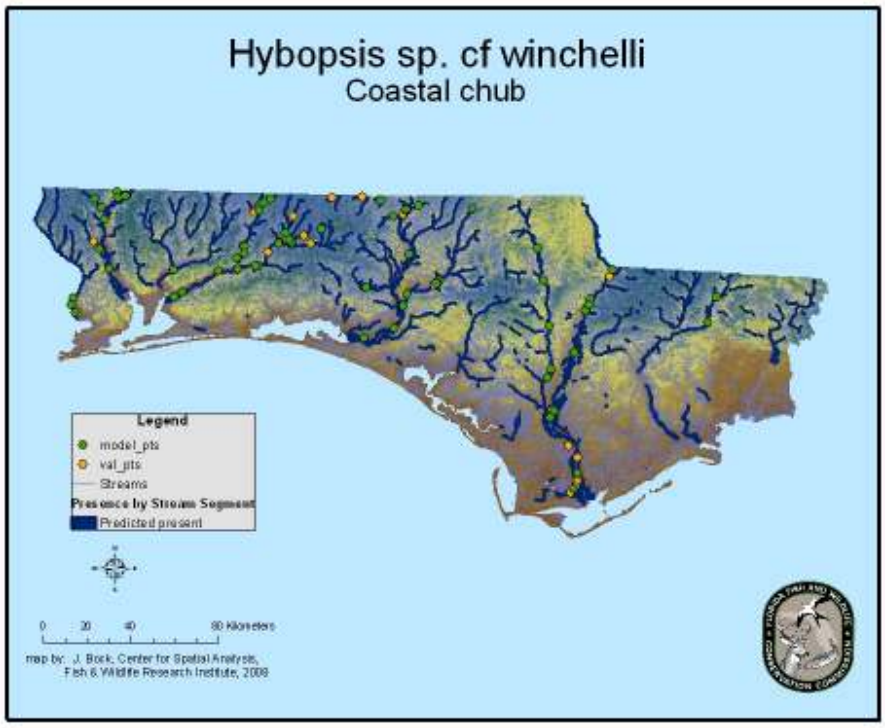


Figure 23. Potential habitat for *Gambusia affinis* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 53) represent the species occurrence points used in the modeling process while val_pts. (n = 18) represent the species occurrence records withheld from the modeling process for independent validation.



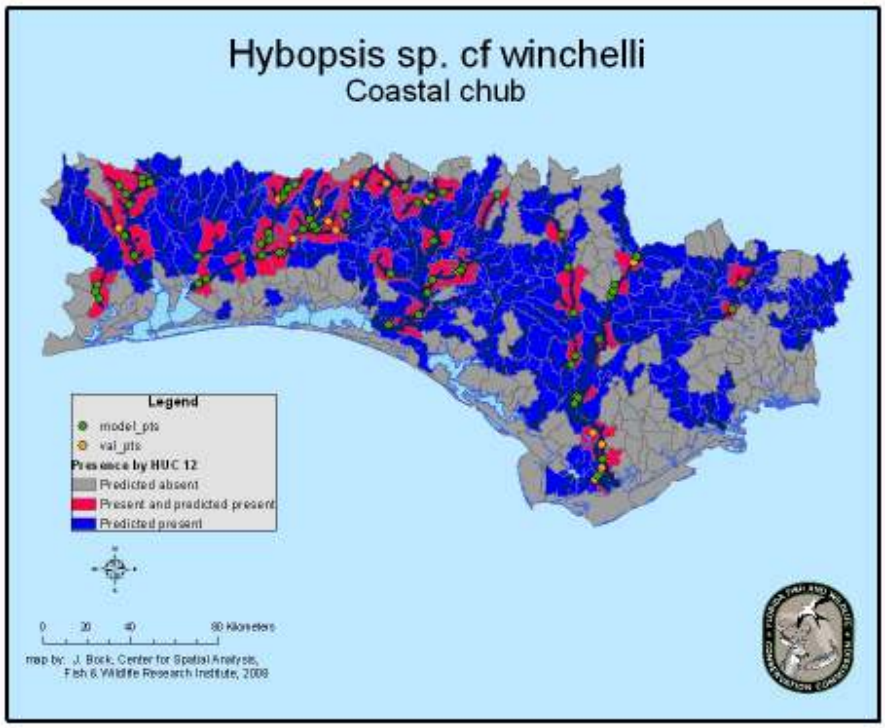
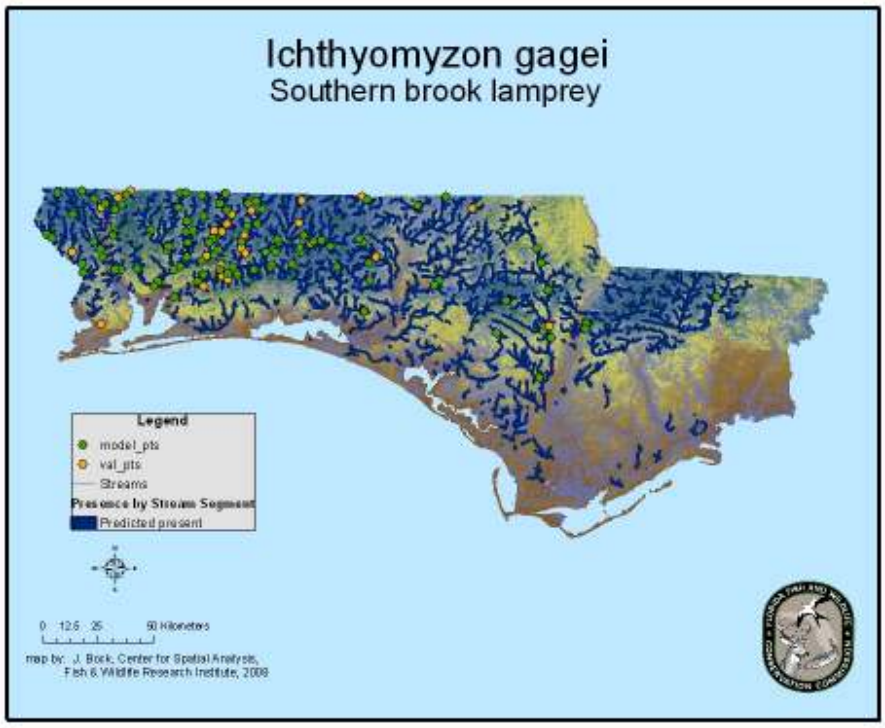


Figure 24. Potential habitat for *Hybopsis sp. cf winchelli* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 88) represent the species occurrence points used in the modeling process while val_pts. (n = 28) represent the species occurrence records withheld from the modeling process for independent validation.



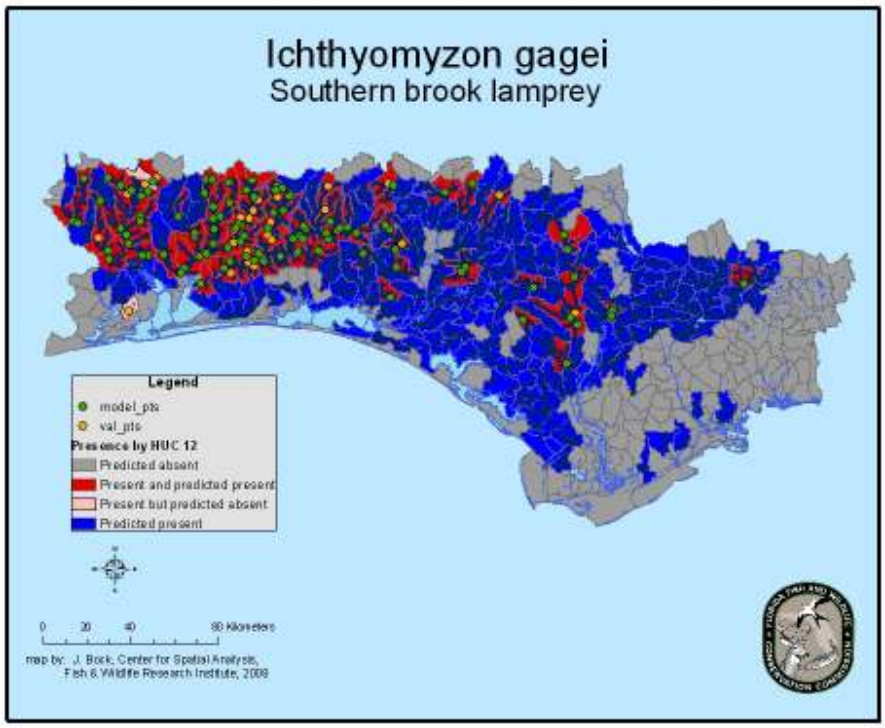
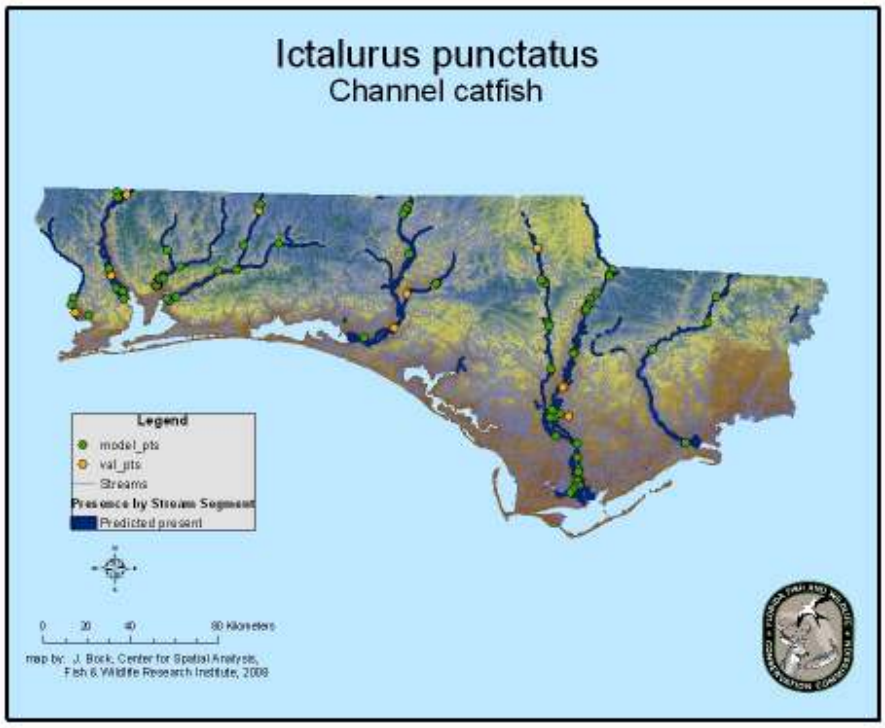


Figure 25. Potential habitat for *Ichthyomyzon gagei* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 151) represent the species occurrence points used in the modeling process while val_pts. (n = 50) represent the species occurrence records withheld from the modeling process for independent validation.



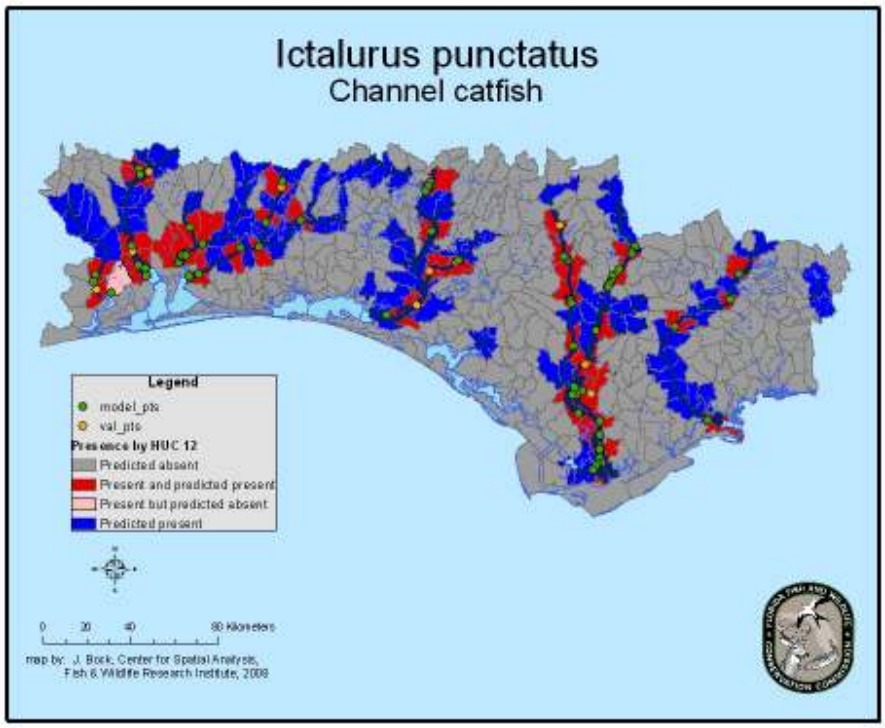
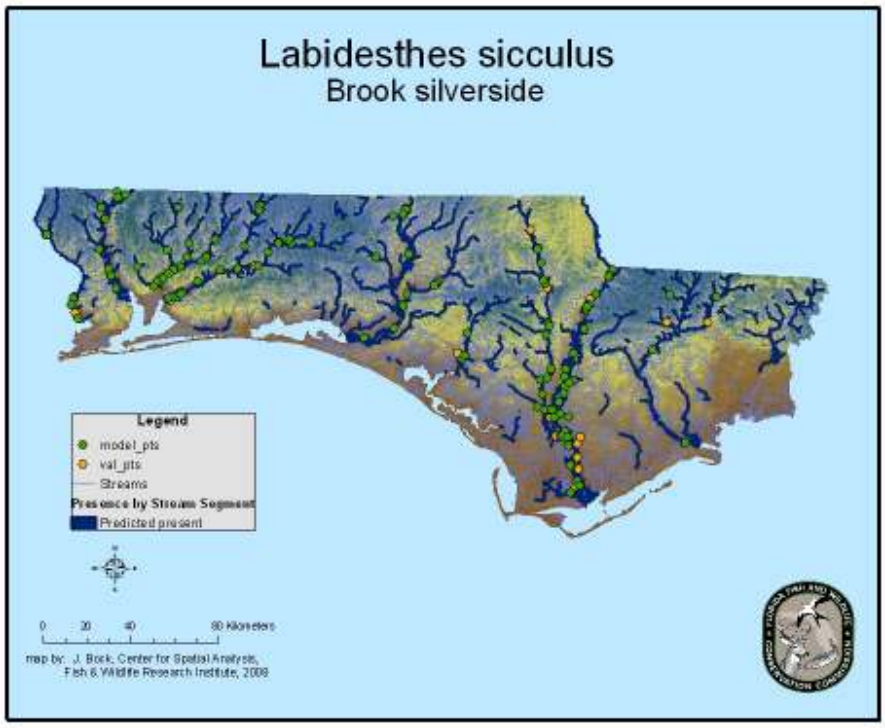


Figure 26. Potential habitat for *Ictalurus punctatus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 91) represent the species occurrence points used in the modeling process while val_pts. (n = 30) represent the species occurrence records withheld from the modeling process for independent validation.



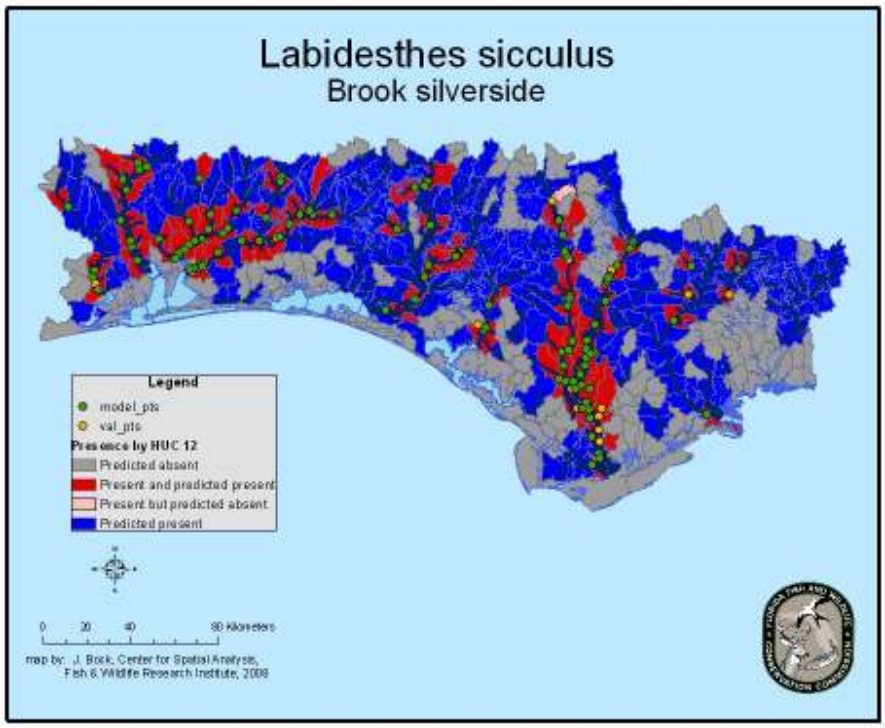
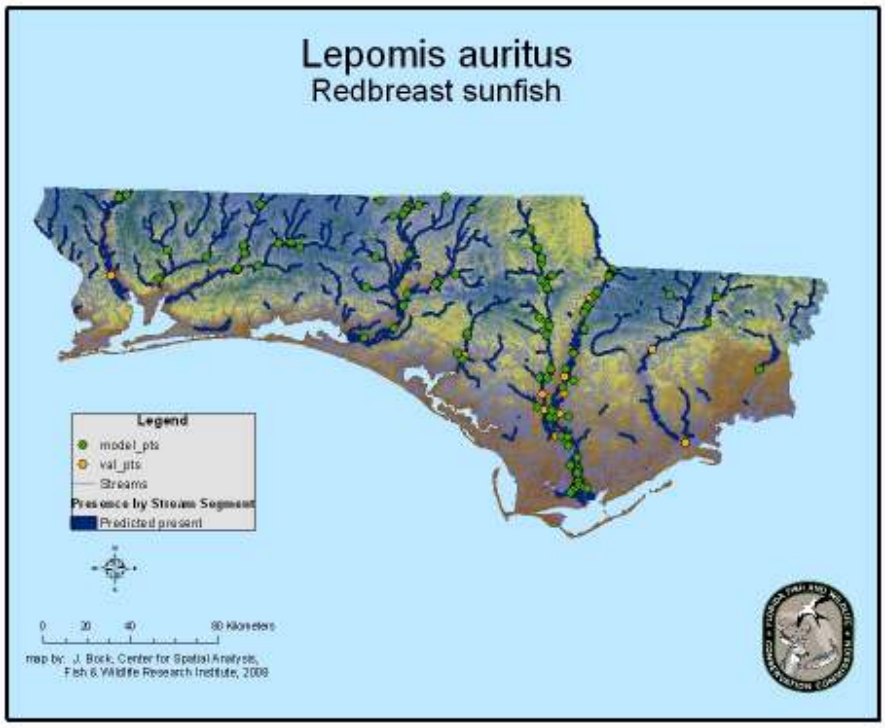


Figure 27. Potential habitat for *Labidesthes sicculus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 145) represent the species occurrence points used in the modeling process while val_pts. (n = 48) represent the species occurrence records withheld from the modeling process for independent validation.



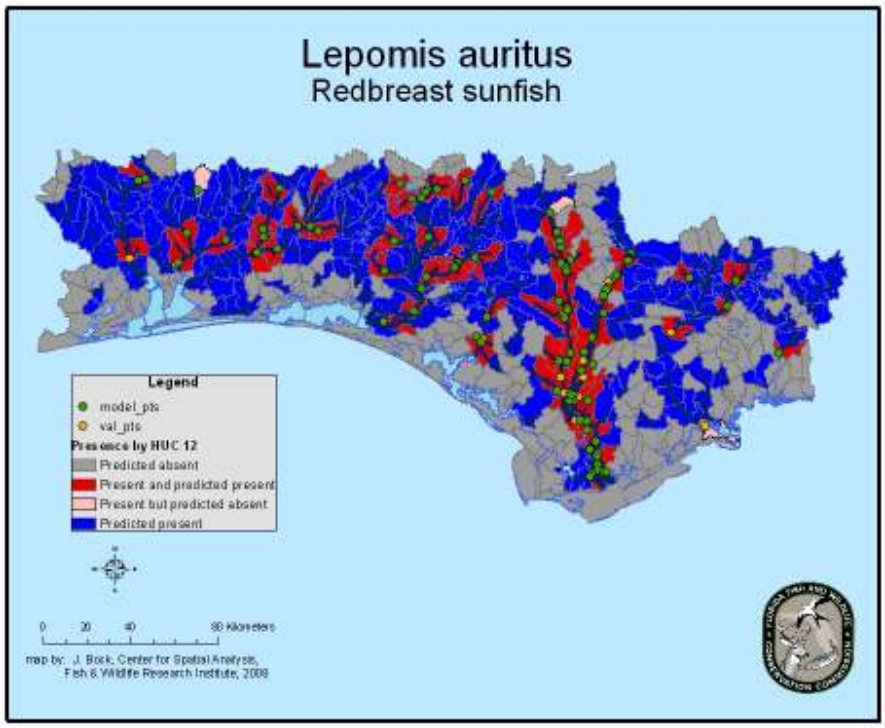
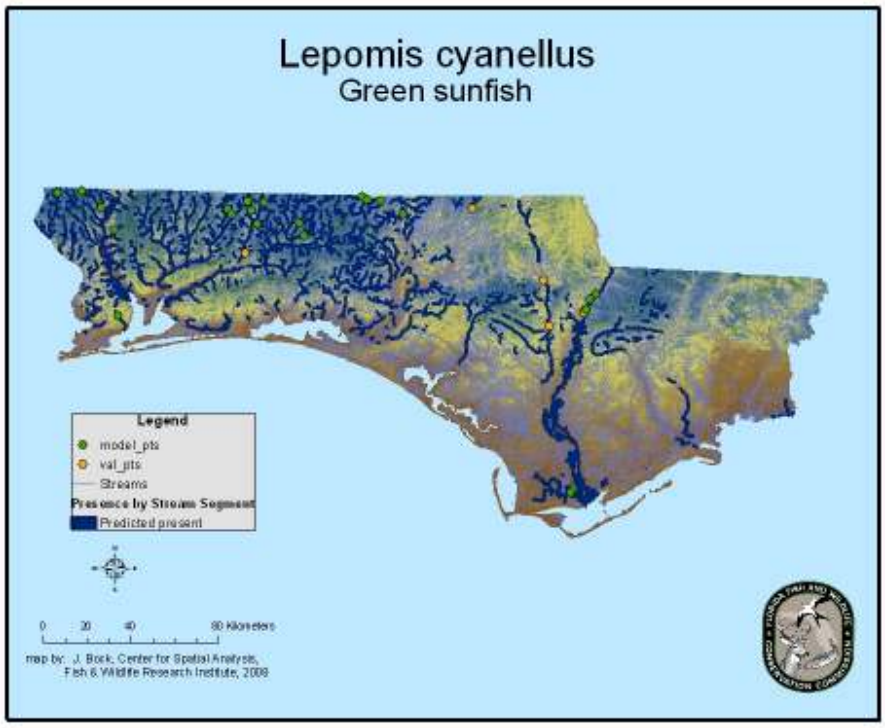


Figure 28. Potential habitat for *Lepomis auritus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 143) represent the species occurrence points used in the modeling process while val_pts. (n = 48) represent the species occurrence records withheld from the modeling process for independent validation.



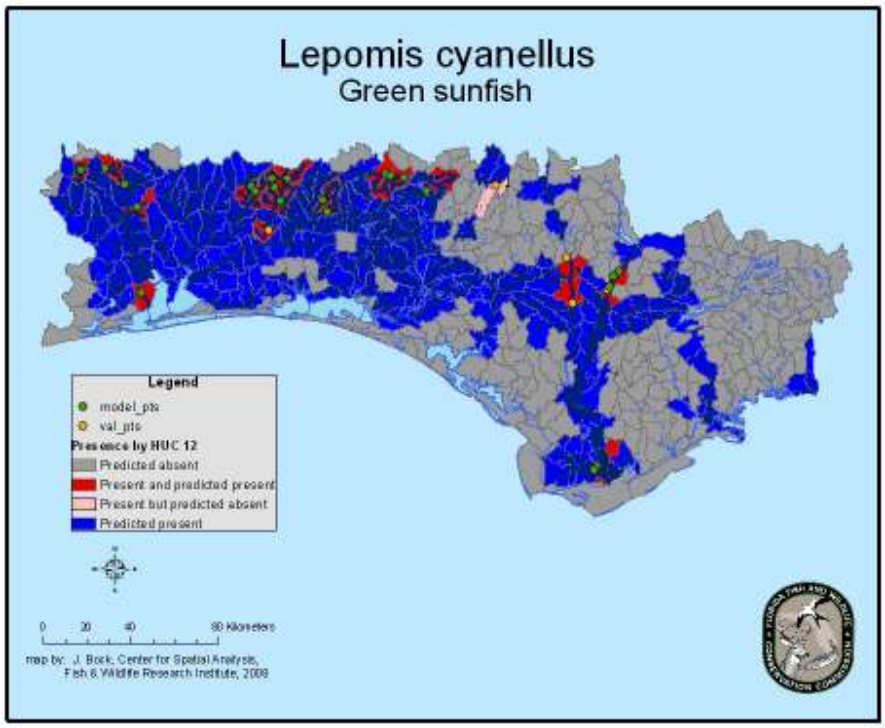
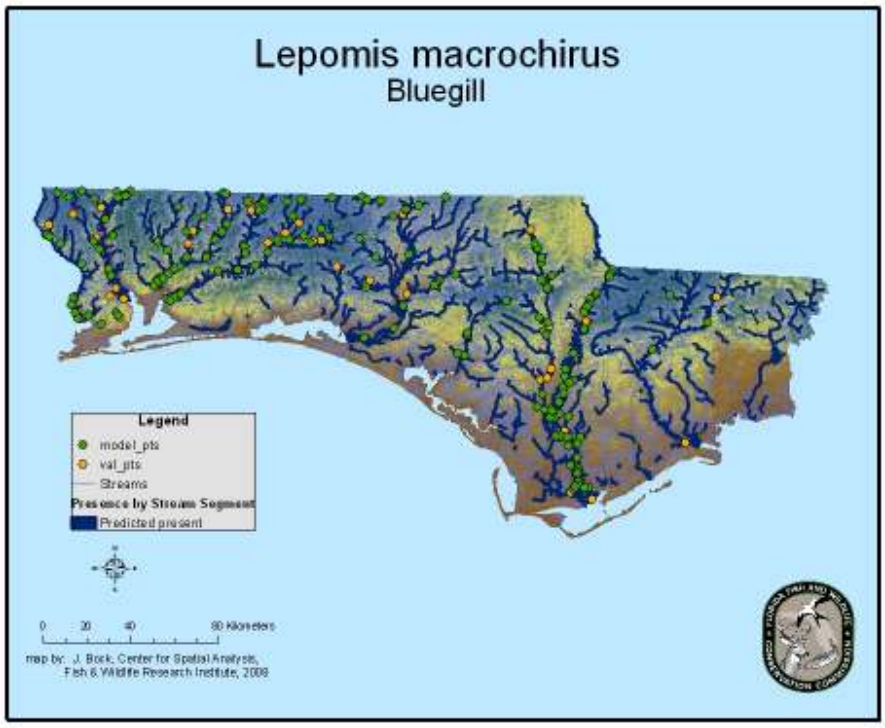


Figure 29. Potential habitat for *Lepomis cyanellus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 24) represent the species occurrence points used in the modeling process while val_pts. (n =8) represent the species occurrence records withheld from the modeling process for independent validation.



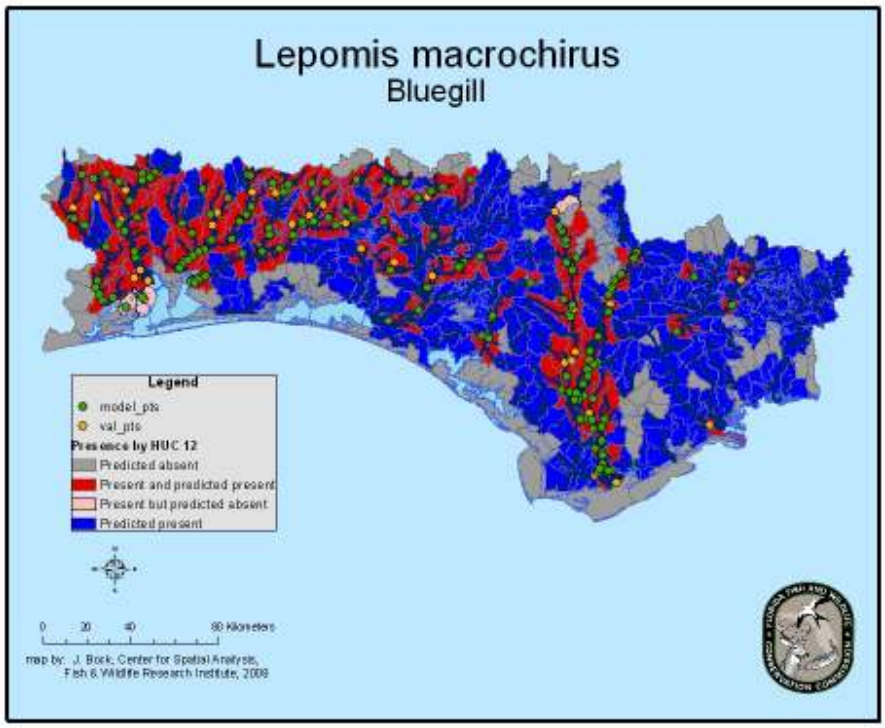
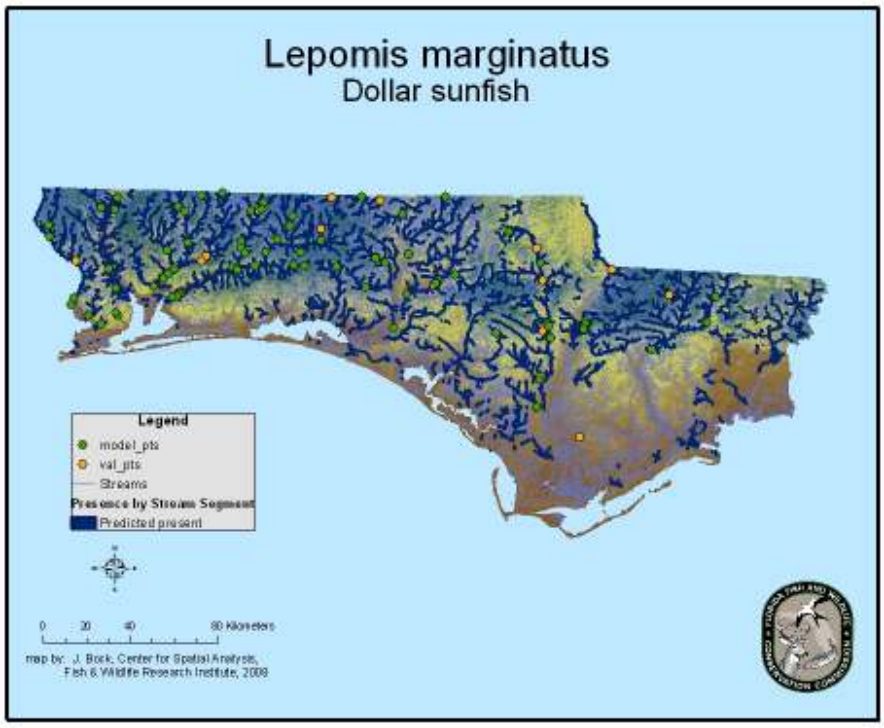


Figure 30. Potential habitat for *Lepomis macrochirus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 247) represent the species occurrence points used in the modeling process while val_pts. (n = 80) represent the species occurrence records withheld from the modeling process for independent validation.



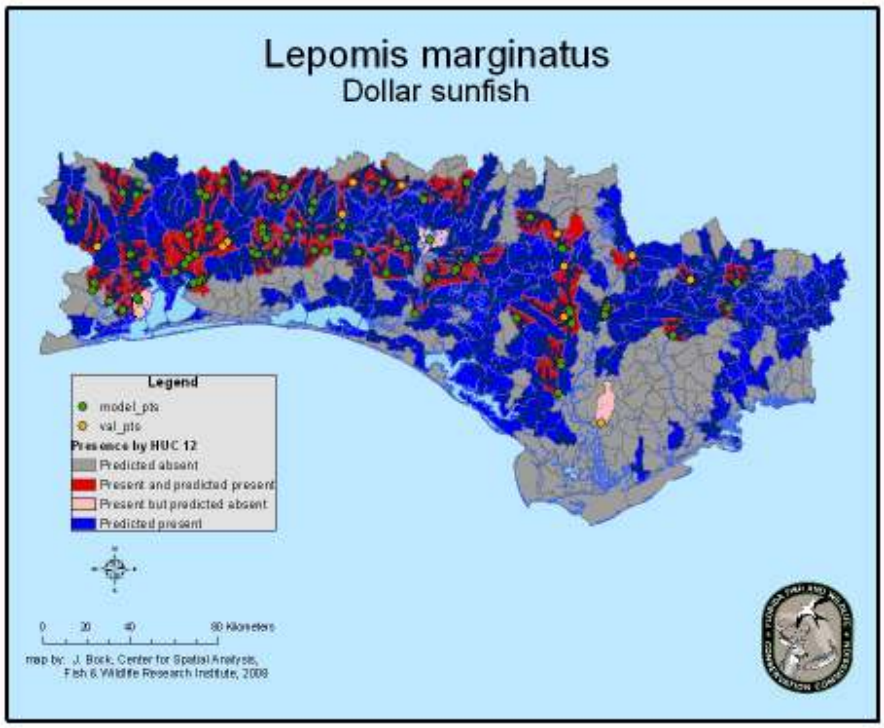
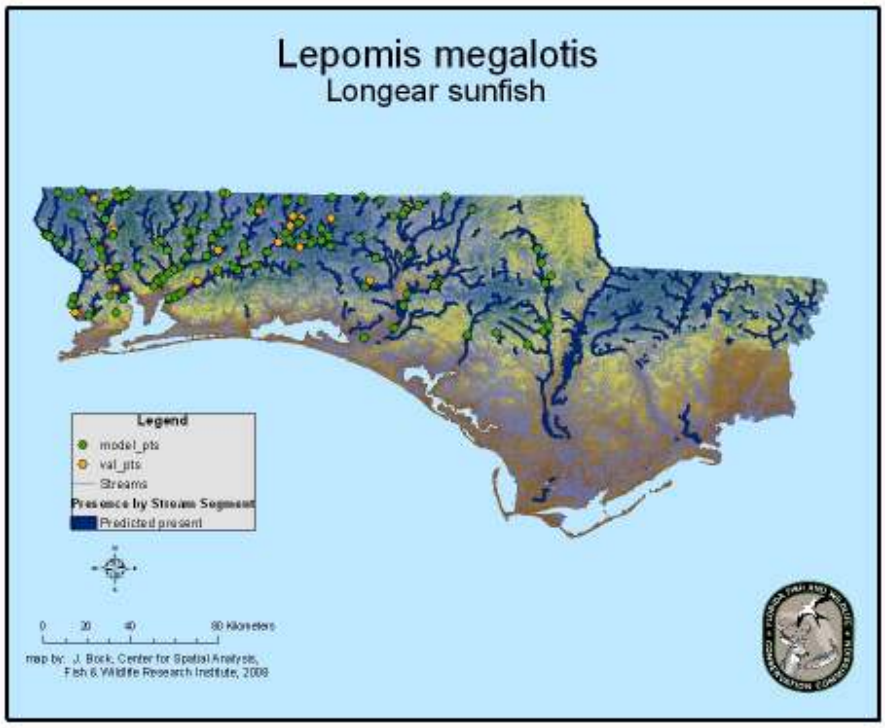


Figure 31. Potential habitat for *Lepomis marginatus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 93) represent the species occurrence points used in the modeling process while val_pts. (n = 31) represent the species occurrence records withheld from the modeling process for independent validation.



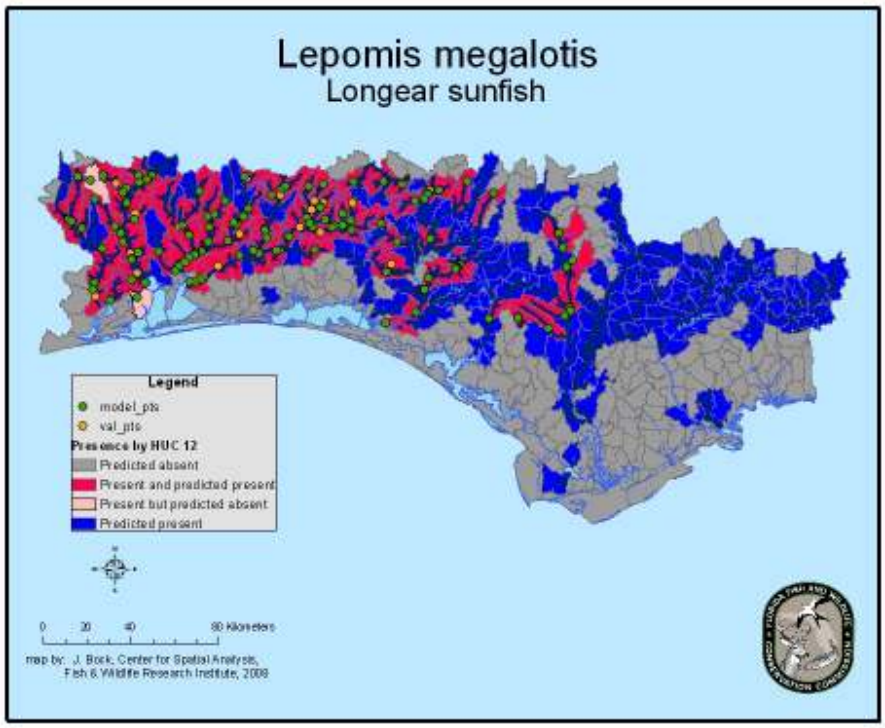
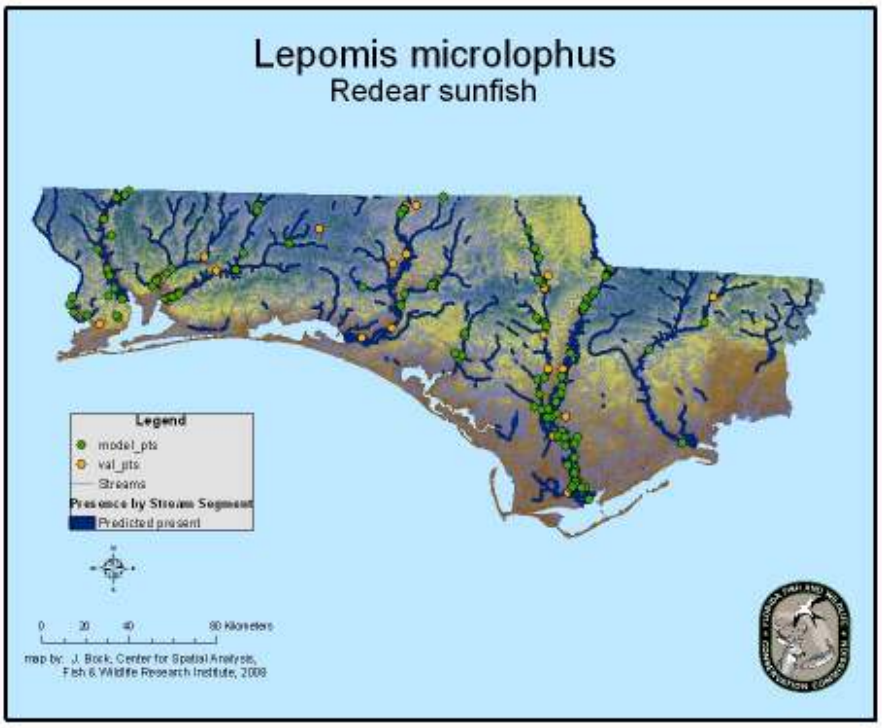


Figure 32. Potential habitat for *Lepomis megalotis* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 180) represent the species occurrence points used in the modeling process while val_pts. (n = 60) represent the species occurrence records withheld from the modeling process for independent validation.



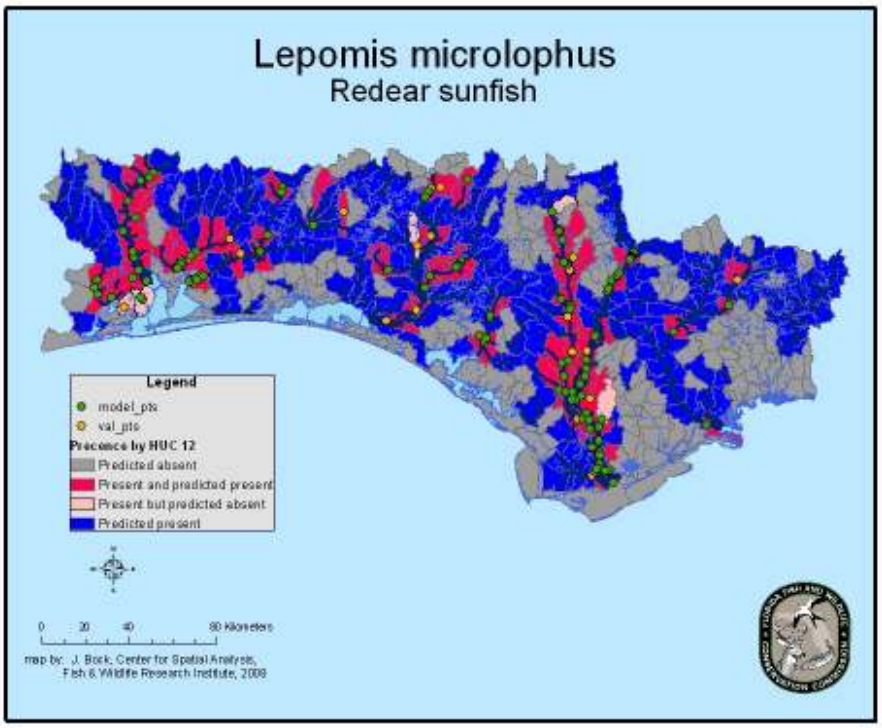
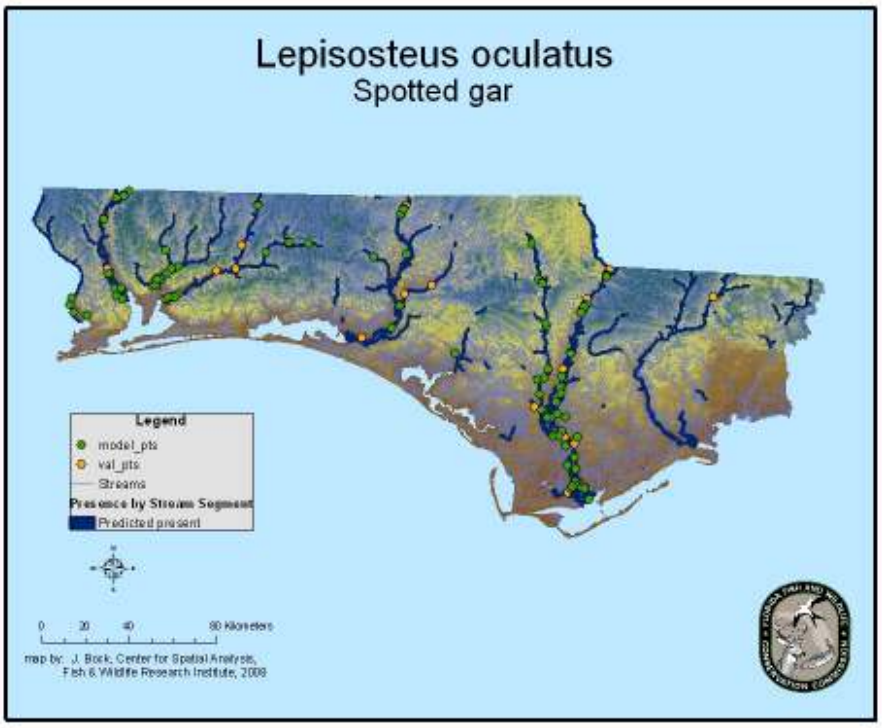


Figure 33. Potential habitat for *Lepomis microlophus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 156) represent the species occurrence points used in the modeling process while val_pts. (n = 52) represent the species occurrence records withheld from the modeling process for independent validation.



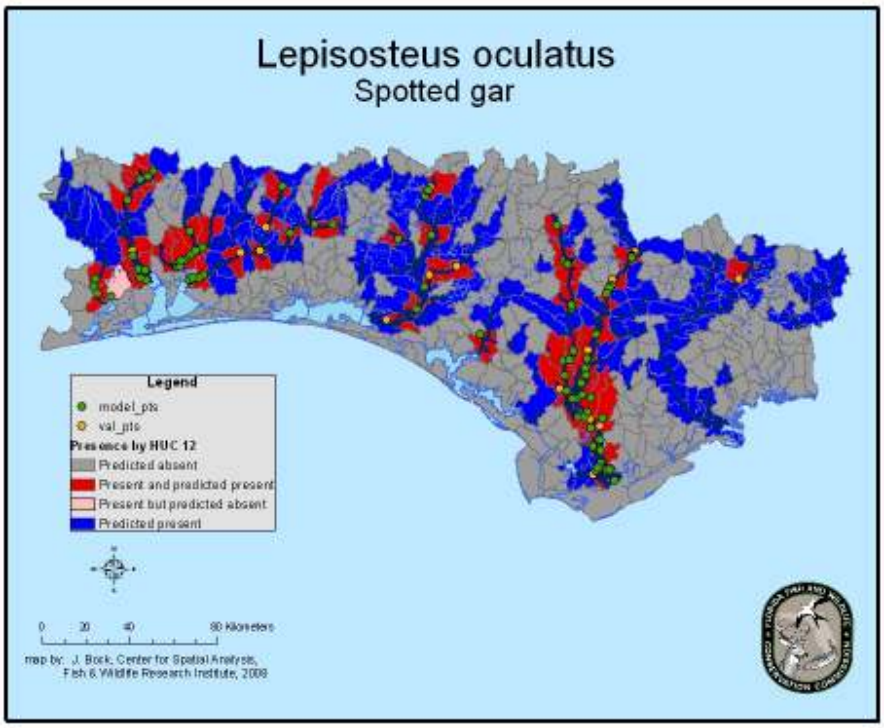
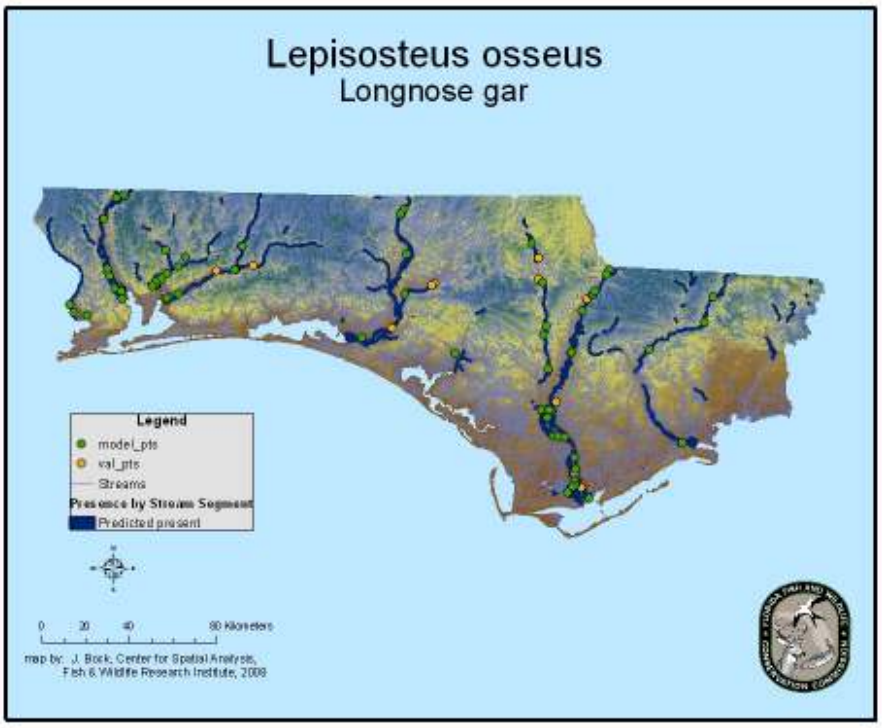


Figure 34. Potential habitat for *Lepisosteus oculatus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 113) represent the species occurrence points used in the modeling process while val_pts. (n = 37) represent the species occurrence records withheld from the modeling process for independent validation.



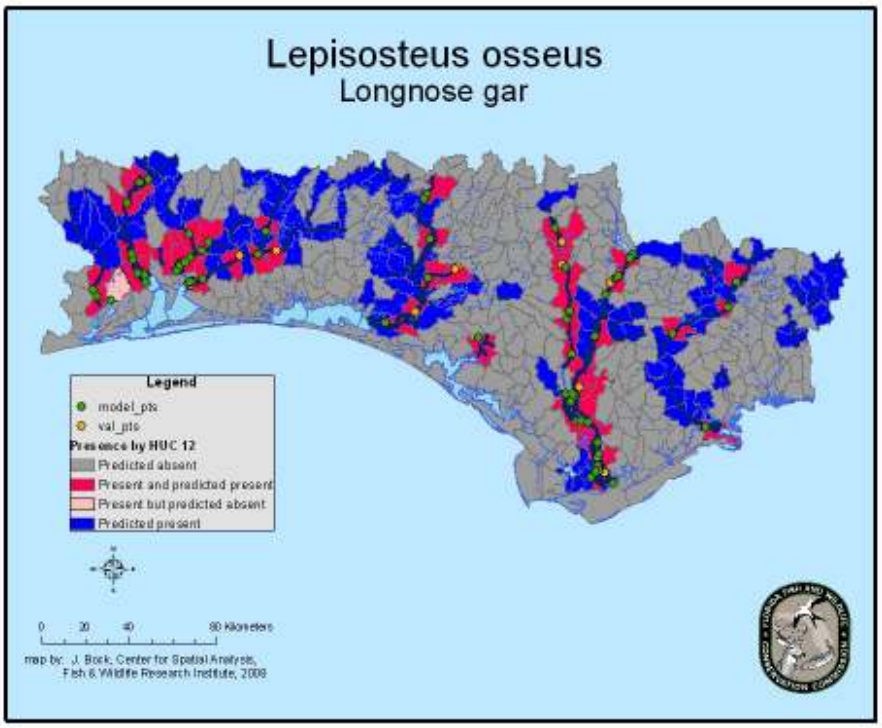
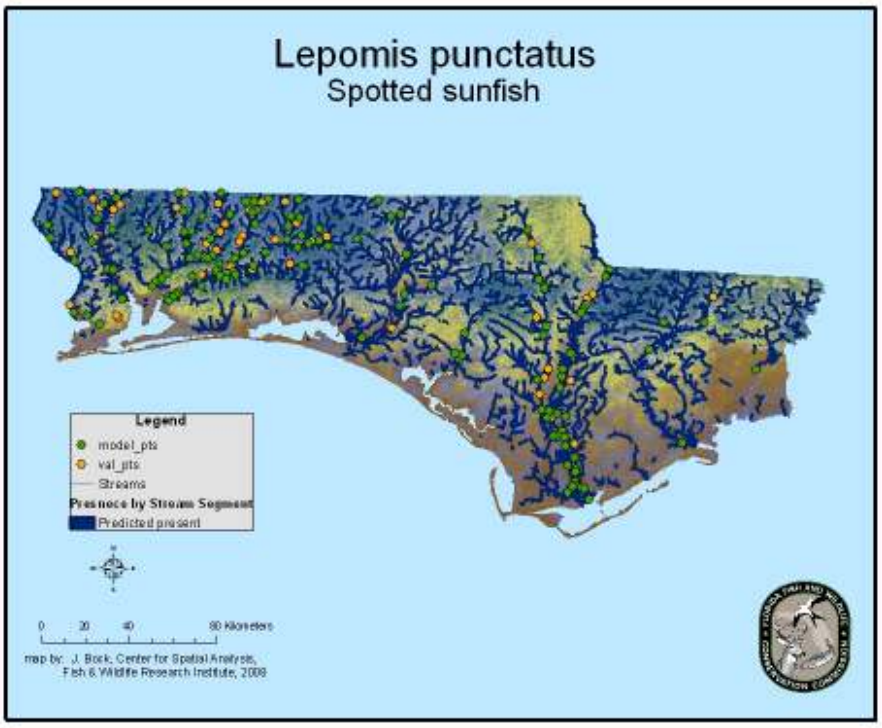


Figure 35. Potential habitat for *Lepisosteus osseus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 77) represent the species occurrence points used in the modeling process while val_pts. (n = 25) represent the species occurrence records withheld from the modeling process for independent validation.



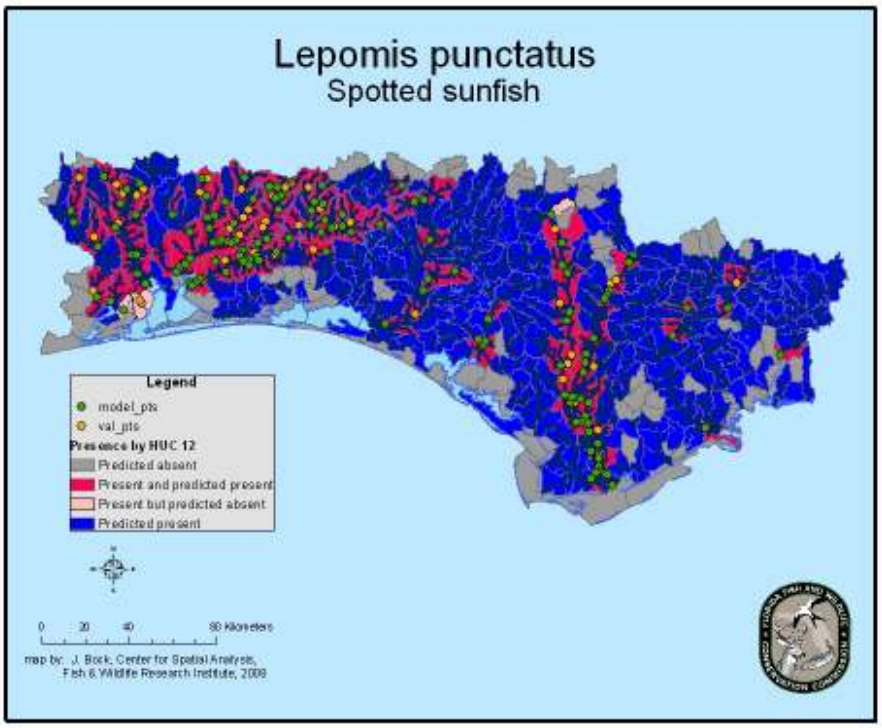
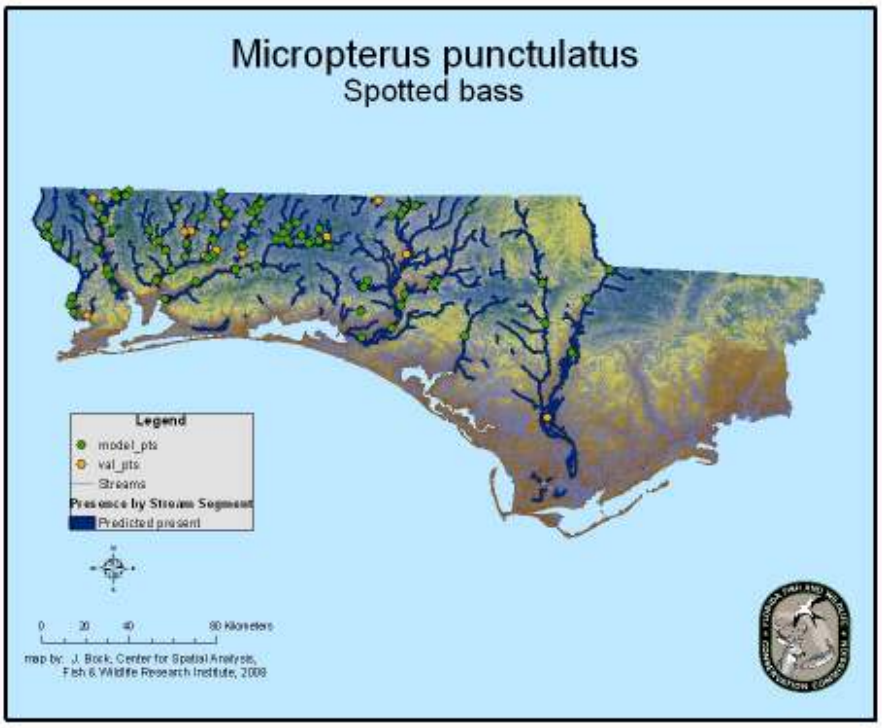


Figure 36. Potential habitat for *Lepomis punctatus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 149) represent the species occurrence points used in the modeling process while val_pts. (n = 50) represent the species occurrence records withheld from the modeling process for independent validation.



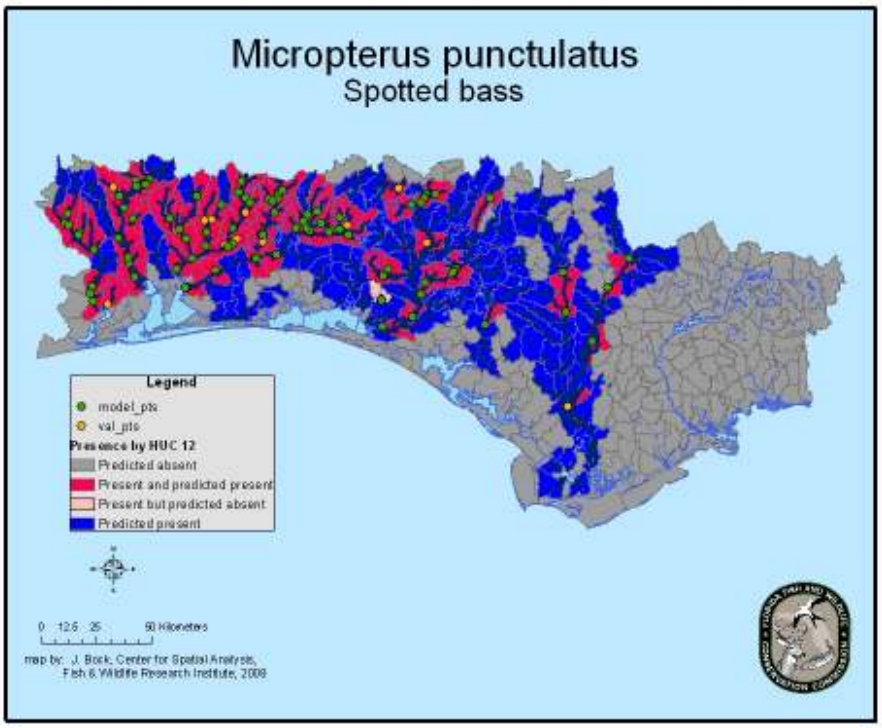
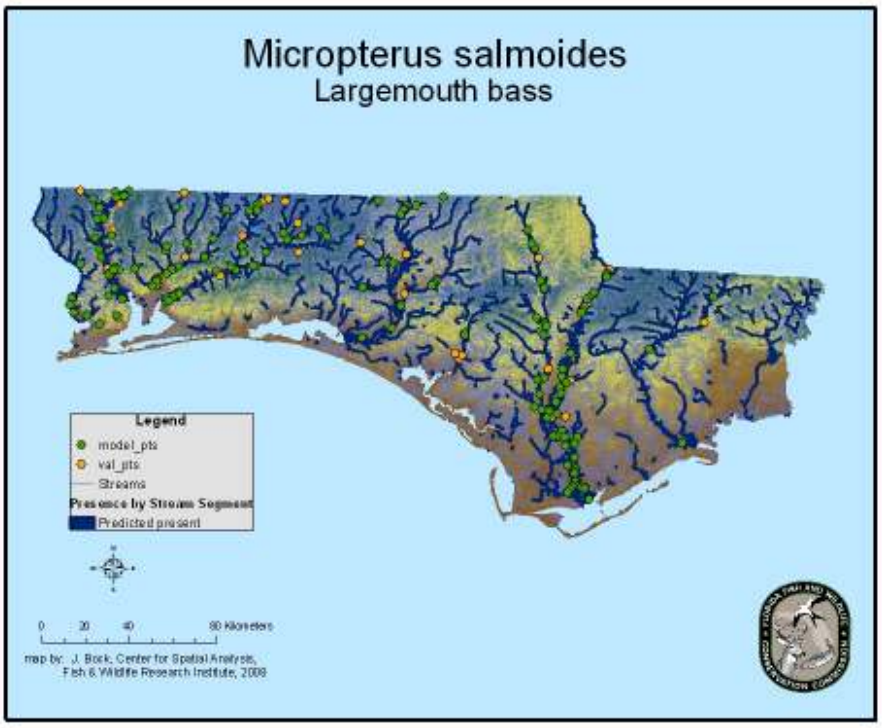


Figure 37. Potential habitat for *Micropterus punctulatus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 134) represent the species occurrence points used in the modeling process while val_pts. (n = 44) represent the species occurrence records withheld from the modeling process for independent validation.



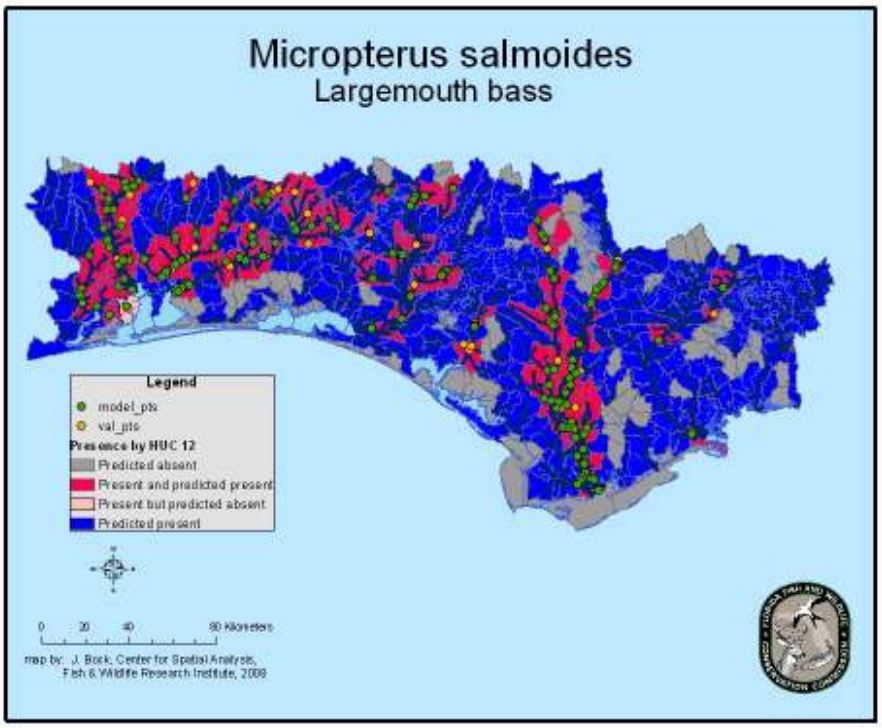
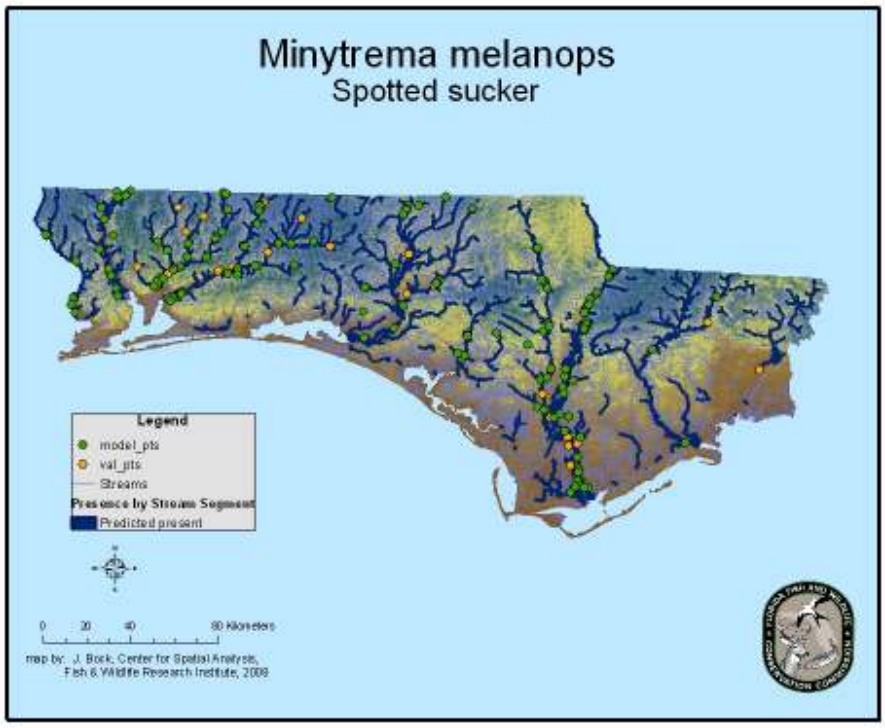


Figure 38. Potential habitat for *Micropterus salmoides* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 215) represent the species occurrence points used in the modeling process while val_pts. (n = 71) represent the species occurrence records withheld from the modeling process for independent validation.



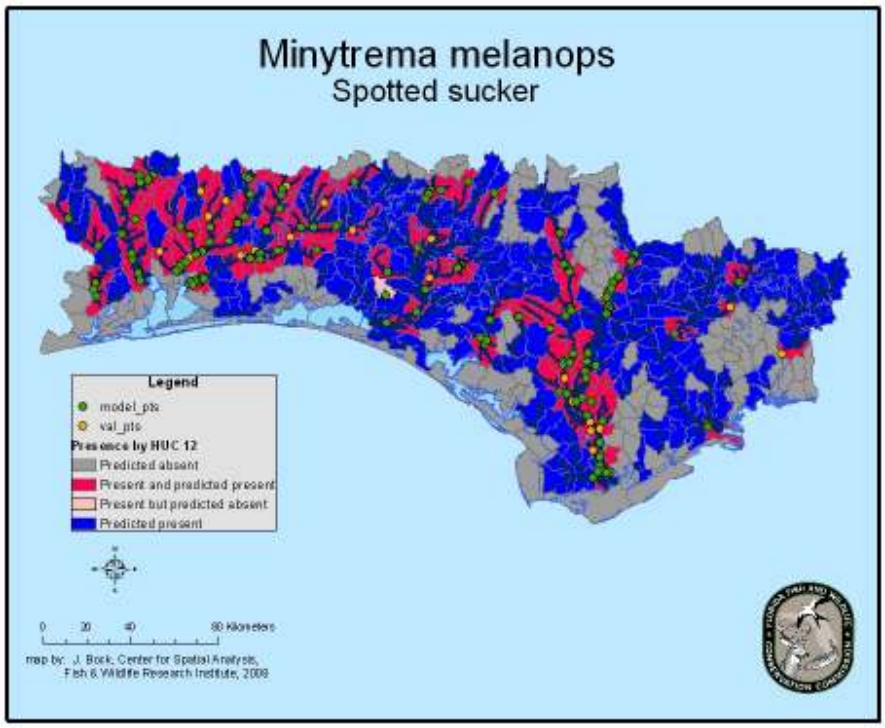
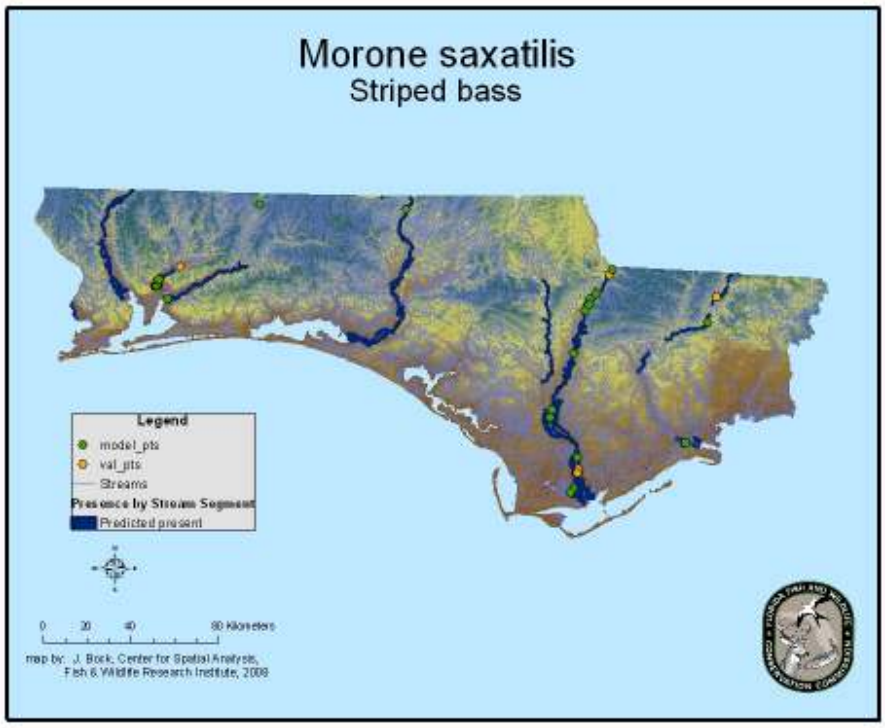


Figure 39. Potential habitat for *Minytrema melanops* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 199) represent the species occurrence points used in the modeling process while val_pts. (n = 66) represent the species occurrence records withheld from the modeling process for independent validation.



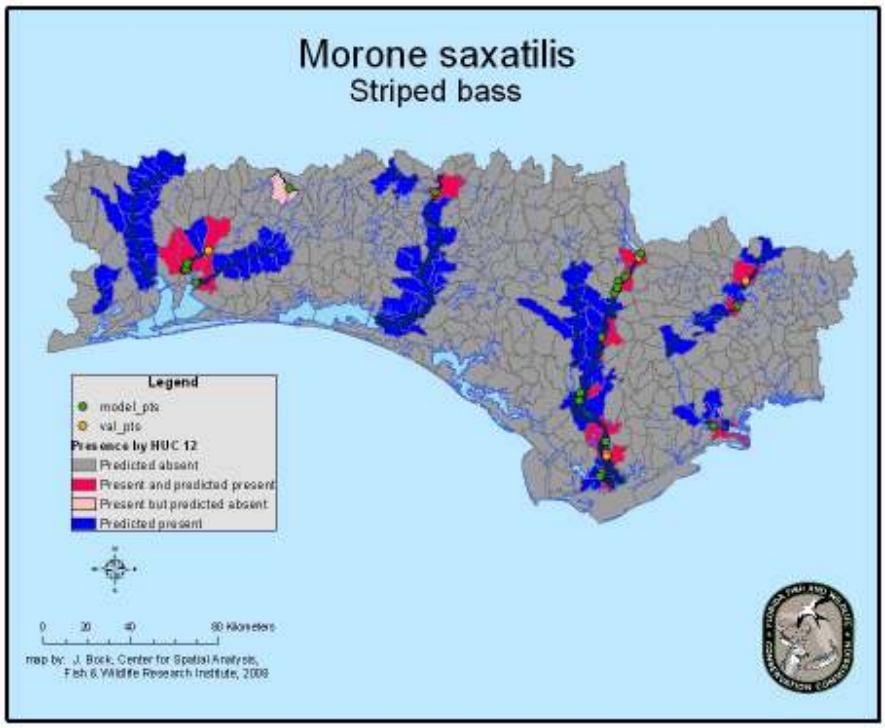
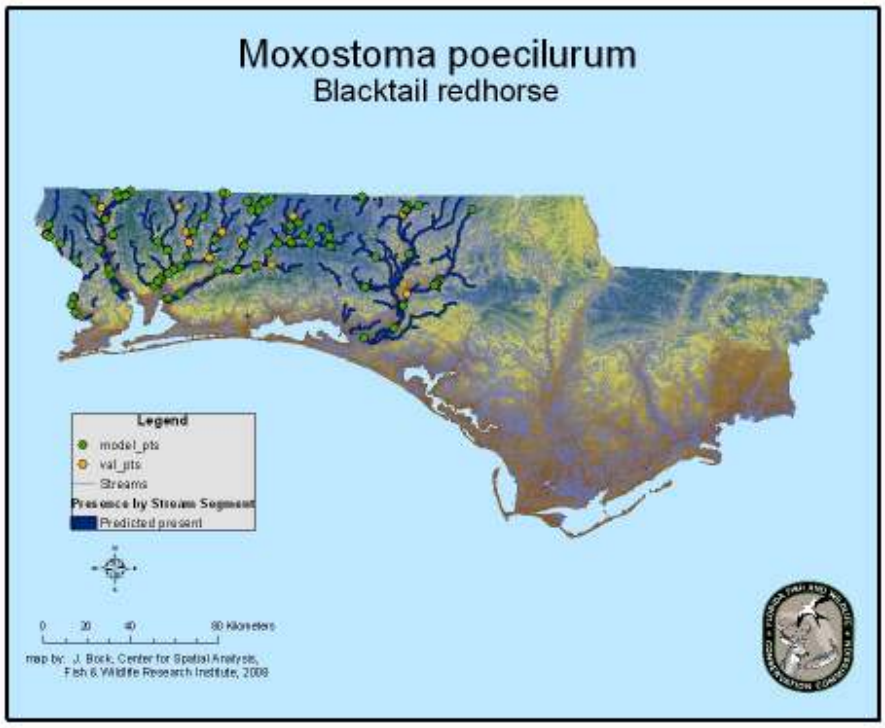


Figure 40. Potential habitat for *Morone saxatilis* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 23) represent the species occurrence points used in the modeling process while val_pts. (n = 8) represent the species occurrence records withheld from the modeling process for independent validation.



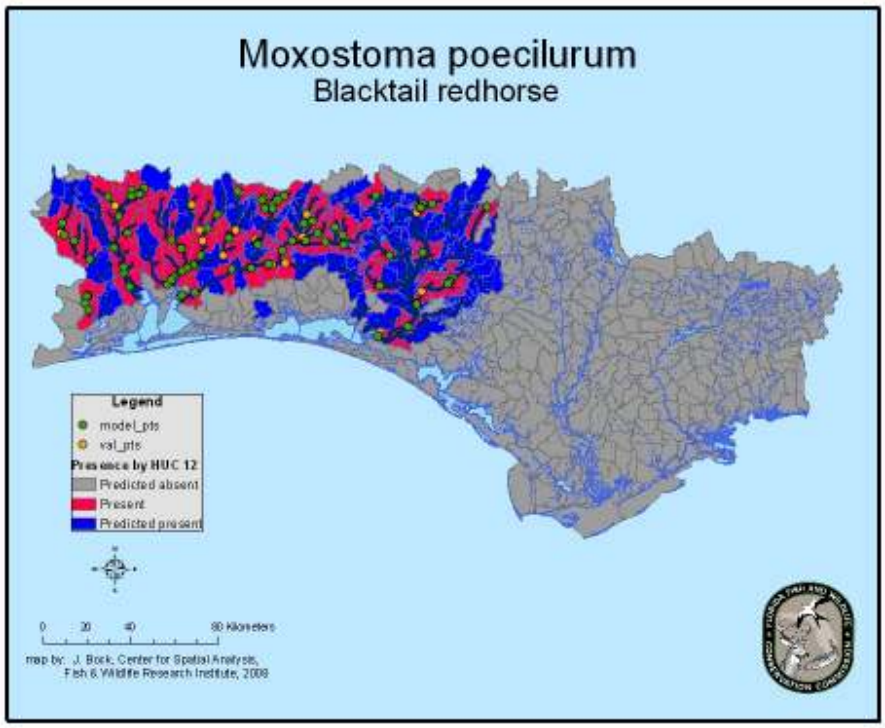
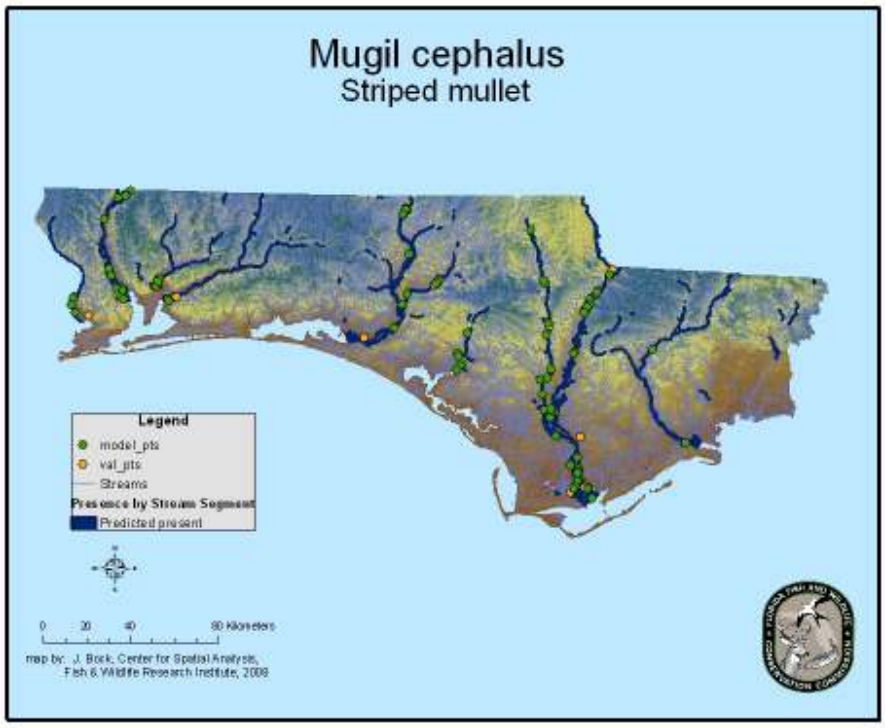


Figure 41. Potential habitat for *Moxostoma poecilurum* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 121) represent the species occurrence points used in the modeling process while val_pts. (n = 40) represent the species occurrence records withheld from the modeling process for independent validation.



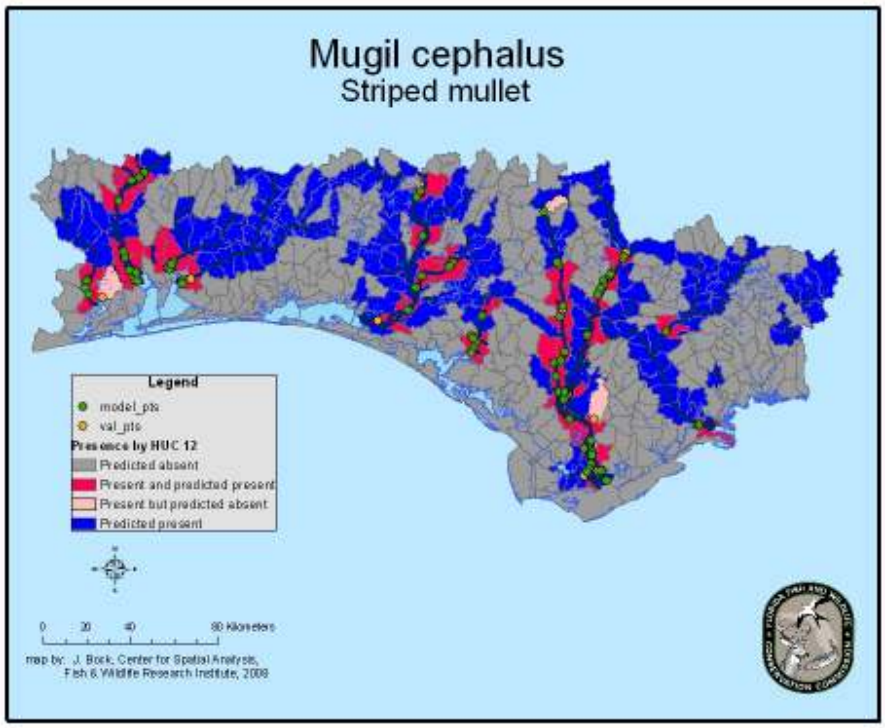
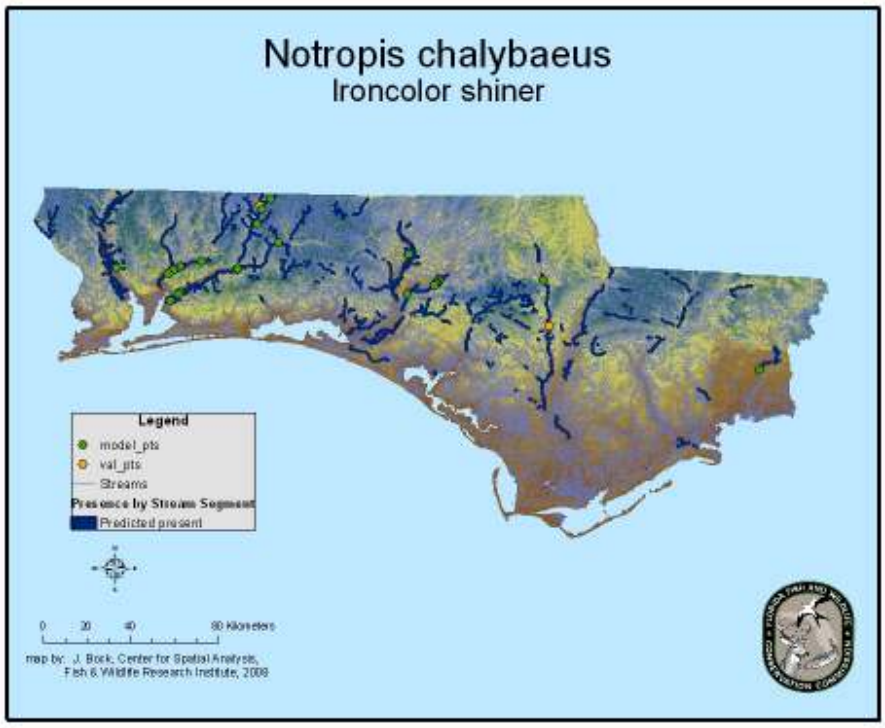


Figure 42. Potential habitat for *Mugil cephalus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 95) represent the species occurrence points used in the modeling process while val_pts. (n = 32) represent the species occurrence records withheld from the modeling process for independent validation.



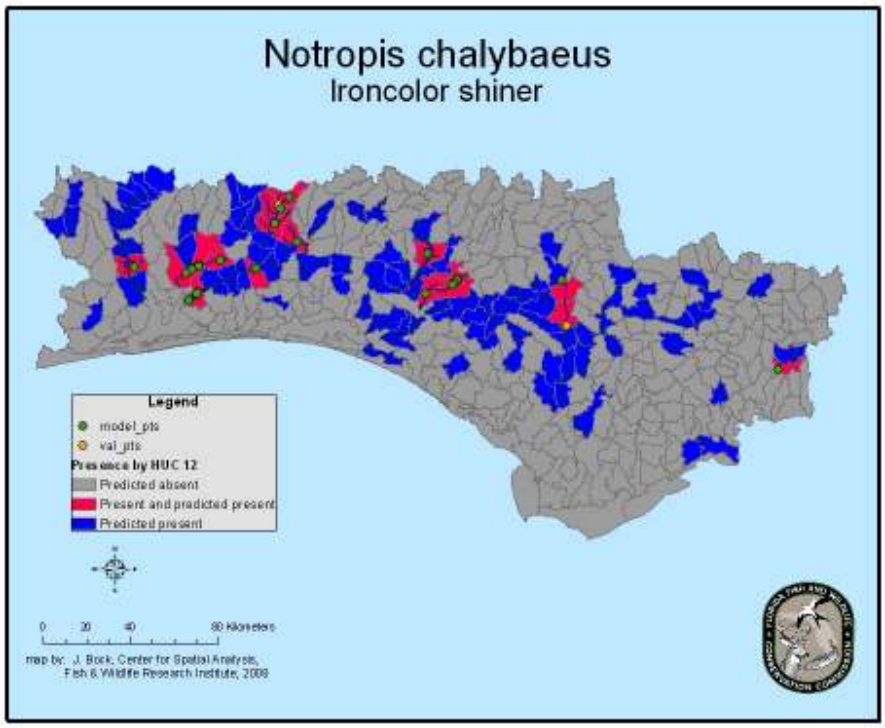
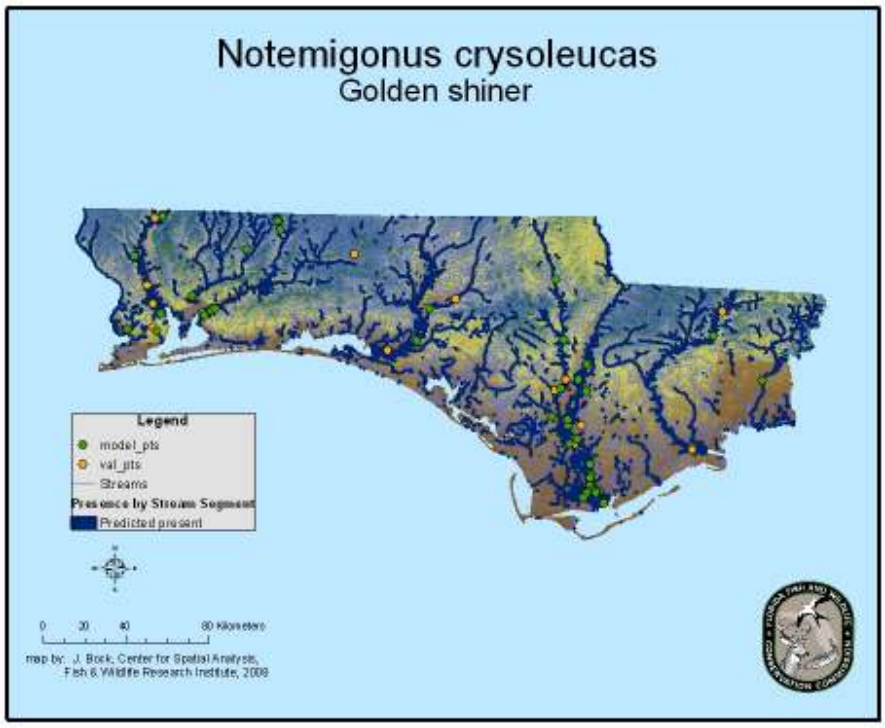


Figure 43. Potential habitat for *Notropis chalybaeus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 26) represent the species occurrence points used in the modeling process while val_pts. (n = 8) represent the species occurrence records withheld from the modeling process for independent validation.



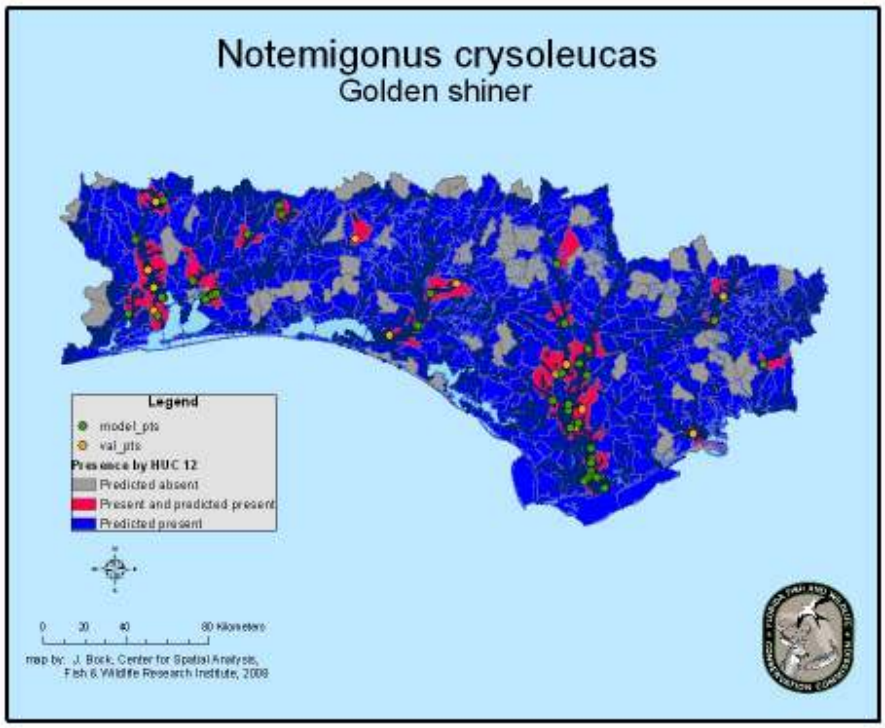
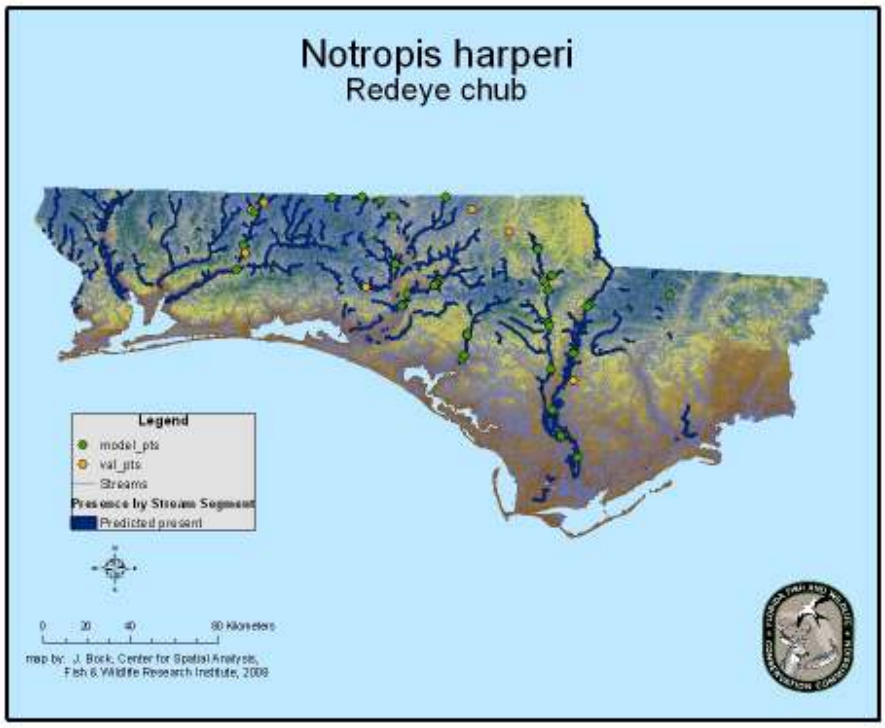


Figure 44. Potential habitat for *Notemigonus crysoleucas* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 44) represent the species occurrence points used in the modeling process while val_pts. (n = 15) represent the species occurrence records withheld from the modeling process for independent validation.



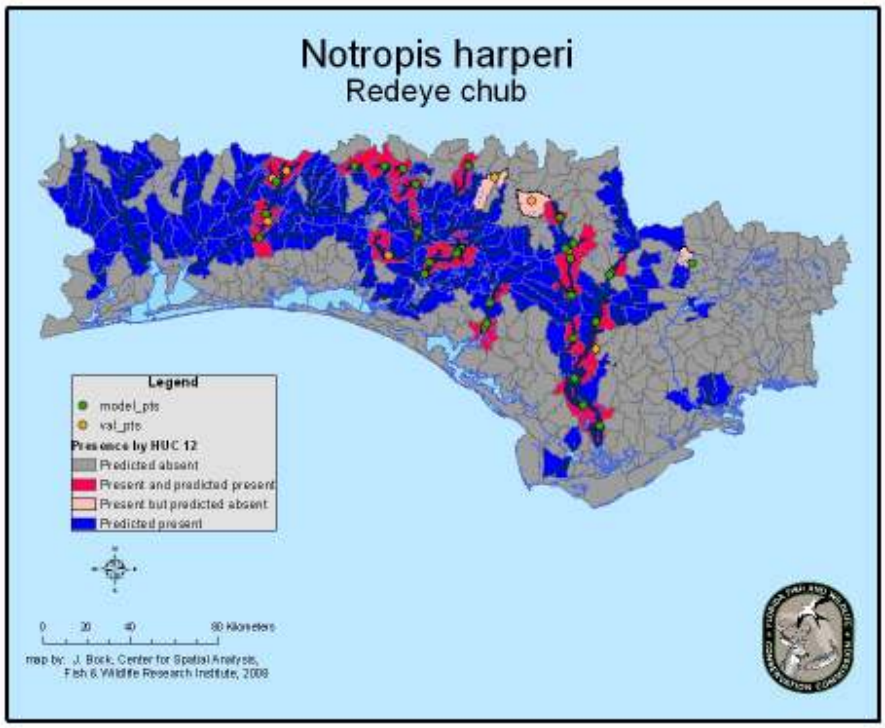
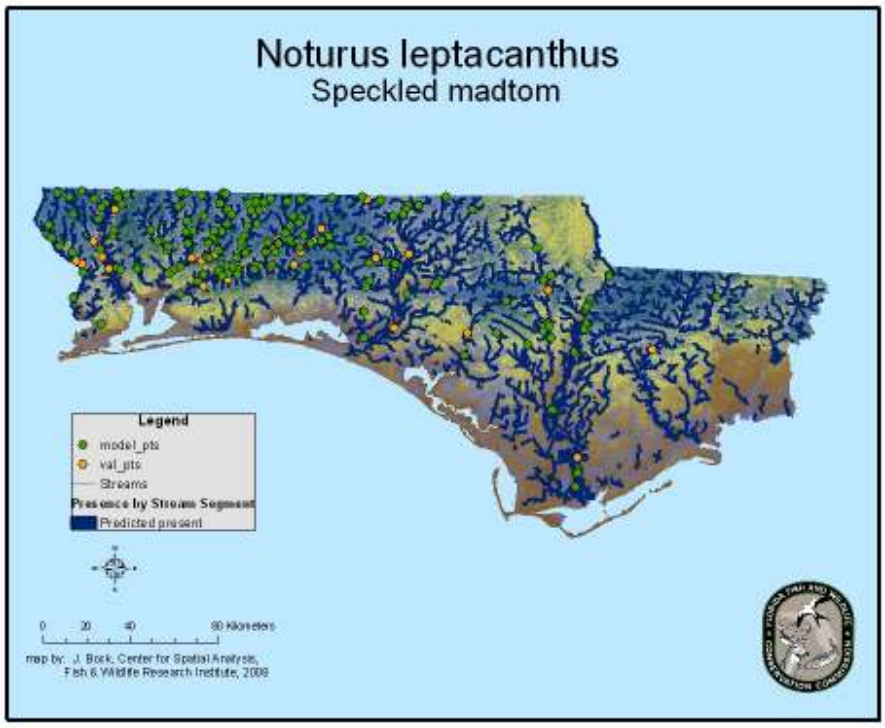


Figure 45. Potential habitat for *Notropis harperi* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 56) represent the species occurrence points used in the modeling process while val_pts. (n = 18) represent the species occurrence records withheld from the modeling process for independent validation.



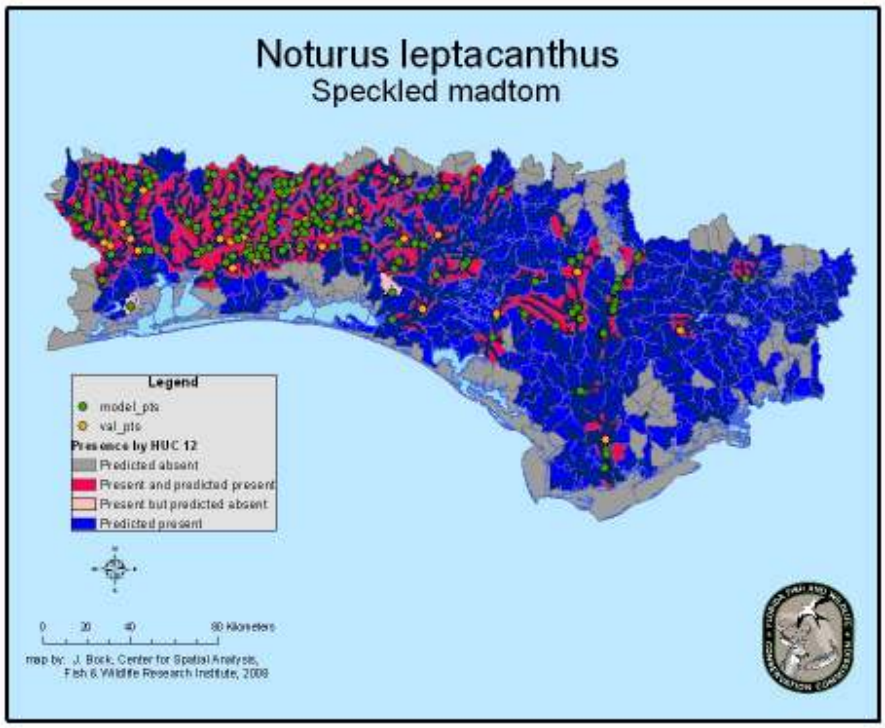
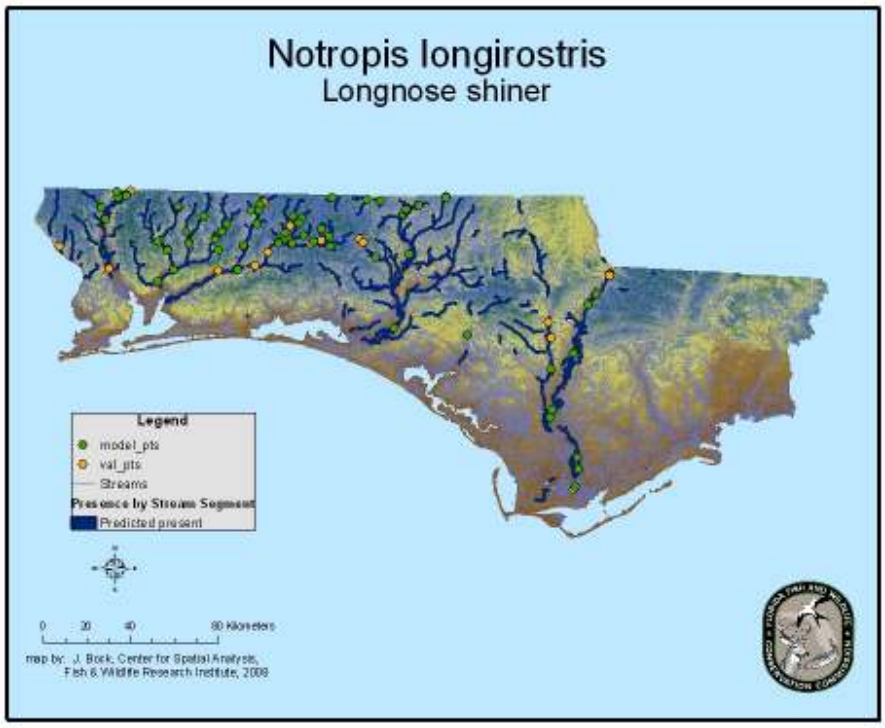


Figure 46. Potential habitat for *Noturus leptacanthus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 237) represent the species occurrence points used in the modeling process while val_pts. (n = 79) represent the species occurrence records withheld from the modeling process for independent validation.



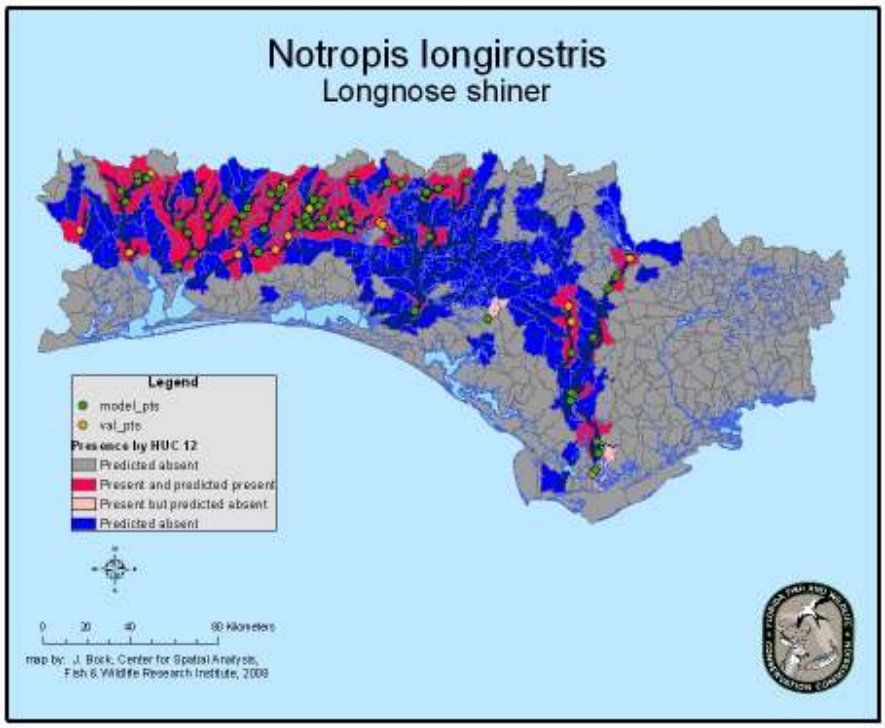
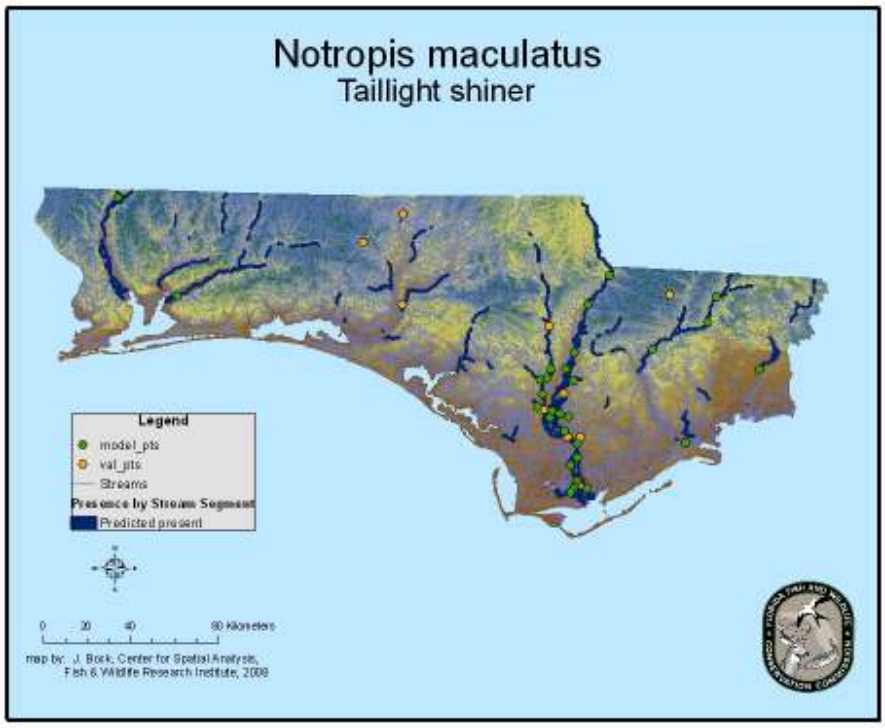


Figure 47. Potential habitat for *Notropis longirostris* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 96) represent the species occurrence points used in the modeling process while val_pts. (n = 32) represent the species occurrence records withheld from the modeling process for independent validation.



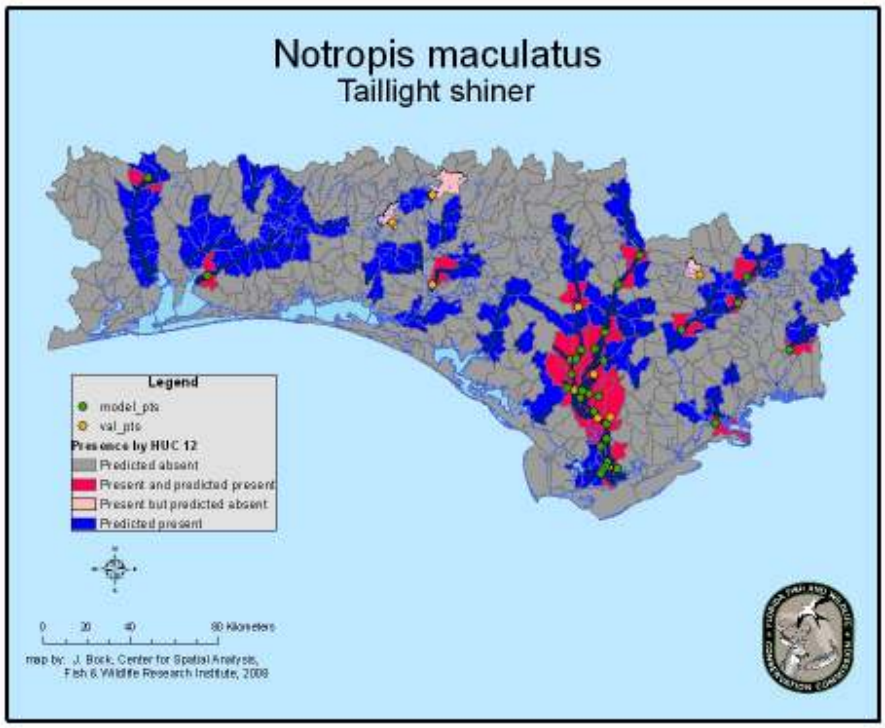
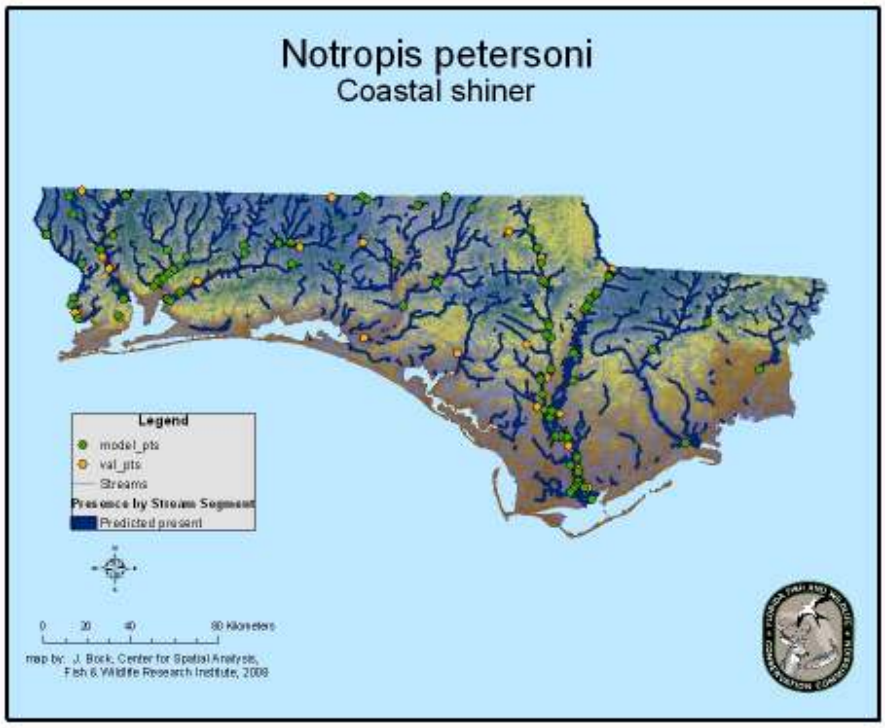


Figure 48. Potential habitat for *Notropis maculatus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 32) represent the species occurrence points used in the modeling process while val_pts. (n = 10) represent the species occurrence records withheld from the modeling process for independent validation.



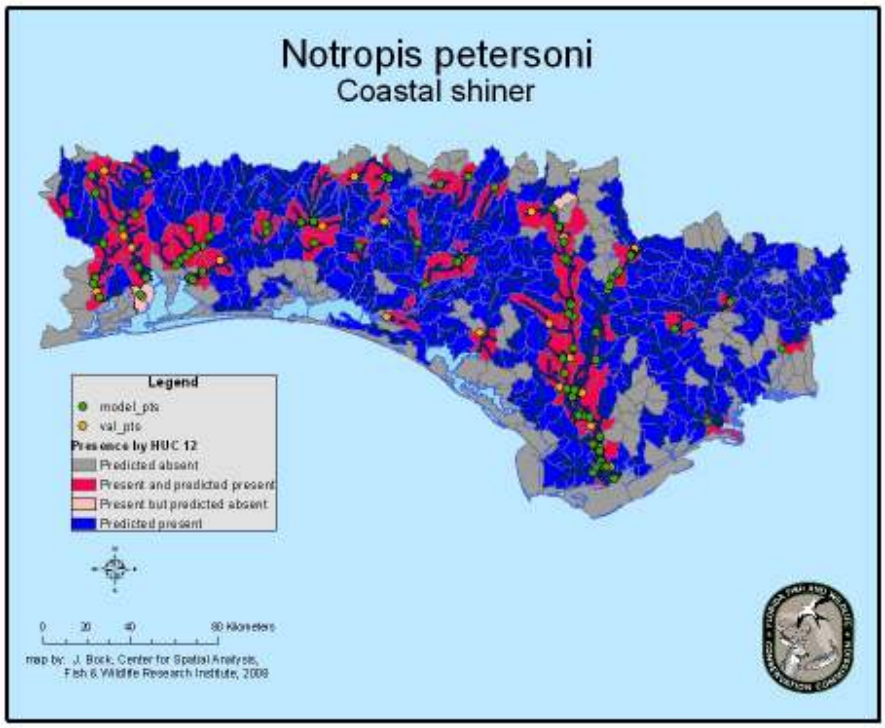
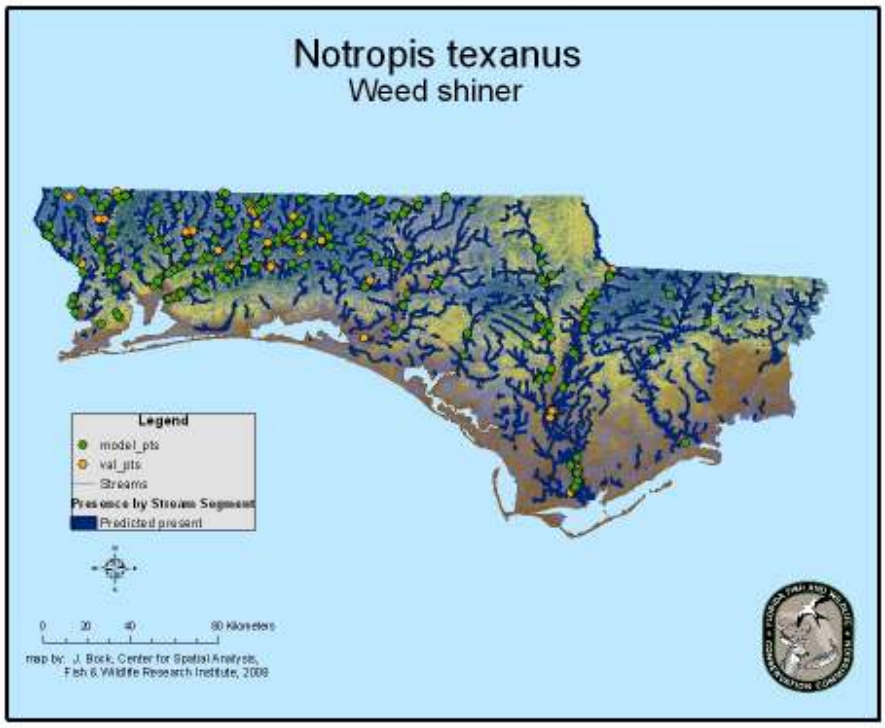


Figure 49. Potential habitat for *Notropis petersoni* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 137) represent the species occurrence points used in the modeling process while val_pts. (n = 45) represent the species occurrence records withheld from the modeling process for independent validation.



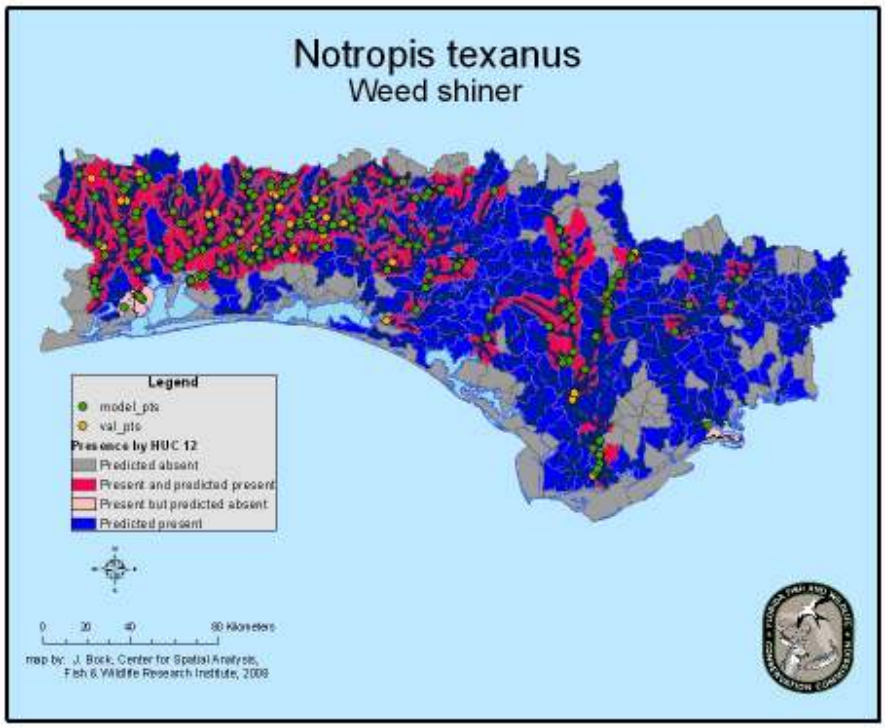
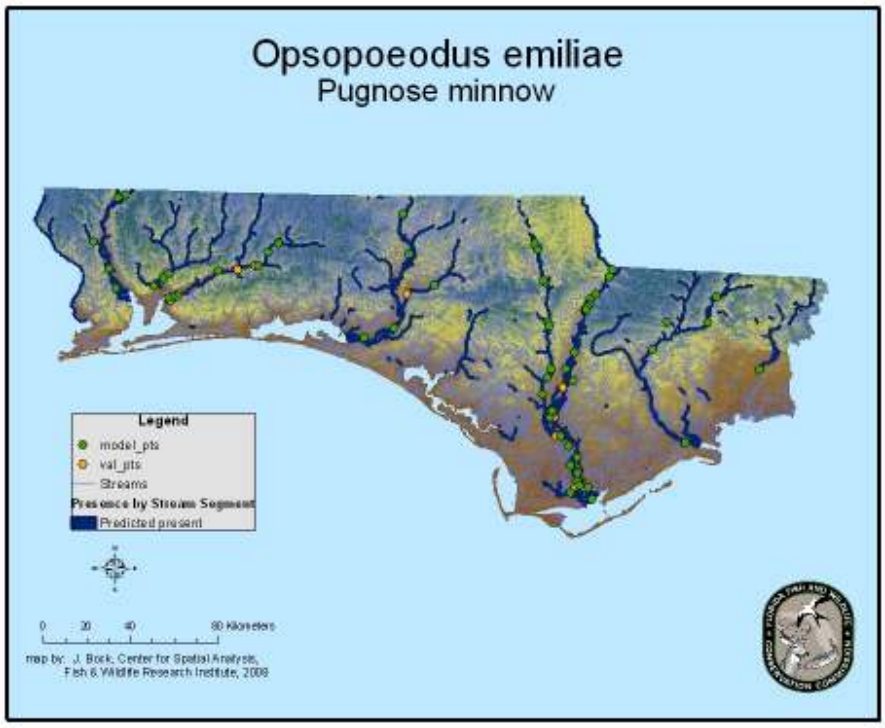


Figure 50. Potential habitat for *Notropis texanus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 289) represent the species occurrence points used in the modeling process while val_pts. (n = 95) represent the species occurrence records withheld from the modeling process for independent validation.



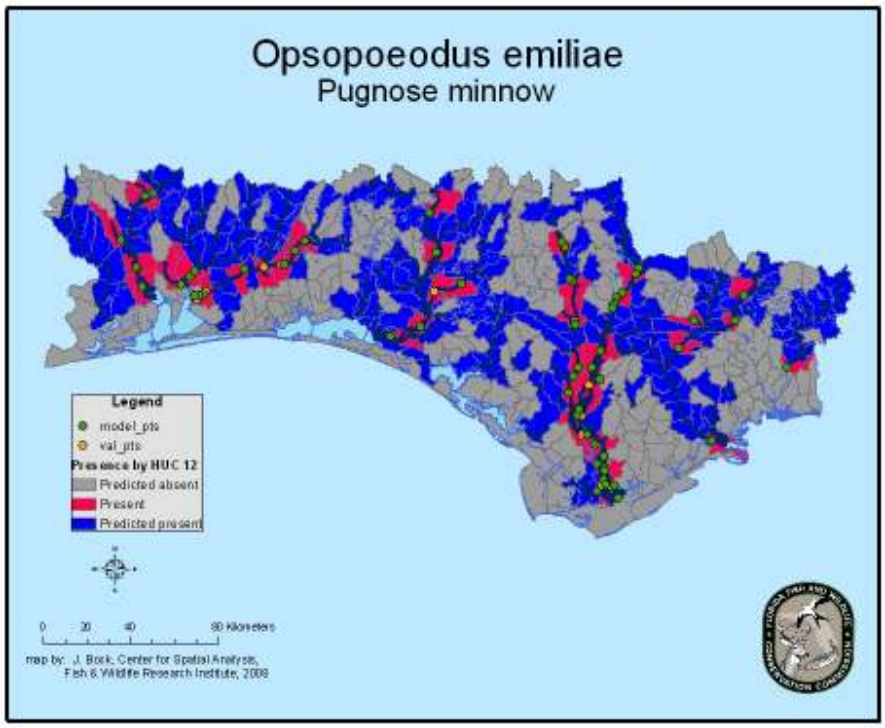
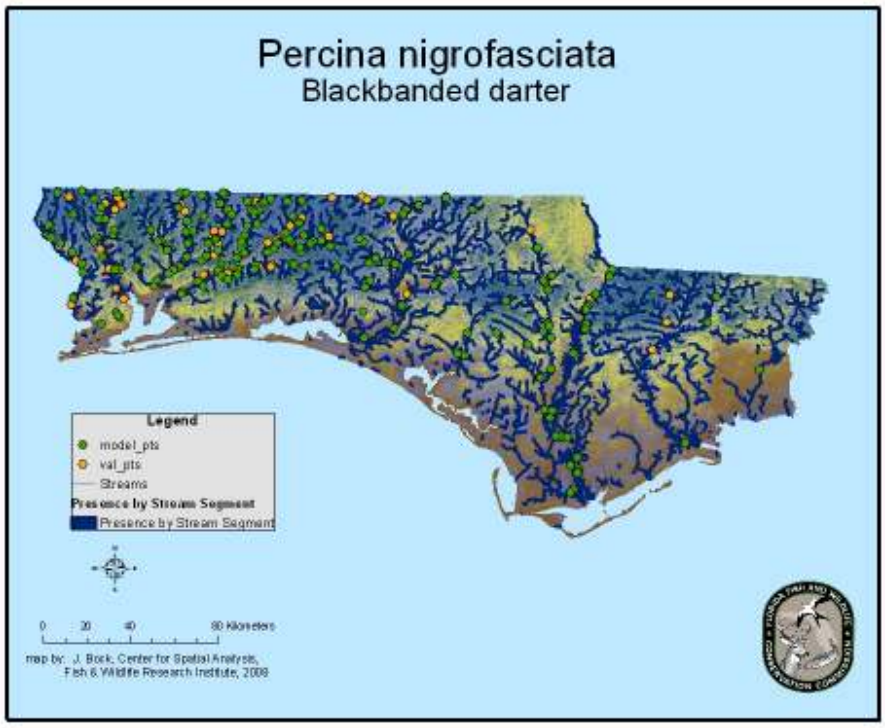


Figure 51. Potential habitat for *Opsopoeodus emiliae* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 65) represent the species occurrence points used in the modeling process while val_pts. (n = 21) represent the species occurrence records withheld from the modeling process for independent validation.



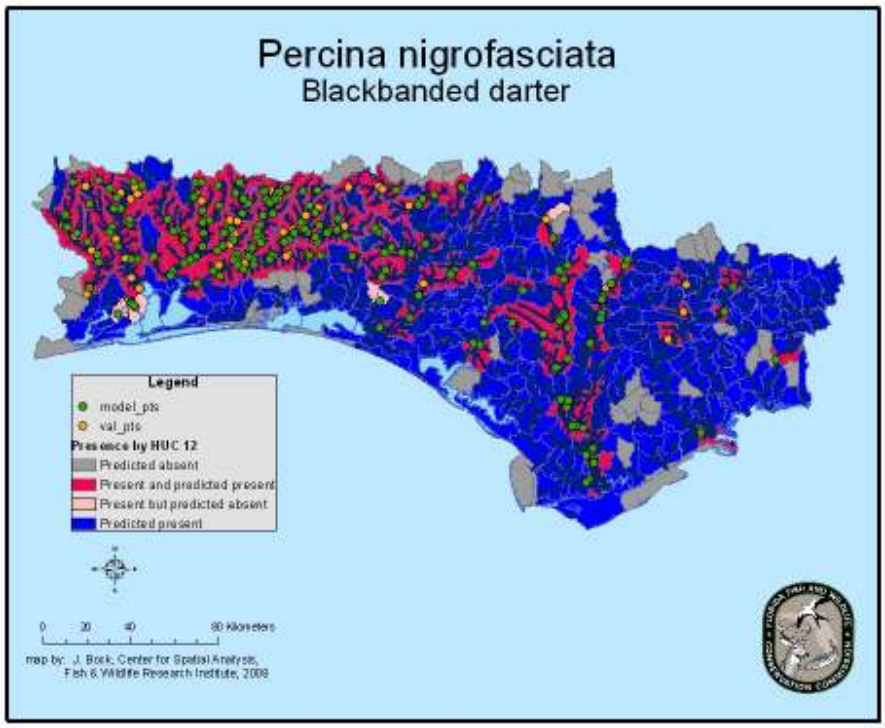
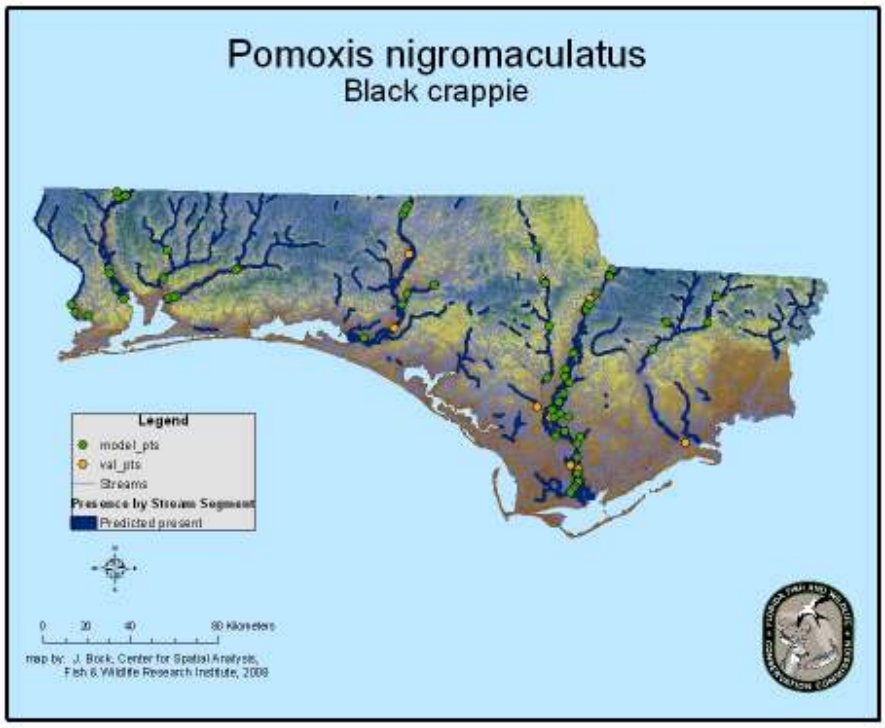


Figure 52. Potential habitat for *Percina nigrofasciata* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 323) represent the species occurrence points used in the modeling process while val_pts. (n = 108) represent the species occurrence records withheld from the modeling process for independent validation.



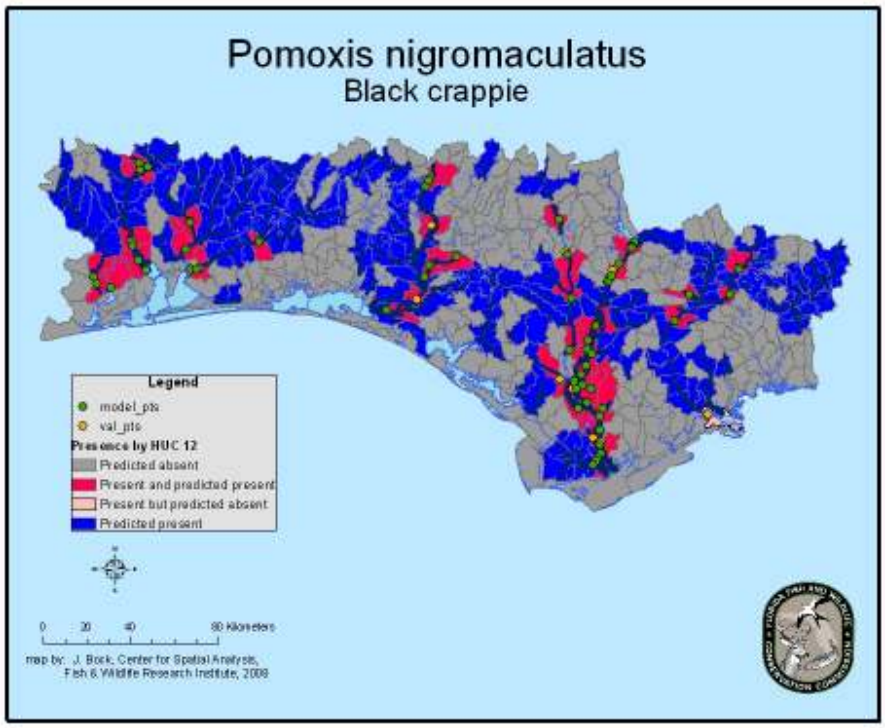
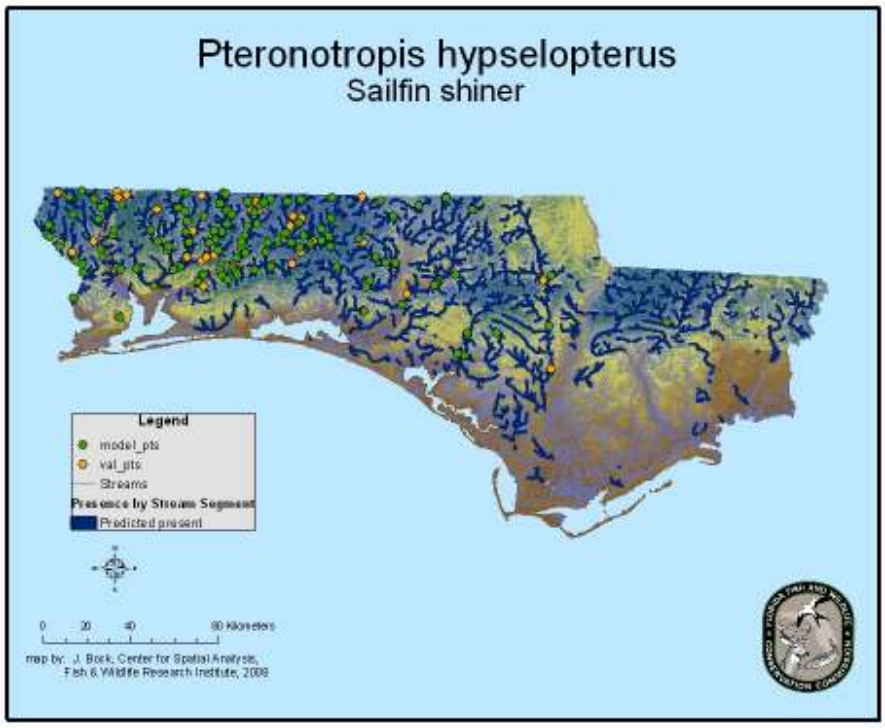


Figure 53. Potential habitat for *Pomoxis nigromaculatus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 67) represent the species occurrence points used in the modeling process while val_pts. (n = 22) represent the species occurrence records withheld from the modeling process for independent validation.



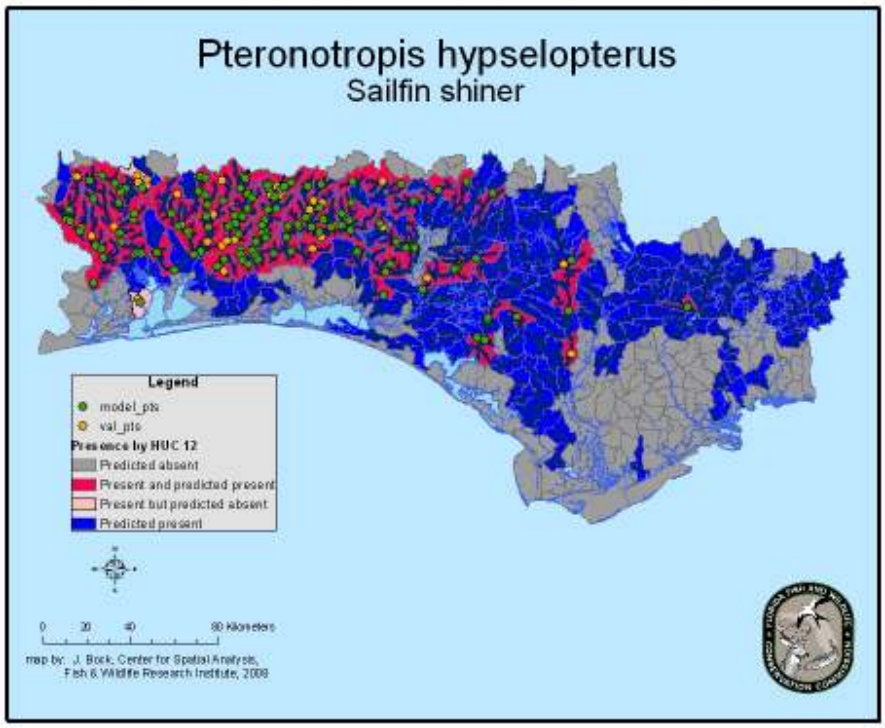
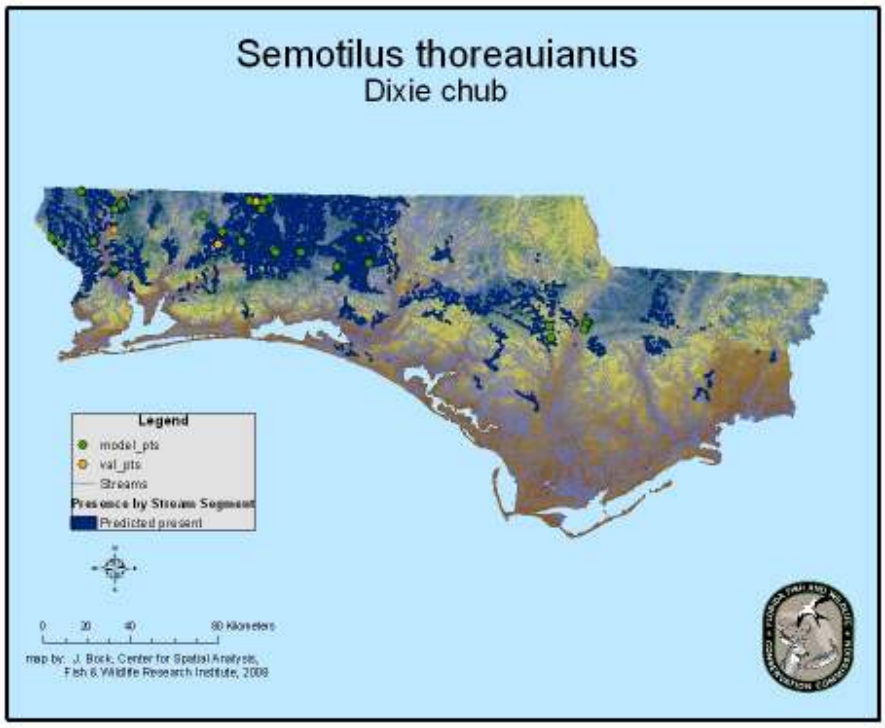


Figure 54. Potential habitat for *Pteronotropis hypselopterus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 198) represent the species occurrence points used in the modeling process while val_pts. (n = 66) represent the species occurrence records withheld from the modeling process for independent validation.



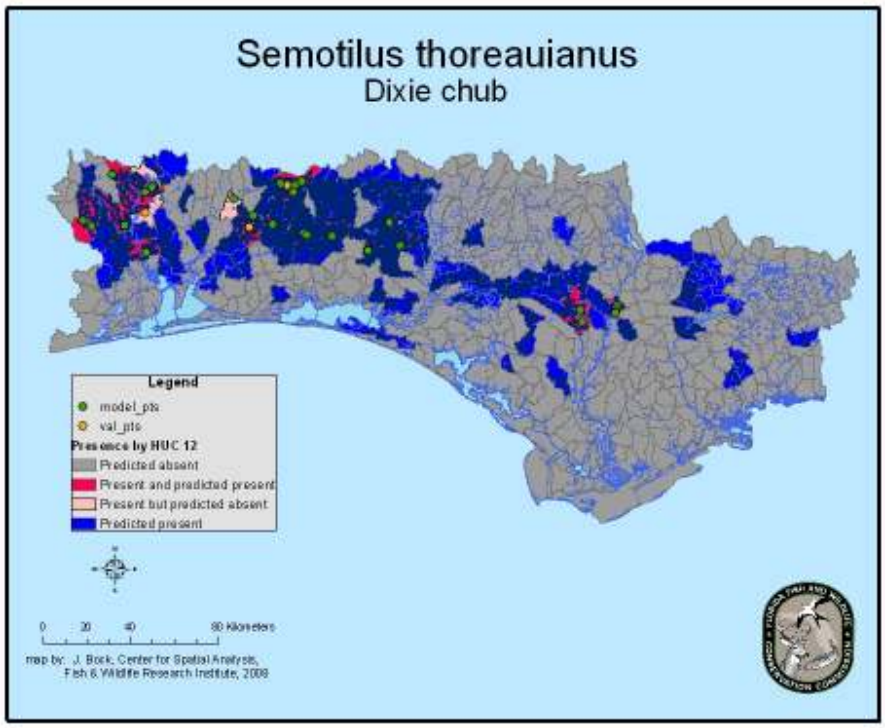
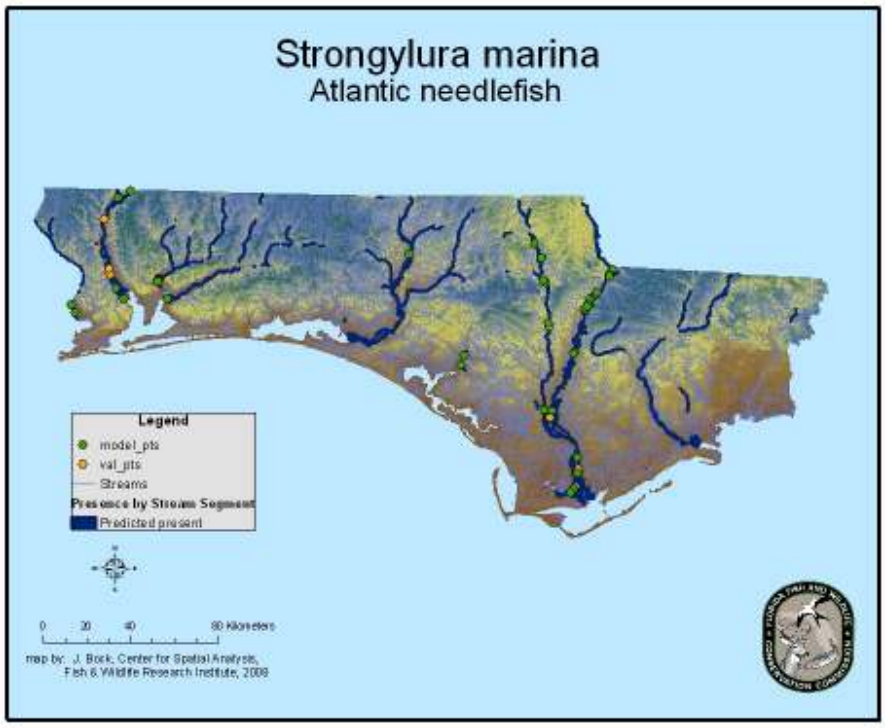


Figure 55. Potential habitat for *Semotilus thoreauianus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 35) represent the species occurrence points used in the modeling process while val_pts. (n = 12) represent the species occurrence records withheld from the modeling process for independent validation.



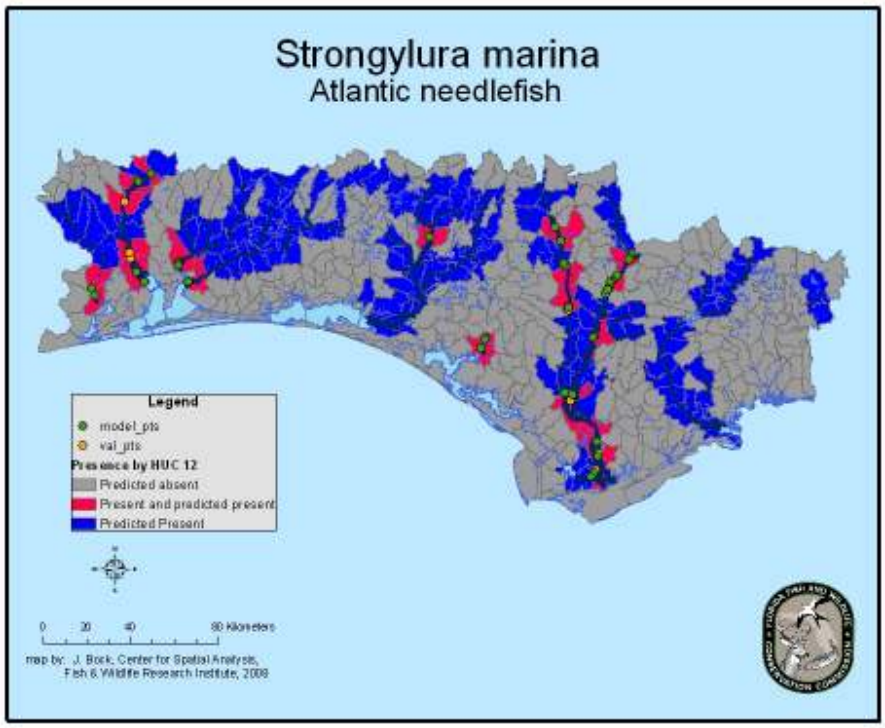
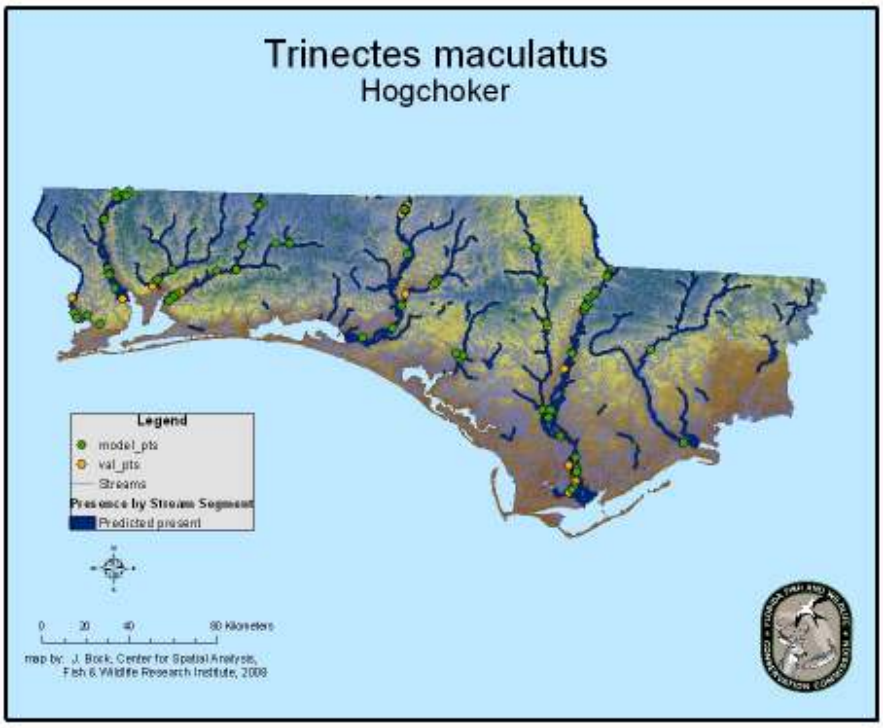


Figure 56. Potential habitat for *Strongylura marina* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 44) represent the species occurrence points used in the modeling process while val_pts. (n = 15) represent the species occurrence records withheld from the modeling process for independent validation.



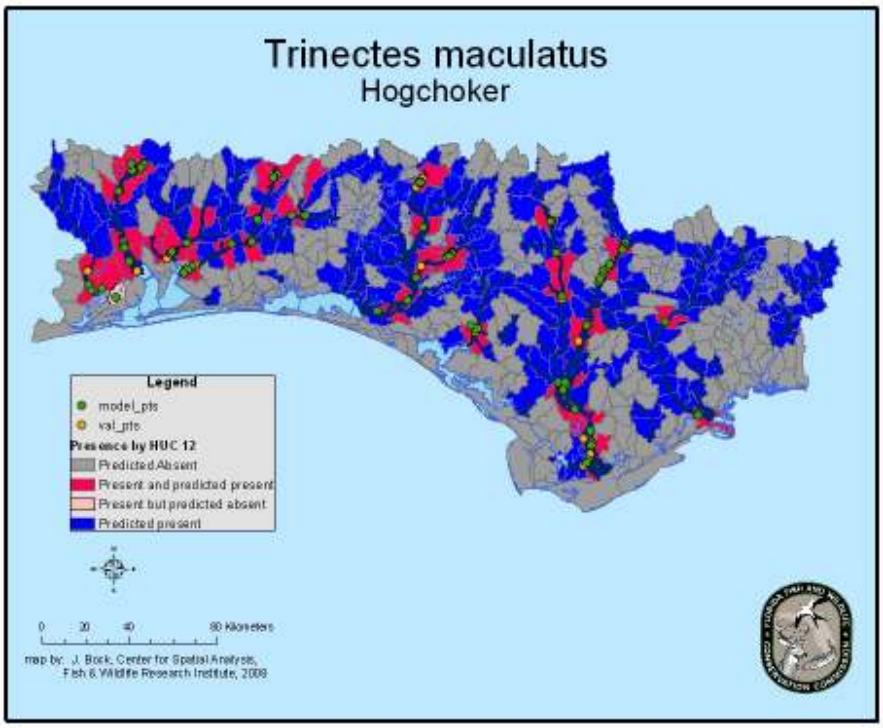


Figure 57. Potential habitat for *Trinectes maculatus* modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 97) represent the species occurrence points used in the modeling process while val_pts. (n = 32) represent the species occurrence records withheld from the modeling process for independent validation.

Models Created Using Only Three Broad Landuse/Landcover Characteristics

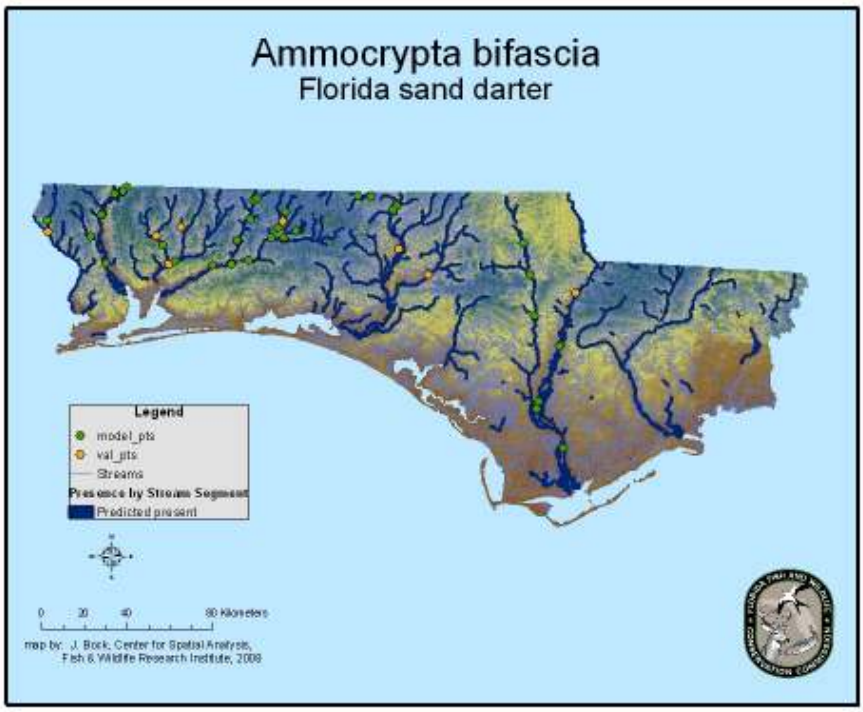
Ten of the models produced using 11 landuse/landcover characteristics, as well as size, Strahler order, connectivity, size discrepancy, flow, sinuosity, surficial geology, and relative gradient, have validation sensitivities between 0.50 and 0.79. It is possible that the inclusion of a large number of landuse/landcover characteristics in the modeling process caused the model to overfit to the model points. To test this, these ten models were rerun using only 3 broad categories of landuse/landcover, as well as all of the other habitat variables used to create the original models. The 3 landuse/landcover characteristics included in these models were percent natural cover, percent human altered cover and percent land used for any type of agriculture. The number of models required to achieve an omission rate of 10% or less ranged from 1 to 12. Commission errors for the models used in the mapping process ranged from 4.98% to 30.17%. The percentage of the study area classified as suitable habitat varied between 3% and 22% (Table 10). Sensitivity values, or the percentage of occurrence points correctly predicted as presence ranged from 50% to 100% when only validation points were considered and from 83% to 94% when all points were considered. The p-values for these sensitivity values were never greater than 0.01 (Table 110).

Table 10. Parameters of the 10 fish species modeled using only 3 landuse/landcover characteristics. Occurrence points describes: the total number of occurrence points for each species (a), the number of points input into GARP for modeling (b) and the number of points withheld for independent validation of the model (c). Range of commission error of the best 20 GARP models used to produce the final potential distributions(d). After the best 20 GARP models were combined, this value represents the minimum number of models that, when summed, agreed to produce a less than 10% omission error (e). The number of runs performed per species (f). The percent of the total study area predicted to be potential habitat by the final potential distribution model (g).

Scientific Name	Occurrence Points Total (a)	Model (b)	Val. (c)	Commission range of 20 models (%) (d)	Number of models used to achieve less than 10% omission error (out of 20) (e)	Runs (f)	%study area predicted (g)
Alosa alabamae	36	27	9	8.67-10.92	1	1000	0.04
Ammocrypta bifascia	61	46	15	9.78-16.02	8	1000	0.14
Carpiodes cyprinus	60	45	15	6.48-7.13	1	1000	0.05
Erimyzon sucetta	72	54	18	22.06-30.17	7	1000	0.22
Erimyzon tenuis	77	58	19	22.65-26.17	2	1000	0.17
Gambusia affinis	71	53	18	16.00-25.06	12	1000	0.21
Lepomis cyanellus	32	24	8	16.92-22.15	2	1000	0.13
Morone saxatilis	31	23	8	4.98-7.22	1	1000	0.03
Notropis harperi	74	56	18	11.89-18.69	4	1000	0.09
Notropis maculatus	42	32	10	8.76-11.07	1	1000	0.04

Table 11. Accuracy statistics for the potential distributions for the 10 fish species modeled using only 3 landuse/landcover characteristics. The ratio of total points falling in areas of predicted habitat to total points (a). Sensitivity, or percent correctly classified as present, for all of the points for a species (b) p-value for total sensitivity, or the chance that the number of points classified correctly could be the results of chance alone (c). The ratio of model points falling in areas of predicted habitat to total model points (d). Sensitivity, or percent correctly classified as present, for all of the model points for a species (e). The ratio of validation points falling in areas of predicted habitat to total validation points (f). Sensitivity, or percent correctly classified as present for all of the validation points for a species (g). P-value for validation sensitivity, or the chance that the number of validation points classified correctly could be the results of chance alone(h).

Scientific Name	Total points classified correctly (a)	sensitivity (b)	p-value (c)	Model points classified correctly (d)	sensitivity (e)	Validation points classified correctly (f)	sensitivity (g)	p-value (h)
Alosa alabamae	32/36	0.89	9.28E-41	24/27	0.89	8/9	0.89	5.69E-11
Ammocrypta bifascia	57/46	0.93	6.16E-44	42/46	0.91	15/15	1.00	1.56E-13
Carpiodes cyprinus	56/60	0.93	5.53E-68	43/45	0.96	13/15	0.87	1.17E-15
Erimyzon sucetta	62/72	0.86	7.95E-31	49/54	0.91	13/18	0.72	7.76E-06
Erimyzon tenuis	70/77	0.91	3.75E-55	54/58	0.93	16/19	0.84	2.80E-10
Gambusia affinis	63/71	0.89	9.01E-46	50/53	0.94	13/18	0.72	4.49E-06
Lepomis cyanellus	30/32	0.94	3.33E-34	23/24	0.96	7/8	0.88	4.45E-06
Morone saxatilis	28/31	0.90	9.93E-25	21/23	0.91	7/8	0.88	1.70E-10
Notropis harperi	66/74	0.89	6.85E-60	51/56	0.91	15/18	0.83	1.29E-13
Notropis maculatus	35/42	0.83	2.41E-42	30/32	0.94	5/10	0.50	2.18E-05



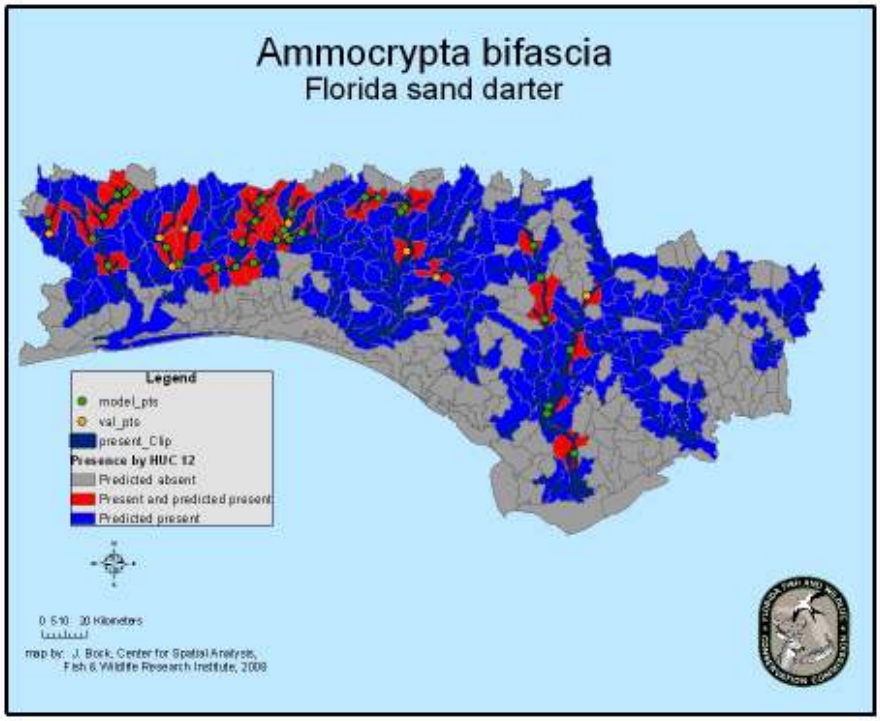


Figure 58. Potential habitat for Ammocrypta bifascia modeled using GARP. Potential habitat shown by stream segment (top) and HUC 12 (bottom). Model_pts. (n = 46) represent the species occurrence points used in the modeling process while val_pts. (n = 15) represent the species occurrence records withheld from the modeling process for independent validation. Only 3 landuse/landcover characteristics were used in the creation of this model.

DISCUSSION AND CONCLUSION

Modeling potential species habitat is an increasingly important tool for ecology, conservation, invasive species management, and climate change research. Multiple studies have demonstrated the ability of species modeling techniques to accurately predict the occurrence of suitable habitat for a species in question using only a few landscape level factors (Stockwell and Peterson 2002, Anderson 2003, Guisan and Thuiller 2005.).

Potential Habitat Maps

Information regarding each speices' potential habitat map is provided below. Information includes: the published range of each species, and whether the predicted range was clipped to the boundaries of the published range.. ….

- *Alosa alabamae* - Occurs throughout the Florida Panhandle. The model for *A. alabame* shows potential habitat for this species existing in the Blackwater and Yellow Rivers. Historical records show Alabama shad in these rivers, however, there are no recent records of them in these rivers (Lee et al. 1980, NatureServe 2009).
- *Alosa chrysochloris – A. chrysochloris'* potential distribution was clipped to its known range because there are no records of it occurring east of the Apalachicola (Lee et al. 1980).
- *Ambloplites ariommus –A. ariommus'* potential distribution was clipped to its known range because there are no records of it occurring east of the Apalachicola (Lee et al. 1980).

- *Ameiurus natalis* - Occurs throughout Florida the Florida Panhandle (Lee et al. 1980).
- *Amia calva*- Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Ammocrypta bifascia* - The published range for *A. bifascia* in Florida extends from the Perdido River east to the Choctawhatchee River and tributaries, with specimens collected from the Apalachicola River being suspected the result of human introductions (Lee et al. 1980). The range potential habitat map was not clipped to this extent because there are several occurrence records for this species in both the Chipola and Apalachicola Rivers. It seems likely that this species has expanded its range eastward at least to the Apalachicola and possibly further.
- *Anguilla rostrata* - occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Carpiodes cyprinus* - - The published range for *Carpiodes cyprinus* in Florida extends east to the Apalachicola River (NatureServe 2009). *Carpiodes cyprinus'* potential distribution was clipped to its known range because there are no records of it occurring east of the Apalachicola
- *Cyprinella venusta* - Range extends east to the Suwannee River drainage (NatureServe 2009).
- *Dorosoma cepedianum* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Dorosoma petenense*- Occurs throughout the Florida panhandle (Lee et al. 1980).
- *Elassoma zonatum* - Occurs throughout the Florida Panhandle (Lee et al. 1980). The predicted potential habitat for this species appears to be strongly influenced by landscape/landuse characteristics. Without field testing it is difficult to

determine whether this represents an actual limit to the species' distribution or whether this is a case of overfitting. The predicted habitat should therefore be interpreted as a very conservative estimate of the extent of potential habitat.

- *Erimyzon sucetta* - Occurs throughout the Florida Panhandle (Lee et al. 1980). The available literature states that this species rarely occurs in streams, preferring ponds, lakes, oxbows, sloughs, swamps, impoundments, and similar waters of little or no flow that are clear and have bottoms of sand or silt mixed with organic debris (NatureServe 2009). However, it is likely that most streams in Florida have a low enough gradient for this species to tolerate.
- *Erimyzon tenuis*- Lee et al. (1980) states that *E. tenuis* is found from the western border of Florida to the Yellow River system, and that the occurrence records in the Choctawhatchee River drainage are based on young *E. sucetta*. However, the occurrence records used in this study show *E. tenuis* occurring as far east as the Chipola River drainage. Additional records which were not included in this study because their locations were only recorded to the drainage basin level show *E. tenuis* as far east as the Ochlockonee River drainage. Therefore the potential habitat was not clipped to the published range.
- *Esox niger* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Etheostoma davisoni* - The published range of E. davisoni extends from the Escambia River drainage east to the Choctawhatchee River drainage (Page and Burr 1991). The potential distribution was clipped to this range.
- Etheostoma edwini - Page and Burr (1991) report the range of *E. edwini* as occupying the area from the St. Johns River drainage west to Perdido River

drainage. It has been introduced in the Choctawhatchee Bay drainage where it is locally replacing *E. okaloosae*. It is common in the western half of its range, and uncommon and localized in the east.

- *Etheostoma swaini* - *E. swaini's* range in the Florida Panhandle runs from the western edge of the state to the Ochlockonee River drainage (Lee et al. 1980).
- *Fundulus escambiae* - *F. escambia* is found in Florida from the Perdido River drainage east to the Suwannee River drainage (Page and Burr 1991). Additional records not used in this study due to a lack of specific locational data indicate that *F. escambia* occurs in far more habitat in subregion 12 than the model indicates. It is likely that predicted potential habitat for this species is strongly influenced by landscape/landuse characteristics and the scarcity of test sites in subregion 12. The predicted habitat should therefore be interpreted as a very conservative estimate of the true extent of potential habitat.
- *Fundulus olivaceous* -Lee et al. (1980) reports that in the Florida Panhandle, *F. olivaceous'* range extends from the western border of the state to the Choctawhatchee River system. This is where the majority of records fall, however additional records not used in this study due to a lack of specific locational data indicate that *F. olivaceuos* occurs as far east as the Ochlockonee River drainage. For this reason, the potential habitat map was not clipped to the range reported by Lee et al. (1980)
- *Gambusia affinis* - Occurs throughout the Florida Panhandle (Lee et al, 1980). Additional records not used in this study due to a lack of specific locational data indicate that *G. affininis* occurs in far more habitat in subregion 12 than the model

indicates. It is likely that predicted potential habitat for this species is strongly influenced by landscape/landuse characteristics and the scarcity of test sites in subregion 12.The predicted habitat should therefore be interpreted as a very conservative estimate of the true extent of potential habitat.

- Hybopsis sp. cf winchelli - NatureServe (2009) gives the range of *Hybopsis sp. cf winchelli* as being from the Perdido River system east to the Apalachicola River basin, but then indicates that records exist of this fish in the Ochlockonee River basin. The records available for this project extend to the Ochlockonee River basin, however, it seems that the range for this species has yet to be fully determined. The potential habitat east of the Ochlockonee basin may serve as a guide for further sampling.
- *Ichthyomyzon gagei* - The Florida range for this species extends from the western border of the state to the Ochlockonee River basin (NatureServe 2009). The potential habitat map has been clipped to this area. At first glance it would appear that landuse/landscape characteristics may have caused overfitting in this model. However, historical records not used for this project indicate that this species is not found in the southern half of subregion 12. Additionally, it would appear that occurrences of this species become less common towards the eastern limits of its range.
- *Ictalurus punctatus* - Occurs throughout the Florida Panhandle (NatureServe 2009).
- *Labidesthes sicculus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).

- *Lepomis auritus*- Both NatureServe (2009) and Lee et al. (1980) gives the Apalachicola River basin as the western limit of this species' range within Florida. However, there are many records of its occurrence as far as the Escambia River basin. Species collected prior to 1990 occur only as far west as the Choctawhatchee River basin. It appears that this species is extending its range eastward, and therefore the potential habitat map was not clipped to the published range.
- *Lepomis cyanellus* - Lee et al. (1980) states that this species occurs only as far east as the Escambia River. NatureServe (2009) repeats this, but shows the species extending as far east as the Apalachicola drainage basin. This seems to indicate that *L. cyanellus* is extending its range eastwards, therefore the potential habitat map has not been clipped.
- *Lepomis macrochirus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Lepomis marginatus* - Occurs throughout the Florida Panhandle (Lee et al. 1980). Additional records not used in this study due to a lack of specific locational data indicate that *L. marginatus* occurs in far more habitat in subregion 12 than the model indicates. It is likely that predicted potential habitat for this species is strongly influenced by landscape/landuse characteristics and the scarcity of test sites in subregion 12. The predicted habitat should therefore be interpreted as a very conservative estimate of the true extent of potential habitat.
- *Lepomis megalotis* - Page and Burr (1991) report that the Choctawhatchee River is the eastern limit L. megalotis' range in Florida. However, records of this

species exist as far east as the Chipola River. It is possible therefore that this species is expanding its range eastward in the Florida Panhandle, so the potential habitat map has not been clipped.

- *Lepomis microlophus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Lepisosteus oculatus* - The Apalachicola River is the easternmost extent of this species' published range (Page and Burr 1991). However, at least one point used in this study occurs in the Ochlockonee River. Therefore the potential habitat map has not been clipped.
- *Lepisosteus osseus* - Occurs throughout the Florida Panhandle (Lee et. al. 1980).
- *Lepomis punctatus*- Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Micropterus punctulatus* - Lee et al.(1980) lists the Apalachicola River as the eastern boundary of *M. punctualatus'* range in the Florida Panhandle. I am not aware of any records of its occurrence further east, so the potential habitat map has been clipped to the Apalachicola River's drainage basin.
- *Micropterus salmoides* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Minytrema melanops* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Morone saxatilis* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Moxostoma poecilurum* - The Choctawhatchee River is the easternmost limit of *M. poecilurm's* range in the Florida Panhandle (Lee et al. 1980). The potential habitat map has been trimmed to this extent.
- *Mugil cephalus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).

- *Notropis chalybaeus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Notemigonus crysoleucas* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Notropis harperi* - *N. haperi's* range runs from the Escambia River to the St. John's River, although it is absent from some drainages within this range. This species is closely tied to springs and spring runs, which was not a factor used in modeling.
- *Noturus leptacanthus*- Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Notropis longirostris* - The Apalachicola River basin is the easternmost limit of *N. longirostris's* range in the Florida Panhandle (Lee et al. 1980). The potential habitat map has been trimmed to this extent.
- *Notropis maculatus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Notropis petersoni* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Notropis texanus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Opsopoeodus emiliae* - Occurs throughout the Florida Panhandle (NatureServe 2009).
- *Percina nigrofasciata* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Pomoxis nigromaculatus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Pteronotropis hypselopterus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).

- *Semotilus thoreauianus* - The Ocholockonee River basin is the easternmost limit of *S. thoreauianus'* range in the Florida Panhandle (Page and Burr 1991). The potential habitat map shows very little habitat occurring beyond this point, and what it does show might guide sampling efforts for this species. Therefore the map has not been clipped to the published range. This fish appears to be one of the few species that drop out of aquatic communities as stream size increases.
- *Strongylura marina* - Occurs throughout the Florida Panhandle (Lee et al. 1980).
- *Trinectes maculatus* - Occurs throughout the Florida Panhandle (Lee et al. 1980).

Models Created Using Only Three Broad Landuse/Landcover Characteristics

The 10 maps created using fewer landuse/landcover characteristics tended to have higher sensitivities than those created using all 11 landuse/landcover characteristics. However, sensitivity actually decreased for *Notropis maculatus*. The potential habitat map for *Ammocrypta bifascia* (Figure 58) is typical of the models produced in the manner described above. Generally, a slightly larger percentage of the study area tends to be classified as suitable habitat than when all 11 landuse/landcover characteristics are included. The addition of suitable habitat usually occurs at the ends of stream stretches that the previous model had classified as suitable, often connecting 2 areas of suitable habitat.

Difficulties

Distribution of species occurrence records.-- The disparity between the percentages of the study area occupied by each subregion and the number of sample sites within each subregion was a possible source of error (Table 12). Subregion 12 contains roughly 20% of the study area, but only slightly more than 1% of the sample sites fall within this

subregion. Therefore, predictions in this area are likely to be the most error prone. In contrast, subregion 14 contains roughly 56% of the study area and 75% of the sample sites. For this reason, predictions in this area are likely to be the most trustworthy.

Table 12. Number of sample sites and area for each subregion in the study area as well as for the entire study area.

Subregion	Sample sites	Area
Subregion 12	7	6708.79km²
Subregion 13	163	8462.77km²
Subregion 14	486	18913.27km²
Total	656	34084.83km²

Additionally, headwaters are underrepresented in sample sites. Only 29 sampling sites are in headwaters, while 146 are in creeks, 137 in small rivers, 160 in large rivers, and 182 in big rivers.

Errors in the base layer.--A disconnect in the base stream layer (and in the original NHD) was discovered just as the project was wrapping up. This disconnect caused the Apalachicola River to be assigned a Strahler order of 7 instead of 8, leaving the Choctawhatchee River as the only river in the study area with a Strahler order of 8. Fixing this misclassification in future modeling projects will likely lead to even greater predictive power. The disconnect also affected size classification, as it caused the accumulate attribute function to terminate prematurely. This issue should be addressed before any further studies are conducted using this data.

Limitations

This study was based on several broad scale habitat factors that are available in a spatially referenced format. Multiple studies have demonstrated the ability of species modeling techniques to accurately predict the occurrence of suitable habitat for a species in question using only a few landscape level factors (Stockwell and Peterson 2002, Anderson 2003, Guisan and Thuiller 2005). However, several habitat characteristics which affect habitat selection among fish are difficult if not impossible to represent spatially over large areas. This is especially true of factors affecting microhabitat selection, such as riffle versus pool habitat. Other attributes which might have improved the predictive power of the models had they been possible to map at the scale of this study include aquatic vegetation, substrate type, dissolved oxygen, and pH.

Trends

As more species were mapped, it became apparent that almost all species were predicted to be present in the largest stream size category, big rivers. This was the case even when the existing literature describes the fish as preferring small streams. Rechecking the species collection sites, and field notes where possible, showed that the fish were indeed collected in larger rivers. Additionally, none of the species that were modeled were predicted to occur in intermittent streams.

Future Research

Overall, GARP was able to predict the location of the validation points with acceptable accuracy. This research can be used as a guide to mapping all of the freshwater fish occurring throughout Florida, as well as other freshwater organisms such as mussels and crayfish. Additionally, GARP has been used to predict how the range of specific

organisms and groups of organisms will respond to climate change, and to predict where invasive species are likely to spread. GARP has also been used to guide field surveys for unknown populations of a rare species, or to help determine which areas are suitable for the reintroduction of threatened species. (Pearson 2007). Additionally, GARP could be used to create more exact potential habitat maps for individual species including habitat factors known to affect the species habitat selection.

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