

Identification and Prediction of Fish Assemblages in Streams of the Albemarle-Pamlico Basin, USA

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Introduction

Set within the Ecological Services Research Program (ESRP) of USEPA's Office of Research and Development, a multi-disciplinary research collaborative (MEERT – Multimedia Ecological Exposure Research Team) has taken on a challenge to develop a regional assessment of several ecosystem services (primarily water quantity, water quality, and fish productivity) in the Albemarle-Pamlico Estuary System (APES, Figure 1), an area encompassing six major drainage basins and spanning three ecoregions (Virginia Highlands, Piedmont, Southeastern/Middle Atlantic Coastal Plain). The collaborative group has developed a modeling system that will produce not only a current accounting of particular ecosystem services in the APES, but also simulate the consequences of altered stressor scenarios (changes in nitrogen and mercury loadings, land use and global climate) on the production of these services. The integrated modeling system is primarily composed of four interacting models:

- SWAT for watershed dynamics and loadings of various contaminants
- WASP for surface water routing and water quality
- BASS for aquatic community modeling
- HSI, a model of fish habitat suitability

These four are set within a software framework (FRAMES) that allows for the models to communicate with each other, access shared data resources, and provides a rich array of data pre- and post-processing functionality.

Our methodology for assessing ecosystem services was first to choose a random sample (stratified by ecoregion) of fifty 12-digit HUCs from across the APES. These basins were sampled from a population of 12-digit HUCs that had been selected using two primary criteria: headwater drainages, to avoid having to simulate surface water inputs from other HUCs; 3rd-4th order perennial streams as pour points. These 3rd-4th order streams are large enough to support recreational fisheries, but small enough to be sampled by backpack electrofishing. This is important as it increases the probability of having past collection efforts and allowing for future collection efforts to support model validation. However, having historic fish samples at the pour points of the sampled HUCs was not a requirement.

This poster details how we provided the ecological model (BASS) with preliminary required information, namely, the initial fish community in the stream segment to be simulated. We had 53 such stream segments (three prototype HUCs for initial methodological/framework testing, and fifty sample HUCs – Figure 2) for which initial fish communities needed to be defined.

Methods

Our approach can be summarized as follows:

- 1) Compile a large dataset of fish samples taken across the region. The spatial extent of these samples is shown in Figure 3. We had five sources of data and a total of 1159 samples.
- 2) Perform a hierarchical cluster analysis on relative abundance data to identify common regional fish assemblages.
- 3) Perform a discriminant analysis using stream and watershed characteristics to relate these metrics to the fish assemblages.
- 4) Use the characteristics of the stream of interest and the results of the discriminant analysis to assign a most likely assemblage to the stream segment in question.
- 5) Given the most likely assemblage, assign an actual fish community to the stream of interest by random selection from the population of other samples that belong to that particular cluster.

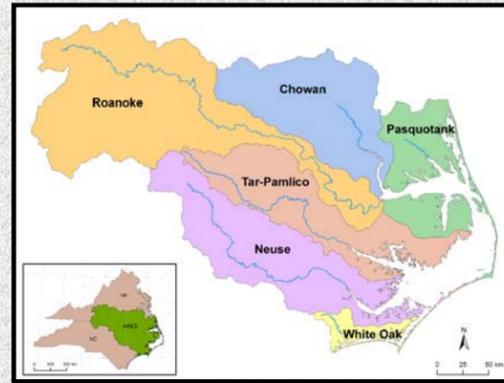


Figure 1. The Albemarle-Pamlico Watershed

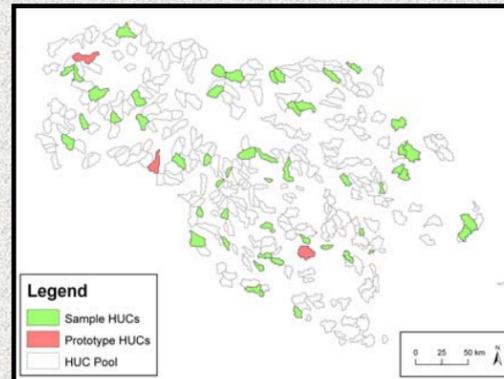


Figure 2. Our prototype and sample 12-digit HUCs

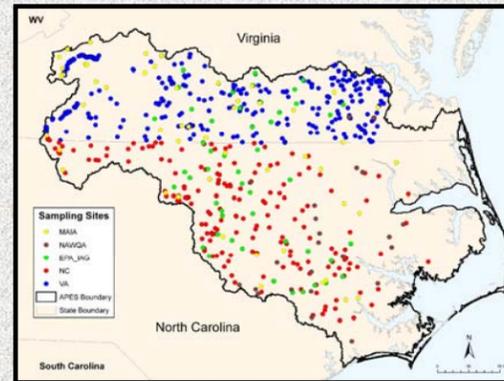


Figure 3. Locations and sources of APES fish samples

Results

A preliminary cluster analysis was performed to identify and remove the least-common communities seen across the dataset (in essence, data outliers). This reduced the dataset from 1159 to 1057 observations. The subsequent cluster analysis on this reduced dataset produced 11 clusters.

A summary of the five primary species in each of the 11 clusters/assemblages, with each species' mean relative abundance in each assemblage, is shown in Table 1. Figure 4 shows the locations of the 11 clusters throughout the APES region. The subsequent discriminant analysis produced a set of functions that were approximately 50% successful in identifying the correct assemblage for any given stream, while a random, uninformed choice would only result in about a 10% success rate. The stream/watershed characteristics used in this analysis are shown in Table 2. "High impact" variables were found to be most significant in discriminating between the assemblages. Variables that were "low impact" did not lend significantly to the discriminant analysis in the presence of the other variables.

These discriminant functions were then used to assign a fish assemblage to each of the three prototype and fifty sample HUCs using the characteristics of each HUC pour point. Because the cluster assemblage is not identical to an actual fish community (its more akin to an aggregation of similar communities), once a HUC was assigned to an assemblage, the actual fish community of a randomly selected member of that cluster of streams was assigned to the HUC in question. For example, if a sample HUC pour point was predicted to belong to cluster 2, one stream out of the 212 members of cluster 2 would be randomly chosen. The actual fish community measured at this site would then be used as the initial fish community of the sample HUC's pour point for subsequent simulation of fish productivity as a quantifiable ecosystem service in the APES.

Future Steps

Summarized results of simulations on all 50 HUCs will be used to quantify the aforementioned set of ecosystem services (water quality, water quantity, fish productivity) for the population of these HUCs (headwater, with 3rd-4th order perennial stream pour points) across the APES region.

Table 1. The top five fish species found in each of the 11 clusters, sorted by Relative Abundance (RA). The number in parentheses in the column heading is the number of member samples for each assemblage.

| Cluster 1 (108) | RA | Cluster 2 (212) | RA | Cluster 3 (33) | RA |
|-------------------------|------|-------------------------|------|------------------------|------|
| Lepomis_macrochirus | 30.4 | Nocomis_leptocephalus | 25.9 | Gambusia_holbrooki | 40.6 |
| Lepomis_auritus | 11.3 | Luxilus_cerasinus | 11.0 | Lepomis_auritus | 6.0 |
| Micropterus_salmoides | 6.0 | Etheostoma_flabellare | 6.8 | Anguilla_rostrata | 5.8 |
| Nocomis_leptocephalus | 3.8 | Phoxinus_oreas | 6.2 | Lepomis_macrochirus | 5.3 |
| Notropis_procne | 3.1 | Clinostomus_funduloides | 5.2 | Enneacanthus_gloriosus | 4.5 |
| Cluster 4 (40) | RA | Cluster 5 (207) | RA | Cluster 6 (170) | RA |
| Enneacanthus_gloriosus | 44.0 | Luxilus_albeolus | 17.6 | Lepomis_auritus | 17.7 |
| Esox_americanus | 12.7 | Percina_roanoka | 15.9 | Notropis_procne | 8.4 |
| Aphredoderus_sayanus | 6.3 | Camptostoma_anomalum | 6.7 | Etheostoma_olmstedii | 7.1 |
| Anguilla_rostrata | 4.8 | Etheostoma_flabellare | 6.2 | Cyprinella_analostana | 7.0 |
| Centrarchus_macropterus | 4.2 | Noturus_insignis | 6.2 | Anguilla_rostrata | 5.5 |
| Cluster 7 (53) | RA | Cluster 8 (48) | RA | Cluster 9 (70) | RA |
| Lepomis_macrochirus | 69.9 | Anguilla_rostrata | 33.3 | Aphredoderus_sayanus | 19.2 |
| Micropterus_salmoides | 7.7 | Aphredoderus_sayanus | 15.3 | Esox_americanus | 14.8 |
| Lepomis_auritus | 3.6 | Lepomis_auritus | 11.6 | Erimyzon_oblongus | 8.8 |
| Lepomis_microlophus | 2.0 | Enneacanthus_gloriosus | 6.0 | Enneacanthus_gloriosus | 6.8 |
| Notropis_hudsonius | 2.0 | Etheostoma_olmstedii | 4.0 | Gambusia_holbrooki | 5.8 |
| Cluster 10 (82) | RA | Cluster 11 (34) | RA | | |
| Nocomis_leptocephalus | 24.9 | Etheostoma_flabellare | 43.0 | | |
| Luxilus_albeolus | 22.0 | Percina_roanoka | 17.4 | | |
| Lepomis_auritus | 7.8 | Luxilus_albeolus | 7.6 | | |
| Notropis_procne | 7.4 | Nocomis_leptocephalus | 6.6 | | |
| Lepomis_macrochirus | 4.5 | Noturus_insignis | 5.9 | | |

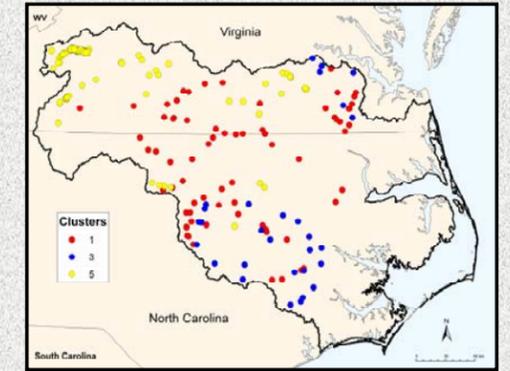


Figure 4a. Locations of a subset of APES fish clusters.

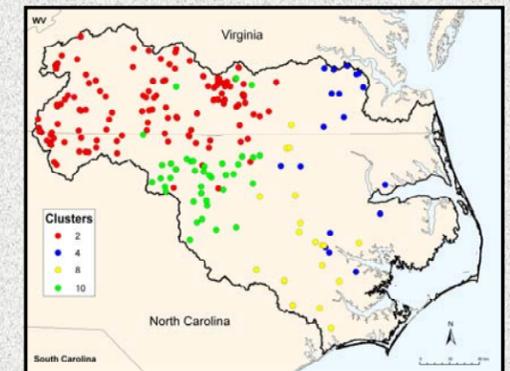


Figure 4b. Locations of a subset of APES fish clusters.

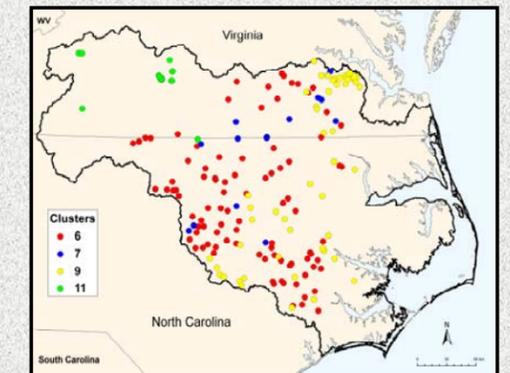


Figure 4c. Locations of a subset of APES fish clusters.

Table 2. Stream/watershed characteristics used in the discriminant analysis. "High impact" column lists those variables found to be most significant for discriminating between the assemblages.

| Independent Variables Tested | |
|------------------------------|--------------------------|
| High Impact | Low Impact |
| Mean Stream Temperature | % Natural Landcover |
| Mean Stream Velocity | Latitude |
| Ecoregion | Watershed Area |
| Mean Stream Slope | % Agricultural Landcover |
| Longitude | % Developed Landcover |
| Mean Stream Elevation | Mean Stream Flow |