DEVELOPMENT AND IMPLEMENTATION OF THE
CHESAPEAKE BAY FISHERY-INDEPENDENT
MULTISPECIES SURVEY (CHESFIMS)

Final Report

Submitted to: Mr. Derek Orner
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EXECUTIVE SUMMARY

Here we report on the results of a large fishery independent survey of fishes in the Chesapeake Bay supported through a research grant to the University of Maryland Center for Environmental Science Chesapeake Biological Laboratory from the National Oceanic and Atmospheric Administration’s Chesapeake Bay Office. Bay wide surveys were conducted three times a year during April, July and September from 2001-2006. Sampling during the surveys employed an 18m² midwater trawl that was deployed in a stepwise fashion at approximately 50 sites throughout the mainstem of the Chesapeake Bay. Additional surveys were conducted in the Patuxent River in an effort to expand the scope of inference. Data collected by the project were entered into a data management system and have been made available to the research community and the general public through a web-based interface at http://hjort.cbl.umces.edu/chesfims.html.

We completed 17 surveys between April 2001 – October 2006. During this period, baywide average temperatures ranged from 13.41-25.95 °C, baywide salinities varied from 10.96-20.36 and baywide oxygen concentrations from 4.25-9.81 mg.L⁻¹. These levels of variability are similar, although less extreme than those reported by earlier baywide surveys conducted during the period 1995-2000. Over the course of the 17 surveys, we occupied 693 stations and collected 520,786 fish weighing 2,205 kg. Only eight deployments (1.15%) resulted in a null catch. The average 20 minute tow resulted in a catch of 811±1135 (mean ± SD) fish. We collected 110 different species of fish. Analysis of these data indicated clear seasonal and spatial patterns of variability with temperature, salinity and dissolved oxygen being implicated as important environmental drivers.
Studies of the ecology of individual species based on specimens conducted during the baywide surveys were also completed. These studies provide data on species-specific patterns of abundance, distribution, growth and diet that will be important inputs to efforts to implement ecosystem-based management within the Chesapeake Bay.

We also conducted extensive statistical analysis of alternative survey designs to estimate variances for design- and model-based estimation approaches. This information will be useful to the development of a complemented baywide fishery survey.

This project was a collaboration of scientists from the University of Maryland Center for Environmental Science, the Department of Animal and Avian Sciences at the University of Maryland College Park, the Maryland Department of Natural Resources, and Versar Corp. This report is divided into six individual chapters that each present a different aspect of the project. In each case, authorship on the work is identified on the chapter title page.
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CHAPTER 1

BACKGROUND, MOTIVATION, AND REPORT STRUCTURE
1.1. BACKGROUND

Fisheries in Chesapeake Bay contribute significantly to U.S. catches at the national and regional levels. Recent National Marine Fisheries Service (NMFS) statistics indicate that between 250,000 - 350,000 metric tonnes (t) of fish and shellfish are harvested annually from Chesapeake Bay waters, with a dockside value of more than $100 Million (Miller 2006a). Maintaining the health of these fisheries is an important but difficult task given the considerable interannual variability in catches of component species (Fig. 1.1). Scientists, managers and the general public recognize that species targeted by fisheries are components of complex ecosystems, whereby the removal of individual targeted species may have ramifications for the entire system (Pikitch et al. 2004). Moreover, changes in ecosystem function or health, may impact the sustainability and profitability of multiple fisheries simultaneously. Yet, the often marked differences in the biology, ecology and pattern of exploitation of different species lead to the development of fisheries management techniques that are based on individual species (Smith 1994). The majority of species subject to fisheries within the Chesapeake Bay are managed on a single species basis, although increasingly there are efforts to develop multispecies or ecosystem-based approaches (Miller et al. 1996, Latour et al. 2003, CFEPTAP 2004, Chesapeake Fishery Ecosystem Plan Technical Advisory Panel 2006).

The potential for biological interactions and technical interactions within traditional single species management has motivated an interest in multispecies and ecosystem-based approaches in the Chesapeake region (Miller et al. 1996). Many of the principal approaches to traditional single species management focus on quantifying maximum sustainable yields so that fisheries can harvest the surplus production. However, when viewed from an ecosystem point of
view, were the surplus production allowed to remain, it would impact other components of the food web. For example, selective removal of a piscivore may allow increased production of its principal prey. In contrast, selective removal of a forage species may cause decreased production of its principal predators. The diversity of fisheries on many fishing grounds means that both predators and prey are often being targeted simultaneously. Thus, the pattern of exploitation in one fishery likely impacts the potential harvest in other fisheries as a result of biological interactions among the individual species. The existence of technical interactions has been another common concern motivating the development of multispecies fisheries. As a result of often similar life histories and habitat requirements, many fisheries catch a variety of species. Often only a few species are the target of the fishery, the other species represent by-catch. However, in some fisheries, all species are potentially of value and are harvested. In such fisheries, management on a species by species basis is clearly unsatisfactory.

In 1996, Miller et al. conducted a literature review and synthesis of information to determine whether the forces that have motivated the development of multispecies approaches in other regions were present in the Chesapeake Bay. They concluded that both biological and technical interactions were present in Chesapeake Bay fisheries. Several species harvested from Chesapeake Bay are either potential competitors (e.g., striped bass *Morone saxatilis*, bluefish *Pomotomus saltatrix*, and the weakfish *Cynoscion regalis*) or predators and prey (e.g., striped bass and menhaden *Brevoortia tyrannus* and Atlantic croaker *Micropogonias undulatus*), and thus their fisheries may experience biological interactions. Miller et al. (1996) provide a hypothetical example in which the linkage between menhaden and croaker is mediated through predation pressure exerted by striped bass, bluefish and weakfish which varies with hydrography.
Motivated by the Miller et al. (1996) white paper, the NOAA Chesapeake Bay Office funded an international workshop to assess the desirability of implementing multispecies or ecosystem-based approaches in Chesapeake Bay (Houde et al. 1998). The workshop report indicates that adoption of multispecies fisheries management would bring the regulation of fisheries in line with the ecosystem-level focus of the Chesapeake Bay Program. Many participants felt that explicit recognition of species interactions, by-catch concerns, competing users, and habitat issues is needed to move fisheries toward a multispecies management ideal that will be desirable in the future. Several important conclusions were reached during the workshop. The workshop participants recommended that coordinated, baywide surveys be performed to estimate key species abundances and that biological data on both economically and ecologically important species that are currently lacking be obtained (Houde et al. 1998). These surveys should form a vehicle within which to estimate the temporal and spatial dynamics of key predator-prey relationships and trophic interactions (Houde et al. 1998). However, at that time no such surveys existed from which the status and trends of the fish community could be assessed.

Following the Houde et al. report, the NOAA Chesapeake Bay program committed to supporting research to study the design of Baywide fishery independent surveys. The intention of the funding was to study alternative survey gear, designs and protocols that would lead eventually to a complemented Baywide survey supported by the States. One element of this funding initiative was a detailed review of ongoing fishery-independent surveys (Bonzek et al. 2007). In addition, two baywide trawl surveys were funded as a result of this initiative.
Scientists with the Virginia Institute of Marine Sciences developed and implemented a trawl program focusing on adult sized fishes. The program called CHESMAPP is still underway. Details of the program can be found at http://www.fisheries.vims.edu/multispecies/. NOAA funded a second trawl program, the results of which we report on here.

With support from the NOAA Chesapeake Bay Office, we conducted a six year fishery-independent survey that focused on forage and juvenile fish in the pelagic realm called CHESFIMS – the Chesapeake Bay Fishery Independent Multispecies Survey. The program build on from a National Science Foundation funded Land Margin Ecosystem study of trophic interaction in the Chesapeake that had surveyed the fish community between 1995-2000. Data from this NSF program revealed the importance of environmental forcing in structuring the forage and juvenile fish assemblage in the Chesapeake (Jung and Houde 2003). By building from this platform we hoped to leverage more information on patterns and scales of variability in the Chesapeake Bay fish assemblage. The CHESFIMS program had four core objectives

**Objective 1.** Conduct a baywide survey of the benthic-pelagic fish community, focusing on young (juveniles, and yearling) fishes in the mainstem of Chesapeake Bay.

**Objective 2.** Conduct pilot surveys of the benthic-pelagic fish community in key tributaries and in the mainstem to generate sampling statistics that will of use in subsequent design improvements.

**Objective 3.** Determine trophic interactions among key components of the pelagic fish community, and examine the implication of the relationships uncovered in empirical studies using bioenergetic modeling.
Objective 4. Conduct statistical analyzes of existing and new data to optimize the complemented benthic-pelagic survey with respect to consistency and accuracy of key parameters.
1.2 REPORT STRUCTURE

The report is divided into five chapters, each one focusing on elements of each core objective. It is important to note that the information presented in this report is by no means comprehensive. A considerable amount of analysis and interpretation remains to be done on the data accumulated. Rather each chapter provides an example of the kind of information and interpretation that can be gleaned from the CHESFIMS data that increases our understanding of the fish assemblage in Chesapeake Bay and may guide the design of future fishery-independent surveys. All chapters are numbered sequentially. Their content is summarized below.

1.2.1. Chapter 2 – Data management and Dictionary

One of the central challenges to undertaking a six-year baywide fishery independent survey is the management and dissemination of the data collected. Each survey generated a huge amount of primary data, including physical oceanographic conditions and fish catches, and secondary data, such as gut content information. Ensuring that data are managed to maintain integrity while at the same time ensuring open access is a central challenge of all large data programs. We invested considerable effort in developing a data management system that achieves this goal. Accordingly, this chapter defines the generally sampling and subsequent sample processing procedures and presents the data management structure that was used in the CHESFIMS program.

1.2.2. Chapter 3. Patterns in the distribution and composition of the fish assemblage in the Chesapeake Bay
This chapter presents and summarizes information on the fish assemblage that we sampled over the six years of the program. Principal findings of the chapter relate to the role of spatial and temporal variability in structuring the fish community. While the analyses are preliminary and further work needs to be completed, the results do indicate the opposing structuring forces of the central up-Bay – down-Bay axis against the seasonal variation in temperature and salinity in structuring the Chesapeake Bay fish assemblage.

This chapter is authored by Thomas Miller and David Loewensteiner and it is anticipated that it will be submitted for peer-review in Estuaries and Coasts.

1.2.3. Chapter 4. Fishery-independent multispecies assessment of the fish assemblage in the Patuxent River, MD

This chapter presents the results of the attempt to expand the baywide survey into a principal tributary of the Chesapeake Bay. Using support from the NOAA Chesapeake Bay Office and the State of Maryland, we conducted an intensive seasonal survey of the Patuxent River. This chapter presents the results of these samples.

The data presented in this chapter are at a preliminary level of analysis, but it is expected that they will be submitted for publication at some point in the future.

1.2.4 Chapter 5. Distribution and diet of Atlantic croaker *Micropogonias undulatus* in Chesapeake Bay

This chapter presents the results of an analysis of the trophic relationships within the Chesapeake Bay fish assemblage. Here we focus on Atlantic croaker, although we note that
similar analysis have been completed for hogchoker (Curti 2005) and weakfish (Miller and Loewensteiner in prep). The analyses presented here are simply representative of the class of analyses that could be conducted. We have selected croaker for inclusion because this study demonstrates the importance of continuing these “basic” science studies because they do provide new insight and evidence of change in processes we thought we understood well. This was the case here where our work on the diets of croaker, a species that has been described as omnivorous (Murdy et al. 1997), indicates that fully 50% of the diet from an energetic point of view of croaker in the mid Bay was derived from bay anchovy.

This chapter represents a chapter in the PhD dissertation of Janet A. Nye. It is anticipated that it will be submitted for publication to Transaction of the American Fisheries Society shortly.

1.2.5 Chapter 6. Design efficiencies of transect and stratified random trawl surveys

This chapter presents the statistical exploration of the survey design used in CHESFIMS and develops appropriate statistical estimators for complemented survey designs. The manuscript was submitted to Fishery Bulletin for consideration for publication but was rejected. It is in revision currently for resubmission to an alternative journal.
1.3 PRODUCTS

In addition to the chapters described above the CHESFIMS programs has resulted in several notable products which are summarized here

1.3.1 Data Sources

Perhaps most importantly from the communities point of view all CHESFIMS data are publicly available and accessible through a custom-designed web interface – accessible at http://hjort.cbl.umces.edu/cfdata.html. This site provides maps of distributions of key species throughout the program, and more importantly access to the raw data through a simple query tool. We are not tracking usage but know from email queries that usage is widespread among agencies, academics and the public.

1.3.2 Student Dissertations and Theses

Four students have completed degree based largely or in part on funding through CHESFIMS. They are

Nye, Janet. A.. Ph.D. Bioenergetic and ecological consequences of diet variability in Atlantic croaker (Micropogonias undulatus) in Chesapeake Bay. April 2008

Michael G. Frisk. Ph.D. Biology, life history and conservation of elasmobranchs with an emphasis on western Atlantic skates. September 2004

Kiersten. L. Curti. MS. Biology of hogchoker in Chesapeake Bay. April 2005

Olaf P. Jensen. MS. Spatial ecology of blue crab (Callinectes sapidus) in Chesapeake Bay. September 2004.
1.3.3 Presentations


CFEPTAP. 2004. Fisheries ecosystem planning for Chesapeake Bay. Chesapeake Fisheries Ecosystem Plan Technical Advisory Panel, NOAA Chesapeake Bay Office, Annapolis.


Figure 1.1. Time series of Chesapeake Bay catches of selected important species. Data from Miller et al. 1996
Figure 1.2. Conceptual example of complex interactions in the Chesapeake Bay piscivore guild (striped bass, bluefish and weakfish) in A) normal years when sufficient energy flows through the bay anchovy and menhaden pathways and B) years when menhaden abundance is reduced leading to increasing competition for spot and croaker by the top piscivores. Numbers in boxes represent the age classes of the predators. The importance of the interaction with respect to energy flow is indicated by the weight of the arrow.
CHAPTER 2

CHESFIMS DATA MANAGEMENT AND DICTIONARY

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2.1. ABSTRACT

A central challenge of any large field program is management of the flow of metadata, data and derived data into the project. Importantly, these aspects of the project must be fully addressed if the data collected during the research are to be of lasting benefit to the research community and beyond. Researchers involved in the Chesapeake Bay Fishery Independent Monitoring Survey (CHESFIMS) were committed to these goals. Here we describe the protocols and procedures used to select stations visited during the survey, the operation of equipment while the station was occupied, the preservation techniques of all collected samples, and laboratory techniques used to process the samples subsequently. A data management and reporting system was developed for CHESFIMS that provides for easy quality assurance and quality checking. The data management system also affords easy, reliable and open access to the data to project staff and to the general public through a web based interface. The structure of the database and analytical tools used to query the database are described.
2.2 INTRODUCTION

Ecosystem-based fisheries management places a high demand on data. For example Murawski (Murawski 2000) notes that expansion from traditional single species approaches to ecosystem-based approaches requires not an abandonment of the traditional data collection systems, but their expansion to include data on a wider array of species, information on trophic relationships, and habitat relationships. Thus progress toward ecosystem-based approaches requires analysis of a wider range of data than are typically available (Choi et al. 2005). Such analyses rely on access to data from a wide range of sources.

In 1996, Miller et al. (1996) conducted a literature review and synthesis of information to determine whether the forces that have motivated the development of multispecies and ecosystem-based approaches in other regions were present in the Chesapeake Bay. They concluded that both biological and technical interactions were present in Chesapeake Bay fisheries. Several species harvested from Chesapeake Bay are either potential competitors (e.g., striped bass *Morone saxatilis*, bluefish *Pomotomus saltatrix*, and the weakfish *Cynoscion regalis*) or predators and prey (e.g., striped bass and menhaden *Brevoortia tyrannus* and Atlantic croaker *Micropogonias undulatus*), and thus their fisheries may experience biological interactions. Miller et al. (1996) provide a hypothetical example in which the linkage between menhaden and croaker is mediated through predation pressure exerted by striped bass, bluefish and weakfish which varies with hydrography. Several fisheries, notably the pound net, are inherently multispecies by nature, and thus technical interactions also clearly exist in Chesapeake Bay (Miller et al. 1996).

Houde et al. (1998) reported the recommendations of workshop to explore the utility and advisability of adopting multispecies approaches in Chesapeake Bay. The workshop report indicated that adoption of multispecies fisheries management would bring the regulation of fisheries in line with the ecosystem-level focus of the Chesapeake Bay Program. Many participants felt that explicit recognition of species interactions, bycatch concerns, competing users, and habitat issues was needed to move fisheries toward a multispecies management ideal that will be desirable in the future. Several important conclusions were reached during the
workshop. The workshop participants recommended that coordinated, baywide surveys be performed to estimate key species abundances and that biological data on both economically and ecologically important species that were currently lacking at time (Houde et al. 1998).

With funding from the NOAA Chesapeake Bay Office, we initiated the Chesapeake Bay Fishery Independent Multispecies Survey to specifically address the deficiency identified in the Houde et al workshop. CHESFIMS was designed to extend and complement a baywide investigation of biological production potential and its temporal and spatial variability that had been conducted 1995-2000. The TIES (Trophic Interactions in Estuarine Systems) research has been conducted in a six-year program that includes baywide surveys three times each year (April, July and October). A broad suite of samples were collected on each cruise including measures of water quality, primary production and community metabolism, zooplankton abundances and biomass, gelatinous zooplankton, ichthyoplankton, and juvenile/adult fish.

2.3. METHODS

2.3.1. Survey Design

The CHESFIMS survey is a complemented design involved both fixed and random stations. The fixed stations were located along fixed transects that had been defined during the early TIES program (Jung and Houde 2003). The TIES program occupied more stations and transects than could be occupied during CHESFMS, and accordingly we sampled a subset of these original stations, selected to ensure a broad spatial coverage throughout the Chesapeake Bay. In addition to these fixed stations, we also included a similarly number of stratified random stations selected in proportion to strata area. Individual strata have distinctive characteristics, and their boundaries broadly corresponding to ecologically relevant salinity regimes and depths above 5 m. The upper Bay (38 45’ to 39 25’N) is generally shallow, with substantial areas with depths less than 5 m, and has well mixed waters with high nutrient concentrations. The bottom topography in the mid Bay includes a narrow channel in the middle of the Bay (37 55’N to 38 45’N) with a stratified water column and broad flanking shoals. This region has relatively clear waters and experiences seasonally high nutrient concentrations and periods of hypoxia. The
lower Bay (37 05’ to 37 55’N) has the clearest waters, greatest depths and lowest nutrient concentrations (Kemp et al., 1999). The strata volumes are 26,608 km$^3$ (Lower), 16,840 km$^3$ (Mid) and 8,664 km$^3$ (Upper).

CHESFIMS was initiated in 2001, employing the TIES trawling procedures, transect design and stratification. Sampling was conducted during spring, summer and autumn from the University of Maryland Center for Estuarine and Environmental Science’s R/V ‘Aquarius. All data from each cruise were identified to cruise as CFYYSS, where CF is for CHESFIMS, YY is for year, and MM is a numeric for season. On most cruises we occupied 31 stations allocated according to the original TIES transect design, and 20 stations allocated according to a stratified random scheme. The transect stations were fixed for the duration of the CHESFIMS program, whereas the stratified random stations were selected anew for each cruise. For the transect design, the $m_i$ stations within the $i^{th}$ transect were selected by restricted random sampling. Each transect was divided into $m_i$ segments of equal size, with one station allocated randomly within each segment. For the transect surveys, the clustering of stations and variable transect lengths resulted in heterogeneous selection probabilities for stations within strata. Starting in 2002, the transect sampling was augmented with an independent, stratified random trawl survey in an effort to optimize the monitoring design. We were restricted to maintaining the transects used for monitoring and so chose stratified random sampling as an appropriate additional sampling design for optimizing the geographic distribution of sampling locations and as a counterpoint to the transect design. In the stratified random surveys, conducted simultaneously with the transect surveys, 20 stations covering the entire bay were allocated to each stratum proportional to their volumes. Latitude and longitude of stations within strata were randomly generated. Weather precluded complete sampling of all 20 stations during some surveys. To the extent possible all activity at each station was standardized. All information obtained during a station was identified as CFYYYMMTTSSS where TT is the transect number (1-30 with RN being used for Random) and SSS is station number (1-999). An example of the allocation of stations in the 2002 stratified random survey is shown in Figure 2.1.

2.3.2. CTD Profiling
Immediately prior to each trawl deployment, a Sea-Bird SBE 25 conductivity, temperature, depth profiler was used to profile the water column. The dissolved oxygen probe was recalibrated before each cruise, and all instruments were calibrated by Seabird annually. To profile the water column the profiler was lowered to the surface and held for 2-5 mins while the instrument equilibrated. The instrument was then lowered slowly and steadily to the bottom. Once the bottom was achieved, the instrument was raised approximately 1 m off the bottom and held for 2-5 minutes at depth to re-equilibrate. Following this second period of re-equilibration, the profiler was slowly raised to the surface.

Each profile resulted in two data files: a communication file and a hexadecimal raw data file. The communication file contained all the station specific details for the deployment. The HEX file contains raw instrument data, often in mV. Following a cruise, the “Seasave” software (Sea-Bird Electronics Inc, Bellevue, WA) was used to convert the data to provide a downcast profile in ASCII format for subsequent analysis. Filename standards generated from the CTD profiling are provided in table 2.1.

2.3.3. Midwater Trawl Deployment

Survey deployments followed the TIES trawling procedures (Jung and Houde, 2003). We continued to use an 18-m² midwater trawl (MWT) with 3-mm cod end mesh as the primary survey gear. MWTs are commonly used to survey pelagic fish including anchovy (Komatsu et al. 2002), walleye pollock (Wilson 2000), and Pacific whiting (Sakuma and Ralston 1997) and in commercial fisheries for many of these same species. The MWT employed in the Bay samples fish 30-256 mm total length of most species effectively, but appears to be less effective for Atlantic menhaden (Brevoortia tyrannus) of all sizes (Jung and Houde 2003).

We used a standardized 20-minute oblique, stepped tow in all deployments. The trawl was towed for two minutes in each of ten depth zones distributed throughout the water column from the surface to the bottom, with minimum trawlable depth being 5 m. The section of the tow conducted in the deepest zone sampled epibenthic fishes close to or on the bottom. The
remaining portion of the tow sampled pelagic and neustonic fishes. All tows were conducted between 19:00 and 7:00 Eastern Standard Time to minimize gear avoidance and to take advantage of the reduced patchiness of multiple target species at night. A temperature-depth mini-logger was attached to the head rope of the trawl for all deployments to record the tow profile. Data from this minilog was inspected immediately after each haul to determine whether the haul had largely met survey criteria. From the autumn 2003 survey onwards an additional minilog was attached to the foot rope of the trawl. By combining data from the top and bottom minilog, the net opening could be estimated for the duration of the haul using a custom MatLab script (Appendix 2.1). Filename standards generated from the minilog data are provided in table 2.1.

Catches were identified, enumerated, measured and weighed onboard. For species for which there were less than 100 individuals caught in the haul, all individuals were measured to the nearest mm for total length (TL), and a total weight of the species caught was measured on a precision spring balance (nearest g). For some species, individuals were of sufficient size that individual weights could be determined, but this was not common. For abundant species (e.g., bay anchovy, white perch etc), a subsampling procedure was used to estimate the catch. In most cases a random subsample of 100 individuals was measured for TL. This subsample was weighed, and the total catch of the species was also weighed. The total number in the catch was then estimated by proportion.

Following complete enumeration of the catch, selected subsamples of target species were preserved. The subsamples of the majority of species were preserved in ethanol. However, for some targeted species, and for larger individuals, subsamples were immediately frozen at -5°C.

Information on each haul was initially recorded on log sheets in the field. Immediately following the cruise, the information was transcribed to an Excel spreadsheet for subsequent export to the project database.

2.3.4. Laboratory Procedures
In the laboratory, individual specimens were removed from ethanol or thawed prior to further processing. Individual length (TL nearest mm) and weight (W nearest 0.1g) and maturity status were recorded for these processed fish. Subsequently, the carcasses were processed for some of the following characteristics: otolith-based ageing, stomach contents, tissue energy density, RNA:DNA ratio. To relate information gathered on individual fish each fish was given a unique identification of the form CFYYMMMTTSSS-SpCodeNNN, where SpCode is a unique two letter code for each species, and NNN is a numeric identifier.

2.3.4.1. Ageing

Sagitall otoliths were dissected from thawed carcasses and cleaned in distilled water. The otolith was weighed, and its maximum dimension recorded. The otolith was affixed to a triple thickness of glass using thermoplastic cement and sections of the otolith were cut. A double blade technique was used to make thin sections through the core of the otolith. This approach requires only one cut for each section and ensures production of uniformly flat sections. Briefly, two 4” diameter diamond wafering blades were mounted on a low speed wheel saw (South Bay Technologies, San Clemente, CA). The two blades were separated by an 0.5 mm stainless spacer. A range of thicknesses of spacers was available, and changed according to the species being sectioned.

Otolith sections were examined under a dissecting microscope at low magnification and age was determined. We employed a double blind technique that we have used successfully in other studies (Frisk and Miller 2006). Briefly, each otolith was read blind by at least two different readers, and the ages compared. If age estimates differed, a third read was taken. If the age of this third reader did not agree with one of the previous estimates, the otolith was discarded as unreadable.

2.3.4.2. Stomach Contents

Whole stomachs were dissected from the carcass. For this application the stomach was defined as that section between the termination of the esophagus and the pyloric caecae. The remainder of the alimentary canal was inspected to ensure no undigested food was
present. Prior to removal of the stomach contents, full stomachs were blotted dry and weighed to obtain a full stomach weight (nearest 0.01g). Stomach contents were then removed and the stomach was subsequently re-weighed to obtain an empty stomach weight (nearest 0.01g). The difference between these two weights represents an estimate of the total weight of prey in the stomach. Stomachs were scored for the presence/absence of food. A feeding incidence of 1.0 indicated the presence of food in the stomach.

Stomach contents were sorted and identified to the lowest practical taxonomic level under a dissecting microscope. Individual items comprising each prey group were blotted dry and weighed to obtain an estimate of the total weight of that prey type in the stomach. For larger prey, length and weight of each individual prey item was also recorded.

2.3.4.3. Tissue Energy Density

For targeted species, tissue energy density measurements were taken. Individual carcasses, less stomachs and otoliths were ground in a commercial meat grinder. For Atlantic croaker, liver tissues were processed separately. Homogenized tissue samples were then freeze-dried at -70C and X Atm for 24 hrs in a 2.5 L capacity freeze drier (Labonco Corp, Kansas City, MO). Dried samples were ground in a commercial coffee grinder and formed into 0.5 – 1.0 g pellets. The pellets were burned in an oxygen rich-environment in a bomb calorimeter (Model 6200, Parr Instruments, Moline, IL) to determine the energy content of the tissue.

2.3.4.4. RNA: DNA-based condition

RNA:DNA has been shown to be a reliable indicator of short term growth in juvenile fish (Peck et al. 2003). We used a fluorometric technique to quantify RNA:DNA levels in samples of axial muscle (Caldarone et al. 2006). Briefly, each tissue sample was extracted in N-lauroylsarcosine (final concentration 1%) in Tris-EDTA (TE) buffer (pH 7.5). After diluting and centrifuging, a portion of the supernatant was combined in a microplate with the fluorophore EB and the total nucleic-acid fluorescence was recorded with a microplate fluorometer. After adding RNase to each well, the plate was read a second time and the resulting fluorescence was attributed to
DNA. RNA concentrations were calculated from the difference in fluorescence between the first and second readings (Caldarone et al. 2001).

2.4. DATABASE DESIGN AND MANAGEMENT

The CHESFIMS program developed a substantial volume of data. Initially, the program used the data management tools that had been developed for the TIES program. However, it was soon apparent that the existing data management scheme was insufficient with respect to data security and integrity, data quality assurance and did not allow for simultaneous multiuser access to the most recent data.

Following discussions with CBL IT professionals we contracted with an independent database consultant to design and implement the CHESFIMS database. Subsequently, discussions among the consultant, CHESFIMS personnel and the CBL IT group it was decided to implement the database as a MySQL database on a SUN Solaris Server at CBL. The advantage of this choice is that routine database management would be handled by the CBL IT group, who would be responsible for archiving, software updates, and any hardware difficulties. The CBL IT group also handles user profiles and ensures security, thereby preventing any unauthorized access. MySQL is an appropriate choice because it can serve as an ODBC server and the majority of software applications can serve as ODBC clients.

2.4.1. Database Design

A database design that strongly reflected the sampling program was developed. The final database design is shown in Fig. 2.2. The database design focuses on station events as the central design element. A unique event number is assigned each time the research vessel stopped to undertake sampling. Physical data collected during each event are stored in one of three tables: CTD, MINILOG_TOP and MINILOG_BOTTOM. Each datalogger records its data by unique scan numbers, thus the combination of event number and scan number provides unique keys for these tables. A CRUISE table was also established to provide convenient hierarchical subsetting of the data. Cruise ID served as a unique key for the CRUISE table. Biological data collected at each event were recorded in separate tables. For each event we recorded the catch
summary by species in the CATCHSUMMARY table. For this table event number and species IDs served as a unique key. To ensure the widest possible use of the data we used ITIS codes as species ID codes. ITIS, the Integrated Taxonomic Information System, is the result of a partnership of federal agencies, included NOAA, formed to satisfy their mutual needs for scientifically credible taxonomic information. The goal of the partnership is to create an easily accessible database with reliable information on species names and their hierarchical classification. The database is reviewed periodically to ensure high quality with valid classifications, revisions, and additions of newly described species. The ITIS includes documented taxonomic information of flora and fauna from both aquatic and terrestrial habitats. The taxonomic information on the catch and species in the diet of the catch are recorded in the SPECIES table. The subset of the catch that was measured onboard the vessel is recorded in the SIZE table. A dummy specimenID variable, combined with event number and species ID provides the key for this table. Information from the secondary processing of the sample is recorded in PROCESSED_FISH and DIET tables. Full details of each table, its data fields, formats and default values are provided in Tables 2.2-2.12.

Following extensive prototyping which involved running frequent dummy queries, the consultant delivered the final database design in May 2006. The initial prototyping was all conducted in MS Access. Subsequently, CHESFIMS staff input all CHESFIMS data into the database in MS Access for the ease that its visual interface afforded. This exercise provided ample opportunity for quality assurance / control. Subsequently, data were exported to populate the final MySQL database structure.

We note that this database has now become the default data management tool for all field collections undertake in the Miller Lab at CBL. Thus, the database continues to expand, now holding data from a wide variety of programs including a parallel midwater trawl survey in the Patuxent River in 2004 that was funded by Maryland Department of Natural Resources, an ichthyoplankton survey of the Patuxent River conducted in 2006 and 2007, seine survey collections for striped bass and menhaden conducted in Maryland waters of Chesapeake Bay in 2006 and 2007.
2.4.2. Data Reporting

Protocols for data access were checked for all principal software clients that were likely to be used by CHESFIMS staff. We verified data access in MS Access, MS Excel, SAS, R, and ArcView. Currently, these software clients can only be used internally within CBL due to security firewalls in place at CBL. However, as described below, we have also implemented a web interface that provides access to all but the processed fish and diet data to the general public via the internet.

We have developed SQL queries for all local clients able to support data queries from the master CHESFIMS database. For example the following code implements the database connection in SAS and extracts all spring cruises

```sql
libname survey ODBC datasrc="miller_survey" user=xxx password=xxx;
libname cf c:\files\cf;
proc sql;
Create table cf.testcatch as
  Select CruiseID FROM survey.cruise WHERE month>4;
run;
```

Similarly, it is simple to make the connection in the statistical package R

```r
Library(ODBC)
cfdata<-odbcconnect("Miller_Survey", uid="xxx", pwd="xxx")
Cruiselist<-sqlQuery(cfdata, "select CruiseID from Cruise where month >4")
```

Of course more complex queries are possible. The next example of the implementation in R extracts data to generate length frequencies for a single species from the database.

```r
## produces a length frequency plot for a single species for all CF cruises
## edit the Size.Species= to change the species - may have to change x and y label limits
## anchovy = 161839, wp=167678, croaker=169283, sb=167680, hc=172982
library(RODBC)

## connect to the database
lfdata<-odbcConnect("Miller_Survey", uid="xxx", pwd="xxx")
```

## use SQL query to retrieve required data

close(lfdata)

2.4.3. Development of Web Interface

Following the successful development and implementation of the SQL database and development of ODBC clients for a variety of commonly used software, our next goal was to develop a web interface for the database. It was quickly determined following discussions with CBL IT staff that off-the-shelf solution would likely not be sufficiently flexible for use. Accordingly, we contracted with an independent web-developer to design and code a specific implementation that we could tailor to our own use.

The contractor was provided with a limited number of minimum requirements. The web interface had to be secure and not provide a portal to the actual data itself. Further, a specific design criterion was that the portal should be sufficiently simple that any potential stakeholder could access the data. Following discussions it was decided that these goals could be met if we restricted the tool to the following data types

Total Catch (number)
Total Catch (weight)
Length data
Average physical parameters (temperature, salinity, dissolved oxygen)
Average surface parameters (temperature, salinity, dissolved oxygen)
Average bottom parameters (temperature, salinity, dissolved oxygen)

The web site was coded using a combination of php, java script and SQL language. The web site is completely open: there is no login or restriction on any user. The web site is accessible from any web browser and has been tested in the principal commercially available
browsers included Internet Explorer v 6, Firefox v 2., Netscape v 7, and Apple Safari. The site is registered with Google and other search engines. A GOOGLE search for CHESFIMS takes the user directly to the main project page, or secondarily to the data tool itself. The main page of the web interface is shown in Fig 2.3. The main page provides instructions about how to use the remainder of the data selection tool. The data tool does not produce results directly to a web, rather the result of any query is an Excel file that provides the raw data. The data tool also provides access to a complete list of all stations visited during the survey program. This can be used to expand estimates of survey CPUEs by accounting for those stations at which there was no catch of the species selected. By navigating through the tabs from the main page, the user can subset the CHESFIMS data by Season, Area, Date or Species. We are particularly pleased that the Area tab allows the user to select regions of the Chesapeake Bay from which to query data graphically by clicking and dragging to define the area of interest (Fig. 2.4).

The results of a query using the data selection tool are shown in Figure 2.5. Prior to saving the data, the user can inspect the data prior to saving. Once the user has ensured the data selected meet the criteria, the user can then save the data. The data are saved to a compressed folder that can be saved locally on the users own hard disk. When uncompressed, the data are saved in a series of comma separated files that can be opened in excel or imported into a software package of the users choice. The compressed files include a master file – called index.csv which provides information on each cruise, and then separate csv files for each cruise. An example of the data included in an individual cruise file is shown in Figure 2.6.


CFEPTAP. 2004. Fisheries ecosystem planning for Chesapeake Bay. Chesapeake Fisheries Ecosystem Plan Technical Advisory Panel, NOAA Chesapeake Bay Office, Annapolis.

Chesapeake Bay Fisheries Ecosystem Advisory Panel. 2006. Fisheries Ecosystem Planning for the Chesapeake Bay. American Fisheries Society, Bethesda, MD.

Chesapeake Fishery Ecosystem Plan Technical Advisory Panel. 2006. Fishery Ecosystem Planning For Chesapeake Bay. American Fisheries Society, Bethesda, MD.


Frisk, M. G., and T. J. Miller. 2006. Age, growth, and latitudinal patterns of two Rajidae species in the northwestern Atlantic: little skate (Leucoraja erinacea) and winter skate (Leucoraja ocellata). Canadian Journal of Fisheries and Aquatic Sciences 63:1078-1091.


Table 2.1. Filename standards and content for electronic information developed on each cruise

<table>
<thead>
<tr>
<th>Filename</th>
<th>Extension</th>
<th>Instrument</th>
<th>Format</th>
<th>Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>CTD</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CFYYMMOTTSS</td>
<td>.con</td>
<td>CTD</td>
<td>ASCII</td>
<td>Communication information for CTD</td>
</tr>
<tr>
<td>CFYYMMOTTSS</td>
<td>.hex</td>
<td>CTD</td>
<td>Hexadecimal</td>
<td>Raw data from CTD profile</td>
</tr>
<tr>
<td>CFYYMMOTTSS</td>
<td>.cnv</td>
<td>CTD</td>
<td>ASCII, CSV delimited</td>
<td>Converted Hex data. File contains converted data for the downcast together with details on each instrument</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MiniLog</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BinXXXXX</td>
<td>.XXX</td>
<td>Minilog</td>
<td>Hexadecimal</td>
<td>Raw data for each minilog deployment. The numbers following the BIN identify the minilog used, and the extension is simply a numeric counter that identifies the number of hauls since the memory was last wiped.</td>
</tr>
<tr>
<td>CFYYMMOTTSS_btm</td>
<td>.txt</td>
<td>Minilog</td>
<td>ASCII, csv delimited</td>
<td>Converted minilog data for a minilog attached to the foot rope. Data columns are identified in the file header</td>
</tr>
<tr>
<td>CFYYMMOTTSS_top</td>
<td>.txt</td>
<td>Minilog</td>
<td>ASCII, csv</td>
<td>Converted</td>
</tr>
<tr>
<td>delimited</td>
<td></td>
<td></td>
<td>delimited</td>
<td>minilog data for a minilog attached to the header rope. Data columns are identified in the file header</td>
</tr>
</tbody>
</table>
Table 2.2. Details of CRUISE Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>CruiseID</td>
<td>Text, 6</td>
<td>Cruise Number (CF0203)</td>
</tr>
<tr>
<td>Program</td>
<td>Text, 2</td>
<td>CF</td>
</tr>
<tr>
<td>Vessel</td>
<td>Text, 50</td>
<td>Aqaurius</td>
</tr>
<tr>
<td>Year</td>
<td>Integer, 4</td>
<td>2002</td>
</tr>
<tr>
<td>Season</td>
<td>Text, 20</td>
<td>Summer</td>
</tr>
<tr>
<td>Month</td>
<td>Integer, 2</td>
<td>7</td>
</tr>
<tr>
<td>Comment</td>
<td>Text, 50</td>
<td></td>
</tr>
</tbody>
</table>
Table 2.3. Details of STATION Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data Type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>EventNum</td>
<td>Number</td>
<td></td>
</tr>
<tr>
<td>StationID</td>
<td>Number</td>
<td>Original station number</td>
</tr>
<tr>
<td>CruiseID</td>
<td>Text</td>
<td>Cruise Number (CF0302)</td>
</tr>
<tr>
<td>Btime</td>
<td>Date/Time</td>
<td>Arrival time on station</td>
</tr>
<tr>
<td>AirTemp</td>
<td>Number</td>
<td>Air temperature (C – from Bridge log)</td>
</tr>
<tr>
<td>Barometer</td>
<td>Number</td>
<td>Air pressure (From Bridge log)</td>
</tr>
<tr>
<td>WindDirection</td>
<td>Text</td>
<td>Wind direction – compass rose – From Bridge Log</td>
</tr>
<tr>
<td>WindSpeed</td>
<td>Text</td>
<td>Wind Speed (From Bridge Log)</td>
</tr>
<tr>
<td>Tide</td>
<td>Text</td>
<td>State of tide (From Bridge Log)</td>
</tr>
<tr>
<td>Weather</td>
<td>Text</td>
<td>Weather conditions (From Bridge Log)</td>
</tr>
<tr>
<td>CloudCover</td>
<td>Text</td>
<td>(From Bridge Log)</td>
</tr>
<tr>
<td>SeaState</td>
<td>Text</td>
<td>(From Bridge Log)</td>
</tr>
<tr>
<td>Transect</td>
<td>Number</td>
<td>Transect for station, cruise sampling design</td>
</tr>
<tr>
<td>Region</td>
<td>Text</td>
<td>Region of Bay (Upper, Mid, Lower)</td>
</tr>
<tr>
<td>Order</td>
<td>Number</td>
<td>Sequential number of station during cruise</td>
</tr>
<tr>
<td>Date</td>
<td>Date/Time</td>
<td>Date of arrival on station</td>
</tr>
<tr>
<td>Depth</td>
<td>Number</td>
<td>Station depth recorded from aft mounted depth sounder (m)</td>
</tr>
<tr>
<td>CTDLat</td>
<td>Number</td>
<td>Latitude of CTD cast</td>
</tr>
<tr>
<td>CTDLong</td>
<td>Number</td>
<td>Longitude of CTD cast</td>
</tr>
<tr>
<td>Gear</td>
<td>Text</td>
<td>Gear used (MW – midwater)</td>
</tr>
<tr>
<td>TLATBegin</td>
<td>Number</td>
<td>Latitude at beginning of tow</td>
</tr>
<tr>
<td>TLongBegin</td>
<td>Number</td>
<td>Longitude at beginning of tow</td>
</tr>
<tr>
<td>TLatEnd</td>
<td>Number</td>
<td>Latitude at end of tow</td>
</tr>
<tr>
<td>TLongEnd</td>
<td>Number</td>
<td>Longitude at beginning of tow</td>
</tr>
<tr>
<td>Ttime</td>
<td>Number</td>
<td>Duration of tow</td>
</tr>
<tr>
<td>CTDFile</td>
<td>Text</td>
<td>Name of CTD conv file</td>
</tr>
<tr>
<td>MLTopFile</td>
<td>Text</td>
<td>Name of mimilog top file</td>
</tr>
<tr>
<td>MLBottomFile</td>
<td>Text</td>
<td>Name of mimilog bottom file</td>
</tr>
</tbody>
</table>
Table 2.4. Details of CTD Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>EventNum</td>
<td>Number</td>
<td>EventNumber from StationID</td>
</tr>
<tr>
<td>Sca</td>
<td>Integer</td>
<td>Sequential number indicating line of data</td>
</tr>
<tr>
<td>Time</td>
<td>Number</td>
<td>Time of scan</td>
</tr>
<tr>
<td>Pressure</td>
<td>Number</td>
<td>Pressure in water column</td>
</tr>
<tr>
<td>Depth</td>
<td>Number</td>
<td>Estimated depth from pressure</td>
</tr>
<tr>
<td>Salinity</td>
<td>Number</td>
<td>Salinity in water column</td>
</tr>
<tr>
<td>Temp</td>
<td>Number</td>
<td>Temperature in water column</td>
</tr>
<tr>
<td>Oxygen</td>
<td>Number</td>
<td>Oxygen concentration in water column</td>
</tr>
<tr>
<td>Oxysat</td>
<td>Number</td>
<td>Percent saturation of oxygen in water column</td>
</tr>
<tr>
<td>Transmis</td>
<td>Number</td>
<td>Transmissivity in water column</td>
</tr>
<tr>
<td>Flourom</td>
<td>Number</td>
<td>Fluorometer value in water column</td>
</tr>
<tr>
<td>Flag</td>
<td>Number</td>
<td>Error flag recorded by CTD</td>
</tr>
</tbody>
</table>
Table 2.5. Details of MiniLogTop Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>EventNum</td>
<td>Number</td>
<td>EventNumber from StationID</td>
</tr>
<tr>
<td>Time</td>
<td>Text</td>
<td>Time at which data was scanned</td>
</tr>
<tr>
<td>Temp</td>
<td>Number</td>
<td>Temperature in water column</td>
</tr>
<tr>
<td>Depthj</td>
<td>Number</td>
<td>Depth recorded</td>
</tr>
</tbody>
</table>
Table 2.6. Details of MiniLogBottom Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>EventNum</td>
<td>Number</td>
<td>EventNumber from StationID</td>
</tr>
<tr>
<td>Time</td>
<td>Text</td>
<td>Time at which data was scanned</td>
</tr>
<tr>
<td>Temp</td>
<td>Number</td>
<td>Temperature in water column</td>
</tr>
<tr>
<td>Depth</td>
<td>Number</td>
<td>Depth recorded</td>
</tr>
</tbody>
</table>
Table 2.7. Details of CatchSummary Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data Type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>EventNum</td>
<td>Number</td>
<td>EventNumber from StationID</td>
</tr>
<tr>
<td>StationID</td>
<td>Number</td>
<td>Original station number</td>
</tr>
<tr>
<td>SpeciesID</td>
<td>Number</td>
<td>Species number from ITIS database</td>
</tr>
<tr>
<td>Split</td>
<td>Text</td>
<td>Sample fraction worked up</td>
</tr>
<tr>
<td>SplitBasis</td>
<td>Text</td>
<td>Sample fraction based on volume of weight</td>
</tr>
<tr>
<td>SubWt</td>
<td>Number</td>
<td>Weight of subsample</td>
</tr>
<tr>
<td>SubVol</td>
<td>Number</td>
<td>Volume of subsample</td>
</tr>
<tr>
<td>TotVol</td>
<td>Number</td>
<td>Total volume of sample</td>
</tr>
<tr>
<td>SubCt</td>
<td>Number</td>
<td>Count of subsample</td>
</tr>
<tr>
<td>TotWt</td>
<td>Number</td>
<td>Total weight of sample</td>
</tr>
<tr>
<td>TotCt</td>
<td>Number</td>
<td>Total count of sample</td>
</tr>
<tr>
<td>Comment</td>
<td>Text</td>
<td></td>
</tr>
</tbody>
</table>
Table 2.8. Details of Size Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data Type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>SizeSpecimenID</td>
<td>Number</td>
<td>Unique ID for each dataline</td>
</tr>
<tr>
<td>EventNum</td>
<td>Number</td>
<td>EventNumber from StationID</td>
</tr>
<tr>
<td>StationID</td>
<td>Number</td>
<td>Original station number</td>
</tr>
<tr>
<td>SpeciesID</td>
<td>Number</td>
<td>Species number from ITIS database</td>
</tr>
<tr>
<td>Length</td>
<td>Number</td>
<td>Total length of fish</td>
</tr>
<tr>
<td>Weight</td>
<td>Number</td>
<td>Weight of fish</td>
</tr>
<tr>
<td>Sext</td>
<td>Text</td>
<td>Sex of fish</td>
</tr>
<tr>
<td>Comment</td>
<td>Text</td>
<td></td>
</tr>
</tbody>
</table>
Table 2.9. Details of PROCESSEDFISH Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data Type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>EventNum</td>
<td>Number</td>
<td>EventNumber from StationID</td>
</tr>
<tr>
<td>SpeciesID</td>
<td>Number</td>
<td>Species number from ITIS database</td>
</tr>
<tr>
<td>FishID</td>
<td>Number</td>
<td>Unique sequential number for each species, eventnum combination</td>
</tr>
<tr>
<td>ProcessedDate</td>
<td>Date/Time</td>
<td>Date when fish was processed</td>
</tr>
<tr>
<td>Length</td>
<td>Number</td>
<td>Total length of fish</td>
</tr>
<tr>
<td>Weight</td>
<td>Number</td>
<td>Weight of fish</td>
</tr>
<tr>
<td>Sex</td>
<td>Text</td>
<td>Sex of fish</td>
</tr>
<tr>
<td>FullStomachWt</td>
<td>Number</td>
<td>Weight of stomach with contents</td>
</tr>
<tr>
<td>EmptyStomachWt</td>
<td>Number</td>
<td>Weight of stomach with contents removed</td>
</tr>
<tr>
<td>Age</td>
<td>Number</td>
<td>Estimated age</td>
</tr>
<tr>
<td>Comments</td>
<td>Text</td>
<td></td>
</tr>
</tbody>
</table>
Table 2.10. Details of DIET Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
<thead>
<tr>
<th>Field Name</th>
<th>Data Type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>DietSpecimenID</td>
<td>Number</td>
<td>Unique ID for each dataline</td>
</tr>
<tr>
<td>FishID</td>
<td>Number</td>
<td>Unique ID from Processed fish table</td>
</tr>
<tr>
<td>PreyID</td>
<td>Number</td>
<td>Species number from ITIS database r</td>
</tr>
<tr>
<td>PreyCt</td>
<td>Number</td>
<td>Count of prey type in stomach</td>
</tr>
<tr>
<td>Length</td>
<td>Number</td>
<td>Total length of fish</td>
</tr>
<tr>
<td>Weight</td>
<td>Number</td>
<td>Weight of fish</td>
</tr>
<tr>
<td>Presence</td>
<td>Number</td>
<td>0,1 index indicating presence</td>
</tr>
<tr>
<td>%</td>
<td>Number</td>
<td>Percent contribution</td>
</tr>
<tr>
<td>Comment</td>
<td>Text</td>
<td></td>
</tr>
</tbody>
</table>
Table 2.12. Details of DIET Table Structure for CHESFIMS SQL Database. The key for each table is shown in boldface

<table>
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<tr>
<th>Field Name</th>
<th>Data Type</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
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<tr>
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<td>Text</td>
<td>Genus</td>
</tr>
<tr>
<td>Species</td>
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</tr>
<tr>
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<tr>
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<tr>
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<td>Text</td>
<td>Trophic mode</td>
</tr>
<tr>
<td>SampleAbbreviation</td>
<td>Text</td>
<td>Abbreviation used in sample processing</td>
</tr>
<tr>
<td>SurveySpecies</td>
<td>Text</td>
<td>Abbreviation used in survey data sheet</td>
</tr>
<tr>
<td>PreySpecies</td>
<td>Text</td>
<td>Abbreviation used in diet data sheet</td>
</tr>
<tr>
<td>Comment</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Figure 2.1 Example of the distribution of samples on an individual cruise
Fig 2.2. Relationships among tables in the CHESFIMS database. Keys for each table are shown in boldface.
Figure 2.3. Main page of the web tool for accessing the CHESFIMS data

A few notes on searching the tool:
- Narrow your search by selecting the information contained within each tab.
- Check boxes for selecting items.
- Click on the table.
- After refining your request, you will be presented with a preview of the data. Please review as this is the result that meets your requirements.
- If you wish to further refine your search terms, you may click "Add Query" which will appear at the top of the page (only when retrieving results).
- When you are ready to view the data, click the "View" menu. It may take up to 20 seconds for us to prepare your data into a file that you can then download.
- Download file by clicking the "Save" file link which will appear in place of the course.
- The data will contain a .csv file providing cruise level information and individual data files for each station.
- If you would like to calculate standardized abundances, please download the "dotted lot file" to identify stations compared but at which there was no catch.
- If you have any further questions, please email Dr. Thomas Miller.
Figure 2.4. The area selection tab on the CHESFIMS data web tool
Figure 2.5. Preliminary results of the data selection tool for a query selecting white perch during the summer in the upper Bay.
Figure 2.6. An example of the data included in a single cruise file produced by a search for data on white perch catches in the upper bay in the summer.
APPENDIX 2.1.

Matlab scripts to estimate average net openings

**Aveop.m**

% a script file that reads a list of stations for a cruise
% and then executes a function - mlcombst for each station
% to calculate the average net opening for that station

```
stalist=textread('H:\chesfims\cf0303\minilog\0303sta.txt','%s');
stas=char(stalist);
cmax=length(stas);
for i=1:cmax
    sta=char(stalist(i))
    aveop(i,2)=mlcombst(cruise,sta);
end
```

**mlcombst.m**

```
function meanopen=mlcombst(cruise,sta)
% mlcombst takes two data matrices read from minilog files on the top and 
% bottom ropes of a trawl, aligns time stamps and creates a single output 
% file 
% Inputs are: 
% top = the ml data matrix from the top rope - data obtained 
% from a call to ml2mat(top rope file name) 
% bottom = the ml data matrix from the bottom rope - data obtained 
% from a call to ml2mat(top rope file name) 
% 

top=ml2mat(strcat('H:\chesfims\cf',cruise,'\minilog\CF',cruise,sta,'_top.txt'));
bottom=ml2mat(strcat('H:\chesfims\cf',cruise,'\minilog\CF',cruise,sta,'_btm.txt'));

% compare the initial time stamps 
if top(1,1)<bottom(1,1)
    is=find(top(:,1)<bottom(1,1));
    indx=max(is);
    top=top(indx:end,:);
elseif top(1,1)>bottom(1,1)
    is=find(bottom(:,1)<top(1,1));
    indx=max(is);
    bottom=bottom(indx:end,:);
end
```
% now merge the two data sets
%

if length(top)>length(bottom)
    maxrow=length(bottom);
elseif length(bottom)>length(top)
    maxrow=length(top);
end

top=top(1:maxrow,:);
bottom=bottom(1:maxrow,:);
mldat=horzcat(top, bottom);
mldat(:,7)=mldat(:,6)-mldat(:,3);
means=mean(mldat,1);
meanopen=means(1,7);
return
Chapter 3

PATTERNS IN THE DISTRIBUTION AND COMPOSITION OF THE FISH ASSEMBLAGE IN THE CHESAPEAKE BAY

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3.1 INTRODUCTION

Agencies, at all levels, are seeking to adopt ecosystem approaches to management (EAM) of fisheries in efforts to ensure long term sustainability of the exploited marine resources and the ecosystems from which these resources are taken (Pauly et al. 2002). The need to adopt EAM is motivated by the recognition that fish populations are components of complex marine ecosystems. Removals by fisheries from these ecosystems have consequences to ecosystem services generally, and in turn ecosystem processes affect the productivity and sustainability of individual fish stocks (Pikitch et al. 2004, Worm et al. 2006). However, EAM require analysis of a wider range of data than are typically available (Choi et al. 2005). Such analyses rely on access to data from a wide range of sources.

The Chesapeake Bay, located on the mid-Atlantic seaboard, is the largest estuary in North America. It is shallow, temperate, coastal plain estuary with high productivity (Nixon 1988). Since European settlement, the bay has experienced heavy exploitation, extensive physical habitat alteration, invasion of exotics and anthropogenic nutrient enrichment (Kemp et al. 2005, Secor and Austin 2006). These forces have had significant impacts on its fishery resources (Miller 2006a). For example, oyster (Crassostrea virginica) fisheries flourished at the end of the 19th Century, with catches in excess of 600,000 t. As a result of both overfishing and disease (Rothschild et al. 1994), current catches are less than 1% of this maximum level. Several other species (e.g., striped bass) have experienced similarly substantial changes in abundance. Together these changes in the Chesapeake Bay ecosystem motivated the regional management jurisdictions to commit to an EAM for the Chesapeake Bay (Chesapeake Bay Fisheries Ecosystem Advisory Panel 2006). A central requirement for the success implementation of EAM is the availability of fishery-independent survey data for both economically and ecologically important species from which biological reference points can be developed.

In 1996, researchers at the University of Maryland Center for Environmental Science instituted a baywide survey of the fish community in Chesapeake Bay as part of a larger project to document and quantify trophic interactions in the estuary (TIES). Surveys of the fish community focused on the small pelagic and benthopelagic components of the fish fauna because these sizes and species represent an important energetic pathway for the ecosystem as a...
whole (Baird et al. 1995). Additionally, this component of the fish community had been largely neglected by existing surveys. Jung and Houde (2003) published a description of the baywide spatial and temporal pattern in community structure of the pelagic and benthopelagic fishes throughout the Bay based on surveys conducted between 1995-2000. Jung and Houde documented an assemblage comprising 36 pelagic and 21 benthic species. They characterized the assemblage as a low diversity, but high dominance system, with catches being dominated by bay anchovy (*Anchoa mitchelli*) by number and by bay anchovy, Atlantic croaker (*Micropogonias undulatus*) white perch (*Morone Americana*) by weight. Jung and Houde (op. cit.) used a multivariate correspondence analysis to quantify changes in the fish assemblage over time. This analysis clearly demonstrated an important seasonal and spatial progression in survey catches. Interannual differences in the abundances, when corrected for season appeared to respond most to variation in the freshwater input to the Bay. Most surprisingly, Jung and Houde’s analysis also indicated an inverse relationship between fish biomass and mean, depth-integrated oxygen concentration. This relationship would appear to indicate that assemblage biomass was highest under the lowest oxygen concentrations. Jung and Houde hypothesized that the oxygen levels in this analysis were serving as a surrogate for benthic production: when benthic production is high, it acts to lower oxygen levels. Thus they suggest that the high benthic production supports high biomass in the fish assemblage. The results of Jung and Houde’s analyses represent hypotheses relating to the bentho-pelagic fish community in Chesapeake Bay. Specifically they hypothesized that

H1: Interannual variation in assemblage structure is caused by differences in the flow of freshwater into the Chesapeake Bay.

H2: Spatial variation in the assemblage responds to the salinity distribution such that clear oligohaline (0-5 salinity), mesohaline (5-18 salinity) and polyhaline (>18 salinity) assemblages can be identified.

H3: There is a strong seasonal succession evident in the fish assemblage that reflects the role of the Bay as a nursery area for anadromous species in the spring/summer period and then the recruitment of bay anchovy in the autumn.
With funding from the NOAA Chesapeake Bay Office, we initiated the Chesapeake Bay Fishery Independent Multispecies (CHESFIMS) Survey to complement the TIES survey. The objectives of the survey were to extend the TIES survey for an additional five years (2001-2006) using the same sampling protocols and to determine the trophic interactions among key components of the pelagic fish community. Here we use the CHEFIMS data to test the specific hypotheses suggested by Jung and Houde’s analysis of the 1995-2000 data.
3.2 METHODS

3.2.1. Field

The CHESFIMS survey is a complemented design involved both fixed and random stations. The fixed stations were located along fixed transects that had been defined during the early TIES program (Jung and Houde 2003). The TIES program occupied more stations and transects than could be occupied during CHESFIMS, and accordingly we sampled a subset of these original stations, selected to ensure a broad spatial coverage throughout the Chesapeake Bay. In addition to these fixed stations, we also included a similarly number of stratified random stations selected in proportion to strata area. Individual strata have distinctive characteristics, and their boundaries broadly corresponding to ecologically relevant salinity regimes and depths above 5 m. The upper Bay (38 45’ to 39 25’N) is generally shallow, with substantial areas with depths less than 5 m, and has well mixed waters with high nutrient concentrations. The bottom topography in the mid Bay includes a narrow channel in the middle of the Bay (37 55’N to 38 45’N) with a stratified water column and broad flanking shoals. This region has relatively clear waters and experiences seasonally high nutrient concentrations and periods of hypoxia. The lower Bay (37 05’ to 37 55’N) has the clearest waters, greatest depths and lowest nutrient concentrations (Kemp et al., 2005). The strata volumes are 26,608 km$^3$ (Lower), 16,840 km$^3$ (Mid) and 8,664 km$^3$ (Upper).

CHESFIMS was initiated in 2001, employing the TIES trawling procedures, transect design and stratification. Sampling was conducted during spring, summer and autumn from the University of Maryland Center for Estuarine and Environmental Science’s R/V ‘Aquarius. On most cruises we occupied 31 stations allocated according to the original TIES transect design, and 20 stations allocated according to a stratified random scheme. The transect stations were fixed for the duration of the CHESFIMS program, whereas the stratified random stations were selected anew for each cruise. In the stratified random surveys, conducted simultaneously with the transect surveys, 20 stations covering the entire bay were allocated to the each stratum proportional to their volumes. Latitude and longitude of stations within strata were randomly generated. Weather precluded complete sampling of all stations during some surveys.
To the extent possible all activity at each station was standardized. Immediately prior to each trawl deployment, a Sea-Bird SBE 25 conductivity, temperature, depth profiler was used to profile the water column. We used an 18-m² midwater trawl (MWT) with 3-mm codend mesh as the primary survey gear (Jung and Houde, 2003). The MWT employed in the Bay samples fish 30-256 mm total length of most species effectively, but appears to be less effective for Atlantic menhaden (*Brevoortia tyrannus*) of all sizes (Jung and Houde 2003). We used a standardized 20-minute oblique, stepped tow in all deployments. The trawl was towed for two minutes in each of ten depth zones distributed throughout the water column from the surface to the bottom, with minimum trawlable depth being 5 m. The section of the tow conducted in the deepest zone sampled epibenthic fishes close to or on the bottom. The remaining portion of the tow sampled pelagic and neustonic fishes. All tows were conducted between 19:00 and 7:00 Eastern Standard Time to minimize gear avoidance and to take advantage of the reduced patchiness of multiple target species at night. A temperature-depth minilogger was attached to the head rope of the trawl for all deployments to record the tow profile. Data from this minilog was inspected immediately after each haul to determine whether the haul had largely met survey criteria. An additional minilog was attached to the foot rope of the trawl. By combining data from the top and bottom miniloggers, the net opening could be estimated for the duration of the haul. Catches were identified, enumerated, measured and weighed onboard. For species for which there were less than 100 individuals caught in the haul, all individuals were measured to the nearest mm for total length (TL), and a total weight of the species caught was measured on a precision spring balance (nearest g). For some species, individuals were of sufficient size that individual weights could be determined, but this was not common. For abundant species (e.g., bay anchovy, white perch etc), a subsampling procedure was used to estimate the catch. In most cases a random subsample of 100 individuals was measured for TL. This subsample was weighed, and the total catch of the species was also weighed. The total number in the catch was then estimated by proportion.

3.2.2. Statistical analysis

Catch data were used to generate catch per unit effort estimates for each species in the survey. These estimates were expanded by including zeros for hauls where that species was not
We calculated the species richness, $S$, as the number of unique species caught per tow. Estimates of $S$ could be aggregated to the region, cruise, season and program level. Because the sensitivity of species richness to the number of individuals caught, we also calculated the Shannon’s diversity index, $H$, for all tows. $H$ is given by

$$H = - \sum p_i \log_2 p_i$$

where $p_i$ is the proportion of species $i$ in the tow. It is not possible to aggregate $H$ at levels higher than the individual tow because $H$ is sensitive to differences in sampling effort (Clarke and Warwick 2001).

Following Jung and Houde (2003), we also calculated k-dominance curves. These are a graphical approach to comparing diversity among different sites. In this approach the ranked abundance, expressed as the proportion of total abundance that is represented by species $i$, is plotted against the species rank. K-dominance curves were calculated using the software Primer (Clarke and Gorley 2001a).

We also used canonical correspondence analysis (Ter Braak 1986) to explore relationships between environmental determinants and species distributions. Prior to conducting canonical correspondence analysis, we examined the correlation structure of the environmental data collected during the cruises. For most parameters, there were strong correlations among surface, bottom and average conditions at each station. For spring and autumn cruises, the correlation between surface and bottom values for each parameter were the strongest in the entire correlation matrix ($r>0.42$ for all pair wise surface vs. bottom comparisons). The relationship was less strong during summer months. Relationships between surface and bottom temperature, oxygen and transmissivity were not strong. However, despite this pattern in summer values, initial, exploratory canonical correspondence analyses were conducted with region, season, year, average water column values for salinity, temperature ($^\circ$C), oxygen (mg.L$^{-1}$), transmissivity and fluorometry values. Catch data for all species were included in the analysis. The constraint that data for all parameters had to be available for a station to be included, restricted the number of stations available for analysis. Missing environmental data meant that only 464 stations could be included. An exploratory analysis tested for the significance of each environmental parameter
using a randomization process with 500 permutations. Based on these analyses, non-significant terms were dropped from subsequent canonical correspondence analyses. Canonical correspondence analysis was conducted using the Vegan package (v. 1.8-6) in R.

To address hypotheses regarding the relationship between fish abundance and dissolved oxygen, we regressed Bay wide average catch per unit effort, estimated in terms of weight (g.min-1) or number (fish.min-1) against depth-weighted dissolved oxygen. Regressions were conducted for both summer and fall separately.

All statistical analyses, except for K-dominance curves estimation, were conducted in R (R Core Development Team 2007) using the base package for standard analysis and graphics. The Vegan package was used for the canonical correlation analysis (Oksanen et al. 2007). Finally the K-dominance curves were implemented in Primer v.6 (Clarke and Gorley 2001b).
3.3. RESULTS

We completed 17 surveys between April 2001 – October 2006 (Table 3.1). During this period, baywide average temperatures ranged from 13.41-25.95 °C, baywide salinities varied from 10.96-20.36 and baywide oxygen concentrations from 4.25-9.81 mg.L⁻¹. These levels of variability are similar, although less extreme than those reported by Jung and Houde (Jung and Houde 2003) for the period 1995-2000. There was a tendency for those cruises that were on average warmer, to also be on average saltier (Fig. 3.1), but no other strong correlations were apparent in the data.

Over the course of the 17 surveys, we occupied 693 stations (Fig. 3.2), and collected 520,786 fish weighing 2,205 kg. Only eight deployments (1.15%) resulted in a null catch. We collected 110 different species of fish (Table 3.2). The average 20 minute tow resulted in a catch of 811±1135 (mean ± SD) fish. When analyzed by logarithmic catch intervals, the frequency distribution of catches appeared multimodal, with modes at approximately 200 and at 2000 fish.tow⁻¹ (Fig. 3.3). We calculated species-specific average biomass CPUEs at the annual, seasonal and regional levels (Figs 3.4-3.6). At the annual level, catches exhibited considerable variability (Fig 3.4). In four of six years Atlantic croaker exhibited the highest CPUES. In the two years in which croaker was not dominant, white perch was the dominant species. In combination, croaker, white perch and bay anchovy comprised at least 60% of the total CPUE in all years. Spot represented substantial CPUE levels in 2005-2006, but otherwise all other species individually accounted for less than 10% of the total CPUE, and often less than 5%. At the seasonal level, average biomass-based CPUEs were again dominated by croaker, white perch and bay anchovy (Fig 3.5). Average CPUEs for croaker and white perch declined over the course of the year, whereas average bay anchovy CPUE increased. At the regional level, CPUE clearly indicate the known salinity tolerances of individual species (Fig. 3.6). White perch dominated catches in the upper Bay, bay anchovy those in the mid Bay and croaker those in the lower Bay.

The average species richness on each cruise was 36.06±7.06 species. Species richness increased over the course of the year, with an average of 32.6±4.72, 35.83±5.04 and 39.16±9.62
species collected in spring, summer and autumn cruises respectively. There was also an increase in the species richness over the course of the course of the sampling program. However, inspection suggests that this increase reflects two aspects of the data: the seasonal effect and the sensitivity of species richness, S, to sample size. Indeed, there is a weakly significant positive relationship between the number of stations occupied on a cruise and the species richness (S=0.287+23.39*Stations, R²=0.17, n=17, p <0.1). Otherwise, there was no obvious change in design, gear or vessel that might have contributed to the increase. At the level of the individual tow and ignoring the null hauls, species richness per haul ranged from 1-21 with a mean of 6.17±3.57. The distribution of species richness per haul was strongly negatively skewed (Fig. 3.7). When averaged by cruise, the seasonal effect on species richness is clear (Fig. 3.7). The distribution of Shanon’s diversity index, H, for each tow was strongly negatively skewed also (Fig. 3.7). The average value of H was 0.524 ± 0.455 (range 0 – 2.12).

K-dominance curves indicated that the Chesapeake Bay fish assemblage is dominated by a relatively few species when assessed either by abundance (Fig 3.8A) or biomass (3.8B). In either case, the top five species never account for less than 60% of the cumulative distribution, and often more than 90%. This is the particularly the case for abundance in fall cruises (Fig 3.8A) for which a single species (bay anchovy) often accounted for in excess of 90% of the cumulative catch by itself. Analysis of similarities indicated that the seasonal differences were significant for biomass (Global R=0.205, p=0.05), and marginally insignificant for abundance (Global R=0.119, p=0.08). A similar pattern was evident when the data were aggregated to examine K-dominance curves at the regional level (Fig. 3.9). As with individual cruise data, at the regional level, the assemblage was less evenly distributed when measured in terms of abundance (Fig. 3.9 A) than when measured in terms of biomass (Fig. 3.9 B). The top five species combined to represent more than 90% of the total abundance, and more than 60% of the total biomass.

Canonical correspondence analysis was conducted using region, season, year, water temperature, salinity, oxygen concentration, and transmissivity. The analysis yielded an ordination dominated by the first five unconstrained axes, with the first axes dominating all
others (Table 3.3) The CCA triplot indicated clear patterns in the weightings of the environmental variables (Fig. 3.10). The first axis which explained 11.8% of the variation in the data, was highly positively correlated with region and salinity, and highly negatively correlated with salinity. The second axis was most strongly related to temperature (+ve) and oxygen (-ve). The effects of region and season were almost orthogonal to each other, as were temperature and salinity. On the plot the effects of temperature and season were in a similar direction, and opposing that of oxygen, indicating that seasonal changes are primarily associated with changes increases in temperature and decreases in dissolved oxygen levels. Similarly, the effects of year and salinity were in the same direction and opposed the effects of region. This combination indicates that salinity is the principal factor associated with interannual differences in community structure, and is the primary factor affecting community difference in the three regions.

We also quantified the relationship between fish catches and oxygen concentrations. The relationship between summertime (July) catch per unit effort and summer time depth weighted oxygen concentration was negative (Fig 3.11A). However, the coefficient of determination was not significant (CPUE=497.36 - 64.08* Oxygen, n=5, r²=-0.15, p=0.539), suggesting a weak relationship. A model of October CPUEs vs oxygen concentrations was however significant, but the slope was reversed (Fig. 3.11 B).
3.4 DISCUSSION

We have documented variability in the fish assemblage of the Chesapeake Bay at annual, seasonal and regional scales. The variation we document is similar in magnitude to that previously demonstrated for the Chesapeake Bay by Jung and Houde (2003), but there are important differences in the pattern between the two studies. For example, in the six years analyzed by Jung and Houde bay anchovy was the dominant species in terms of biomass in four of the six years. In none, of the years we studied, was bay anchovy dominant in terms of biomass. In contrast, croaker dominated only in one year of the period examined by Jung and Houde, whereas it dominated in four of the six years we report on hear. Croaker is known to exhibit substantial interannual variation in abundances (Montane and Austin 2005, Hare and Able 2007). Thus it is possible that in combination the 12 year data set reflect periods of contrasting croaker abundances. The possibility of this is reinforced by the observation that croaker were in high abundance in the later years of the TIES program, and in the earlier years of the CHESFIMS program. However, we also note that Jung and Houde took a slightly different approach to analyzing the TIES data than selected here. For example, they chose to expand their catches by a catchability coefficient derived from a comparison of bay anchovy abundance in TIES survey catches and that estimated from an anchovy egg production model (Jung and Houde 2004). Thus, at the moment, we are unable to determine whether the reported differences do indeed reflect underlying ecological shifts or differences in methodology. At present, we are converting the TIES data to the same data management system used by CHESFIMS and thus we should be able to distinguish between these two alternatives in the near future.

Our analyses reinforce the overall spatial patterns demonstrated by Jung and Houde (Jung and Houde 2003). There are clear spatial differences in the fate of production in Chesapeake Bay. In the upper portion of the Bay, most of the primary and secondary production supports substantial populations of white perch. In both the analyses reported here and those reported by Jung and Houde, white perch represented approximately 70% of the total fish biomass in the survey. As one moves southward the dominance of white perch declines and shifts to first bay anchovy and then to croaker, which comprises approximately 40% of the biomass in the lower Bay region. This shift in dominance reflects changes in known salinity tolerances of these
species, as demonstrated by the canonical correlation analysis. However, this pattern also suggests the likelihood that the ultimate fate of secondary production in the Chesapeake Bay ecosystem is likely dependent on the salinity distribution in the Bay. Thus the balance of freshwater input and marine inflow determine whether the production is internalized within the system (high run-off years leading to high white perch abundance) or potentially exported out of the system (low run-off years leading to high croaker abundance).

Jung and Houde (Jung and Houde 2003) clearly demonstrated the importance of the environmental oxygen levels in controlling the distribution and abundance of fish. These findings were reinforced by the analysis of the CHESFIMS data. Environmental oxygen exhibited its influence orthogonally to salinity, and in opposition to season. In addition, Jung and Houde found that summertime baywide fish biomass was strongly negatively linearly related to summertime environmental oxygen concentrations. This unexpected finding suggested that fish biomass could be expected to be lower under conditions of more favorable oxygen concentrations. They hypothesized that the pattern they reported indicated higher levels of community respiration under more favorable oxygen environments, thereby leading to an increased volume of hypoxic water during the strongly stratified summer months. We repeated this analysis using the CHESFIMS database. A negative relationship was found between baywide fish biomass and depth-averaged oxygen concentration during summer, but this relationship was not as strong or as compelling as that reported by Jung and Houde. Inspection of the results suggest the weaker pattern results from unexpectedly low biomasses for the measured oxygen concentration in 2002 and 2003. We extended Jung and Houde’s analysis by considering the correlation between fish biomass and oxygen in September. Surprisingly, this relationship exhibited an opposite sign to that found in summer. The striking change in the sign of the correlation points to a need to understand the role of the spatial and temporal distribution of oxygen in the Chesapeake Bay on the production and distribution of fish. We suggest several alternative hypotheses. First, the reported patterns may simply reflect differential vulnerability to the midwater trawl caused by differences in the distribution of oxygen. The mid water trawl has lower efficiency in the bottom waters. Thus if oxygen concentrations served to alter only the vertical distribution of fish and not their overall abundance, then period of low DO would result in a higher fraction of the fish assemblage being vulnerable to the midwater trawl. This
hypothesis could be tested by examining regional relationships between sub pycnocline oxygen and catch. If the hypothesis is correct, there should be a negative relationship between these two variables. Alternatively, environmental oxygen levels might, as Jung and Houde hypothesized lead to higher production at higher DO levels. This would increase the rain of organic materials to sub-pycnocline levels, thereby leading to an overall decline in DO. If this hypothesis is correct, water column stratification should be a significant covariate in the relationship between fish biomass and DO. At stations were stratification is weak, we should find the expected positive relationship between fish biomass and Do, and the slope of this relationship should become increasing more negative as the stratification index increases.

The analyses reported herein have been conducted at a coarse spatial scale. We have designated only regional level spatial variation. However, it is likely that there is considerable finer scale spatial pattern. Analysis at a finer spatial scale has the potential to develop predictive models of fish abundance from environmental covariate using General Additive Models (Curti 2005, Jensen et al. 2005). More significantly, geostatistical approaches to interpolating the distribution of abundance offer the possibility of more reliable estimates of abundance than are possible from traditional design-based approaches (Jensen and Miller 2005, Jensen et al. 2006). It is envisaged that both approaches will be applied to the CHESFIMS data for selected species. Not only do the model-based geostatistical approaches offer the potential of developing abundance indices, but they also offer the potential of yielding insight into the likely spatial overlap of predators and prey. This is an important requirement for estimates of trophic demand and predator-prey interactions that are the foundation for ecosystem-based approaches to fisheries management (CFEPTAP 2004).

In summary, we have documented patterns of spatial and temporal variability in the fish assemblage of the Chesapeake Bay. These patterns suggest important differences in the fate of secondary production regionally, and potentially inter-annually. Moreover, we have also documented the relationship between environmental oxygen and fish biomass. However, these analyses are merely exploratory. More detailed analyses of the combined TIES and CHESFIMS data would be beneficial to distinguish real pattern from methodological differences. Such analyses are forthcoming.
3.5 LITERATURE CITED

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Table 3.3. Results of canonical correspondence analysis of station level average environmental conditions, and the composition of the catch

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Unconstrained Eigenvalues

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Percent variation explained

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Tests of Factor Significance

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Figure 3.1. Scatterplot of baywide average physical conditions for the 17 CHESFIMS cruises. Lines are loess fits to the data, and are shown for illustration only.
Figure 3.2 The distribution of stations visited during CHESFIMS from Spring 2001 – Autumn 2006.
Fig. 3.3. The distribution of fish per tow in CHESFIMS survey tows from Spring 2001 – Autumn 2006
Fig 3.4. Annual species composition in fish biomass (CPUE – g.min-1) based on MWT collections during CHESFIMS cruises from Spring 2001- Autumn 2006
Fig 3.5. Seasonal species composition in fish biomass (CPUE – g.min⁻¹) based on MWT collections during CHESFIMS cruises from Spring 2001- Autumn 2006
Fig 3.6. Regional species composition in fish biomass (CPUE – g.min-1) based on MWT collections during CHESFIMS cruises from Spring 2001- Autumn 2006
Fig. 3.7. The distribution of species richness based on MWT collections during CHESFIMS cruises from Spring 2001 - Autumn 2006
Fig. 3.8 The distribution of species richness per cruise based on MWT collections during CHESFIMS cruises from Spring 2001-Autumn 2006
Fig. 3.9  K-dominance curves for A) abundance and B) biomass based on MWT collections during CHESFIMS cruises from Spring 2001- Autumn 2006. Note data are color-coded by season: springtime cruises are shown in blue, summer cruises are shown in red, and autumn cruises in orange. All cruises conducted in the same year have the same symbol.
Fig. 3.10  K-dominance curves by region for A) abundance and B) biomass based on MWT collections during CHESFIMS cruises from Spring 2001- Autumn 2006. Note data are color-coded by region: upper bay data are shown in turquoise, mid bay in blue, and lower bay in green.
Fig. 3.11. Results of a canonical correlation analysis of CHESFIMS MWT and CTD data. Symbols represent individual MWT hauls.
Figure 3.12. Relationship between baywide average catch per unit effort (g.min⁻¹) and depth-weighted dissolved oxygen for A) July and B) September. The relationship for July was CPUE = 497.36 – 64.08* Oxygen, n=5, r²=0.15, p=0.539. The relationship for September was CPUE = -719.46 +125.31 * Oxygen, n=6, r²=0.49, p=0.07.
Chapter 4

FISHERY-INDEPENDENT MULTISPECIES ASSESSMENT OF THE FISH ASSEMBLAGE IN THE PATUXENT RIVER, MD

Thomas J. Miller and David A. Loewensteiner

Chesapeake Biological Laboratory

University of Maryland Center for Environmental Science

Solomons, MD 20688
4.1 INTRODUCTION

Fisheries in the Chesapeake Bay contribute significantly to U.S. catches at the national and regional levels. Recent National Marine Fisheries Service (NMFS) statistics indicate that between 250,000 - 350,000 metric tonnes (t) of fish and shellfish are harvested annually from Chesapeake Bay waters, with a dockside value of more than $100 Million (Miller 2006b). Maintaining the health of these fisheries is an important but difficult task given the considerable interannual variability in catches of component species. Scientists, managers and the general public recognize that species targeted by fisheries are components of complex ecosystems, whereby the removal of individual targeted species may have ramifications for the entire system (Kaiser and Jennings 2002). These changes in ecosystem function or health may impact the sustainability and profitability of multiple fisheries simultaneously. Yet, fisheries management techniques were developed for the single species case (Smith 1994). This is true of exploited species in the Chesapeake Bay for which all exploited species are managed on a single species basis under the aegis of The 1987 Chesapeake Bay Agreement.

In 1996, Miller et al. conducted a literature review and synthesis of information to determine whether the forces that have motivated the development of multispecies approaches in other regions were present in the Chesapeake Bay. They concluded that both biological and technical interactions were present in Chesapeake Bay fisheries. Several species harvested from Chesapeake Bay are either potential competitors (e.g., striped bass *Morone saxatilis*, bluefish *Pomotomus saltatrix*, and the weakfish *Cynoscion regalis*) or predators and prey (e.g., striped bass and menhaden *Brevoortia tyrannus* and
Atlantic croaker *Micropogonias undulatus*, and thus their fisheries may experience biological interactions. Additionally, several fisheries, notably the pound net, are inherently multispecies by nature, and thus technical interactions also clearly exist in Chesapeake Bay (Miller et al. 1996).

Houde et al. (1998) reported the recommendations of workshop to explore the utility and advisability of adopting multispecies approaches in Chesapeake Bay. The workshop report indicated that adoption of multispecies fisheries management would bring the regulation of fisheries in line with the ecosystem-level focus of the Chesapeake Bay Program. Many participants felt that explicit recognition of species interactions, bycatch concerns, competing users, and habitat issues is needed to move fisheries toward a multispecies management ideal that will be desirable in the future. Several important conclusions were reached during the workshop. The workshop participants recommended that coordinated, baywide surveys be performed to estimate key species abundances and that biological data on both economically and ecologically important species that are currently lacking be obtained (Houde et al. 1998). These surveys should form a vehicle within which to estimate the temporal and spatial dynamics of key predator-prey relationships and trophic interactions (Houde et al. 1998).

Several fishery-independent surveys for the assessments of important fish and shellfish stocks in the Chesapeake Bay are currently ongoing. The Virginia Trawl survey has been conducted and regularly expanded since the 1950's, so that it now encompasses all of the main tributaries and the mainstem of the Chesapeake Bay in Virginia. The data
are widely available (www.fisheries.vims.edu/vimstrawldata/), and have been utilized in the assessment of several key species. Similarly, striped bass seine surveys have been conducted since 1954. These surveys conducted in both Maryland and Virginia focus on sampling recruiting juvenile striped bass in tributaries to the Chesapeake Bay. However, other species, common in the littoral zone, are also sampled in this survey. In response to gaps in survey coverage, the NOAA Chesapeake Bay Office funded two, Baywide surveys. The Chesapeake Bay Fishery Independent Multispecies Survey (CHESFIMS) built on from an early NSF-funded study of the fish production in the Chesapeake Bay. CHESFIMS. This survey samples all species of fish in the benthic-pelagic realm, but focuses on anchovy and year-of-year of commercially important species. Likewise, the Chesapeake Bay Multispecies Monitoring and Assessment Program (CHESMAP - http://www.fisheries.vims.edu/chesmmap/) samples the fish community on a baywide basis, but focuses on commercially-important sizes of fish. Together these two programs provide a synoptic view of the entire fish community in the mainstem of the Chesapeake Bay.

The tributaries of the Chesapeake Bay are important features for the ecology of many fishes that utilize the Bay. Anadromous fish utilize the tributaries for spawner and they serve as important nursery areas for many such species (Secor and Houde 1995). Other species use the tributaries as feeding areas later in the year (e.g. menhaden and Bay anchovy – Thomas Miller, pers. Comm). Tributaries in the Virginia portion of the Chesapeake Bay are extensively sampled as a part of the VIMS trawl program. This sampling platform has lead to considerable insight into the dynamics of fish in
Chesapeake Bay tributaries. However, no systematic effort has been mounted to assess the importance of tributaries in the Maryland portion of Chesapeake Bay. Maryland tributaries are sampled as a part of the juvenile striped bass survey, but this focuses on shallow littoral habitat. Earlier work associated with the permitting of power generation plants on several tributaries do provide data on the fish community and patterns of habitat usage in the 1960s. For example, McErlean et al. (1973) report the results of an extensive four year sampling program involving seines, beam trawls and otter trawls in the Patuxent River. They report clear cycles in seasonal diversity in the River during the period of study (Summer 1963 – Spring 1967), with peaks in diversity in the Spring associated with the immigration of anadromous species, and lower diversity in the Winter. Even though these studies were extensive, they focused on patterns in fish abundance and did not provide an ecosystem context for their work.

Here we report on a one-year study of the fish community in the Patuxent River, MD. The objectives of the study were to conduct frequent sampling of the fish community, using gear that parallel those being used in the mainstem of the Chesapeake Bay by the CHESFIMS survey, to quantify patterns of movement, production and trophic dependencies in the river, and between the river and the mainstem. Thus the study was termed PAXFIMS. The objectives of the program were (i) to conduct a temporally-intensive survey pelagic and epi-benthic fish community, focusing on young (juveniles, and yearling) fishes in the Patuxent River and (ii) to determine trophic interactions among key components of the pelagic fish community, and examine the implication of the relationships uncovered in empirical studies using bioenergetic modeling.
4.2 METHODS

4.2.1. Field Methods

Survey work was conducted year round from January 2004 – February 2005. Cruise scheduling was based on the thermal regime in the river (Fig. 4.1). The average temperature cycle in the mesohaline section of the river varies from a low of 2.6°C in the fifth week of the year (February) to 27.6°C in the 31st week of the year (August). When the expected daily temperature change in the river is plotted, two broad peak rates of temperature change are apparent (Fig. 4.2). Using the 2°C.day⁻¹ isoline as a criterion, the weeks of peak change are between weeks 9 - 22 in the spring, and between weeks 39 - 49 in the autumn / winter. Accordingly the 14 planned surveys were scheduled to focus most heavily on these times when temperature changes are most rapid. This scheme resulted in more frequent surveys in the periods of rapid change during spring and autumn when the system is expected to change most rapidly. All surveys were conducted from the University of Maryland Center for Environmental Sciences’ RV Aquarius. An engine failure on the fourth cruise forced us to abandon the cruise. Delays produced by the necessary repairs precluded any rescheduling of ship time.

All surveys were conducted from the University of Maryland Center for Environmental Sciences’ RV Aquarius. Each survey was conducted as a completely randomized design. Twenty stations were randomly selected based on river kilometer, and distributed from Solomons to Abingdon Cove. On each survey, we sampled both the pelagic fish community using a midwater trawl, and the benthic community using an otter trawl. We sampled up to 20 benthic stations, and a subset of up to 10 of pelagic stations.
The benthic component of the survey was conducted during daylight hours (~0600 – 1700) of the first day, and the midwater trawl was deployed during nighttime (~1900 – 0500) on the evening of the second day. The midwater trawl had a mouth opening of 5.7 x 4 m, an 3.8 – 7.6 mm mesh body, and an 3 mm mesh cod-end. The net was instrumented with depth-temperature loggers on the head rope and the foot rope during all deployments. These data were used subsequently to calculate the deployment profile and average net opening for all deployments. The midwater trawl was fished in a single, stepped oblique tow for 10 minutes. Where station depth permitted the net was held at each of 10 depth intervals for 1 minute, to ensure the entire water column was sampled. At shallow stations the number of depth intervals was adjusted according to conditions. The benthic survey employed a 9m semi-ballon otter trawl with 38 mm mesh in the body and 7mm mesh in the cod end. The trawl was equipped with a tickler chain. This net was fished for 5 minutes on the bottom at 1kn. Following all deployments the water column was profiled with a SEABIRD SBE 25 CTD which recorded temperature, salinity, depth, fluorescence profiles for the station.

All fish and crabs collected in the midwater and otter trawls were identified, enumerated, and the total weight for each species recorded. For species with high levels of abundance, random sub-samples of between 30-100 individuals were measured for length and preserved on ice for subsequent dietary analysis. For less abundant species, the entire catch was measured for length and preserved. All fish were handled according to procedures approved by the University of Maryland Center for Environmental Sciences’ Animal Care and Use Committee.
4.2.2. Laboratory Methods

In the laboratory, individual fish were thawed and their individual length and fresh weight determined. The stomach (between the oesophagus and the pyloric sphincter) was removed and weighed. A qualitative assessment of the stomach fullness was made. The stomach was then opened, and its contents transferred to a clean glass Petri dish. The empty stomach was reweighed. The stomach contents were identified the lowest taxonomic level practical. For large prey items, the weight and size of individual prey were determined. For smaller prey items, the bulk weight and where possible to the total number of prey were determined.

For selected species the age of fish in the sub-sample was also determined. Ageing was based on otolith section readings. For fish assumed to be age 1+ the otolith was mounted in Spurr resin, sectioned through the core using a South Bay Technologies Wafering Saw to yield a thin (~ 1mm) section. The number of annulae in the section was determined under a dissecting microscope at 40X magnification. Each otolith was read twice, blind to improve aging accuracy. For YOY fish, individual otoliths were mounted in Spurr resin, sectioned through the core, mounted and polished using a graded series of polishing media and read at 400 – 1000X under a compound microscope.

4.2.3. Statistical Analysis

4.2.3.1 Abundance and distribution

Catches per station for individual species were converted to catch per unit effort (CPUE) by dividing either the catch in number or weight by the duration of the tow.
Mean (±SD) CPUEs were calculated for each survey as the simple average of station CPUE. A general linear model was fit to the CPUEs for each species to assess whether CPUEs were significantly different among cruises. Station-specific CPUEs were considered independent observations.

Two approaches were used to quantify the distribution of each species. Simple bubble plots were generated for each species where the area of the bubble is directly proportional to CPUE at the station. The plots were inspected visually to describe changes in the spatial distribution of each species. Additionally, two-stage general linear models were used to quantify the impacts of temperature, salinity and dissolved oxygen on the distribution of each species (Jensen et al. 2005). This modeling approach identifies the effect of the environmental variables on predicting presence (1st stage) and subsequently on predicting abundance given presence (2nd stage). The model uses penalized regression splines to describe the response of either presence or abundance given presence (Wood and Augustin 2002). Independent fits are estimated for each stage of the model. Thus, each environmental variable can affect presence and abundance differently. The first stage of the model can be described as

\[
P(\text{presence}) = s_1(\text{temperature}) + s_2(\text{salinity}) + s_3(\text{DO}) + \varepsilon
\]

Where the s’s are spline fits for each environmental variable. Similarly the second stage of the model is given by

\[
\text{Abundance} = s_4(\text{temperature}) + s_5(\text{salinity}) + s_6(\text{DO}) + \varepsilon
\]
The individual s terms reflect the degree of non-linearity in the responses. Values of s=1 indicate a linear fit, values greater than 1 indicate increasing non-linearities.

4.2.3.2. Size distributions and growth

Estimates of individual total lengths, measured on the vessel, were used to construct size distributions. Distributions were developed for individual cruises, without regard to the location of fish within the river on that cruise. Distributions were developed for midwater and bottom trawls separately where possible.

Length frequency distributions were analyzed using model-based, hierarchical clustering as an approach to modal analysis. The analysis identified the mixture of Gaussian distributions that best described the observed length frequency. An iterative expectation-maximization method was used to provide the maximum-likelihood estimate of a suite of parameterized Gaussian mixture models. The algorithm used a Bayesian Information Criterion to determine the number of distributions in the mixture. The algorithm was implemented using the EMClust package within R.

Based on the fitted mixture model, the modes from individual cruises were related longitudinally to provide estimates of growth. Mean sizes of appropriate modes were plotted against the mid-date of the cruise to develop approximate growth curves.
4.3 RESULTS

We completed 11 cruises over a 12 month period. One of the cruises had to be abandoned because of an engine failure on the research vessel (Table 4.1). Given the way in which the sampling was tied to the thermal regime in the river, it was not possible to reschedule this cruise.

4.3.1 Abundance and distribution

Bay anchovy was the most abundant species collected in trawls during the PAXFIMS cruises. The average catch per unit effort in the midwater trawl was 26.2 fish.min⁻¹ (19.9 g.min⁻¹). The equivalent catches in the bottom trawl were substantially lower (3.45 fish.min⁻¹; 5.66 g.min⁻¹) reflecting differences in selectivity between the two gear. Catches in both gear varied over the course of the year. Figure 4.4 shows the seasonal pattern of CPUEs in the midwater trawl. Patterns were similar, although lower in the bottom trawl. CPUEs were significantly different in the midwater trawl (F₉,₁₀⁹=13.28, p<0.001) and bottom trawl (F₁₀,₁₅₈=3.46, p<0.004). The increase in abundance evident from late summer to late autumn represent the recruitment of anchovy spawned that summer to the gear.

The seasonal distribution of bay anchovy indicated a broad distribution from April – December (Fig. 4.5). In the initial winter surveys, bay anchovy was confined to the stations near the confluence of the Patuxent River and the Chesapeake Bay (Fig. 4.5). Recruitment of the new year class was evident in the distributions, but recruitment did not appear to be spatially concentrated as it was in white perch. Bay
anchovy remained abundant in midwater trawl catches throughout the remained of the year.

Application of two-stage GAMs to the distribution of bay anchovy indicated significant effects of environmental variables on the distribution of bay anchovy in the Patuxent River. The first stage GAM which seeks to predict presence of bay anchovy at individual locations. Results indicated significant contributions of bottom temperature, salinity and dissolved oxygen to forecasting presence (Table 4.2). Overall the model 37.3% of the deviation in the data. Spline fits for individual environmental parameters were variable (Fig 4.6). The fit for temperature indicated bay anchovy abundance was a linear increasing function of temperature, but a linear decreasing function of salinity. There was an indication of a broad peak in abundance with respect to dissolved oxygen of approximately 7-8 mg/L. (Fig 4.6).

The second stage of the GAM for bay anchovy seeks to predict abundance given presence in the sample. All three environmental parameters were again assessed for their contribution to the predictive ability of the mode. Results indicated a significant effect of temperature and dissolved oxygen, but not of salinity. Overall the model 37.9% of the deviation in the data. Spline fits for individual environmental parameters were variable (Fig 4.7). The fit for temperature indicated bay anchovy abundance was a linear increasing function of temperature, but a linear decreasing function of salinity. There was an indication of a broad peak in abundance with respect to dissolved oxygen of approximately 7-8 mg/L. (Fig 4.7).
The GAM analysis of the bottom trawl data was used to predict catches in the midwater trawl to examine the forecasting ability of the GAM. The forecasting ability of the GAM should be judged by the $r^2$ value rather than a direct comparison of observed and predicted values. The Pearson correlation between observed and predicted was $r=0.43$, indicated that the GAM could explain just over half of the variability in the observed catches of white perch in the midwater trawl. The relationship between the two variables is shown in Figure 4.8.

White perch was the next most abundant species collected in trawls during the PAXFIMS cruises. White perch CPUEs were higher in the bottom trawl than in the midwater trawl. The average catch per unit effort in the bottom trawl was 9.68 fish.min$^{-1}$ (608.6 g.min$^{-1}$). The equivalent catches in the midwater trawl were substantially lower (3.55 fish.min$^{-1}$; 261.1 g.min$^{-1}$) reflecting differences in selectivity between the two gear. Catches in both gear varied over the course of the year. Figure 4.9 shows the seasonal pattern of CPUEs in the midwater trawl. There was no clear seasonal pattern in total CPUE either expressed in number or weight. Although, because the midwater trawl selects for smaller sized individuals, this gear was able to detect the pulse of biomass of white perch recruits (Fig. 4.10). CPUEs were not significantly different through the season either in the midwater trawl ($F_{9,109}=0.82$, $p<0.6$) and bottom trawl ($F_{10,77}=0.96$, $p<0.4$).

The distribution of white perch changed over the course of the surveys (Fig 4.10). Initially, the perch were distributed downriver toward its confluence with the Chesapeake
Bay. By March, adults had started to move upstream. The center of mass of the perch
distribution remained in the upper portion of the sampling domain until reproduction in
early summer. Young-of-year white perch gradually became dispersed throughout the
Patuxent, until the species was almost uniformly distributed throughout the river but early
Autumn.

Application of two-stage GAMs to the distribution of white perch indicated
significant effects of environmental variables on the distribution of white perch in the
Patuxent River. The first stage, which seeks to predict presence of white perch in bottom
trawl catches, indicated significant contributions of bottom temperature and salinity to
forecasting presence, but not of bottom oxygen. Overall the model explained 31.8% of
the deviation in the data. Spline fits for individual environmental parameters were
variable (Fig 4.11). The fit for temperature indicated a peak of predicted presence at
about 10°C. Spline fits forecasting white perch presence for salinity was linear, with
higher probabilities of presence at lower salinities (Fig 4.11).

The second stage of the GAM for white perch seeks to predict abundance given
presence in the sample. All three environmental parameters were again assessed for their
contribution to the predictive ability of the mode. Results indicated a significant effect of
both temperature and salinity, but no significant effect of dissolved oxygen. Overall the
model did not explain a substantial fraction of the deviation in the data. Spline fits for
individual parameters were broadly similar to those observed in stage I, with a non-linear
spline for temperature, and broadly linear effects for salinity and oxygen (Figure 4.12)
The GAM analysis of the bottom trawl data was used to predict catches in the midwater trawl to examine the forecasting ability of the GAM. The forecasting ability of the GAM should be judged by the r^2 value rather than a direct comparison of observed and predicted values. The Pearson correlation between observed and predicted was r=0.51, indicated that the GAM could explain just over half of the variability in the observed catches of white perch in the midwater trawl. The relationship between the two variables is shown in Figure 4.13.

### 4.3.2 Size distributions and growth

The E-M clustering algorithm provided an adequate fit to the observed length frequency distributions in the midwater trawl (Fig. 4.14). The algorithm identified a single mode in the length frequency distributions for PF0402, PF0403 and PF0406. A second mode was identified in PF0405, but it was not felt to be reliable as it accounted for only 3% of the observed catch (Table 4.2). Thus, overall the model represented the bay anchovy population as being comprised by a single age class from March – June. This is in line with what is known about the reproductive biology of bay anchovy. The average of the single mode increased from 44.6 mm TL on March 4, 2004 to 66 mm TL on June 16, 2004 (Table 4.2). These data suggest a growth rate for this cohort during this period of 0.21 mm.day^-1.

Subsequently, the algorithm identified two clear modes in the length frequency distributions for cruises PF0407 - PF0411 (Fig. 4.14). The smaller size mode
reflects the recruitment of young of year bay anchovy, likely spawned in the mainstem of the bay in June and July, to the survey gear. This mode was first observed in August when it comprised 86% of the observed length frequency distribution. The proportion of the population represented by this mode remained approximately constant throughout the remainder of the survey. The size of this mode increased from 39.6 mm TL in August to 49.4 mm TL in November, yielding an estimated growth rate of 0.11 mm.day-1.

Length frequency fits for bay anchovy collected in the bottom trawls were not as compelling as those observed for the midwater trawl. For bottom trawl length frequencies, insufficient numbers of fish were caught in PF0402, PF0403, and PF0412. Even in other cruises, abundances were low compared to midwater trawl catches. Accordingly, no further analysis of these data will be presented.

Length frequency fits to white perch data from the bottom trawl and midwater trawl were similar. The bottom trawl length frequencies will be the focus of the discussion that follows, and midwater trawl data will only be referenced if it contrasts with or provides additional support for the bottom trawl patterns. The E-M clustering algorithm provided an adequate fit to the observed length frequency distributions in the bottom trawl (Fig. 4.15). The algorithm identified a minimum of two distributions in all of the length frequencies, except that for PF0410 (Table 4.3). This was similar in the midwater trawl length frequency modeling, except that it was PF0409 that was found to comprise a single mode. A third, smaller mode was initially identified in PF0405 in the midwater trawl and in PF0406 in the bottom trawl length frequencies (early June). This mode was detected intermittently until the end of the surveys in December. It represents the production and recruitment of young of perch to the river. The size modes that
dominate length frequencies for the bulk of the sampling reflect separate age classes. The smaller of the two modes (mean size = 88mm TL in March) are the survivors from the 2003 year class. The larger and broader size mode (mean size = 177mm TL in March) likely represents a mixture of age classes from earlier years.

Individual size modes were assigned to putative year class to permit a rudimentary growth analysis (Fig. 4.16). Simple linear regressions fitted to size at date of capture data were used to estimate daily growth rates. These analyses indicated that the Age-0 fish (2004 year class) were likely growing at 0.23 mm.day-1 from late summer to early winter. The age-1 fish (2003 year class) appeared to be growing approximately linearly throughout the year. Linear regression of length on date of capture provides an estimated growth of 0.19 mm.day-1. The mixed age-2+ mode shows no steady increase in size during the survey, indicating that these fish have attained approximate maximum size.

4.3.3. Multivariate Analyses

A non-metric multidimensional scaling analysis was able to detect differences in the fish community caught in the midwater trawl. The two-dimensional ordination had a low stress value (Fig. 4.17), indicating that there were clear groupings, but the fact that the stress value was not equal to zero indicates that there residual variation, not explained by the ordination still remains. Inspection of Fig. 4.17 reveals a clear seasonality in the ordination of stations, suggesting a clear seasonality in the midwater trawl catches. In general “winter” cruises, i.e., those conducted in March, April and December are clustered in the lower left of Fig. 4.17, whereas, “summer” stations are
in the top right. A cluster analysis of these data however, did not indicate distinct

groupings of stations by cruise, suggesting the existence of a substantial amount of non
seasonal pattern in the data set. Some of this variability can be explained by patterns in
the catches of individual species. For example, Fig 4.18 shows the CPUE of bay anchovy
overlain on the nMDS ordination. From this plot it is clear that stations with a high
anchovy catch are found in the upper right corner of the ordination. A similar pattern
results for other species with higher salinity affinities, e.g., croaker and weakfish.
Conformation plots using white perch and hogchoker (Fig. 4.19) as representative of
freshwater and mesohaline end members further clarify that salinity is another dominant
response in the nMDS ordination. A broadly similar pattern was evident in an nMDS
analysis of the catches in the bottom trawl portion of the survey, and are thus not
presented here.

To further explore the pattern in the distribution of catches a PCA was used. The
first three axes of the ordination explained 88% of the variability in the data (Table 4.5).
The loadings indicate that temperature was strongly positively correlated with the first
PCA axis, whereas salinity exhibited no correlation with this axis. Conversely, salinity
was highly correlated with the second principal component axis, whereas temperature
exhibited only a weak correlation with this axis. The relationships between the data and
their loadings is exhibited in Figure 4.20
4.4 DISCUSSION

We conducted a year-long survey of the fish community in the Patuxent River as part of an initiative to support the increased sampling needs for ecosystem-based approaches to fisheries. The results of the work indicate the potential for a single multispecies survey to replace ongoing single species approaches. However, given that we have only a single year of data, further parallel sampling would be required to determine whether the temporal pattern in existing single species surveys is replicated in the multispecies approaches.

As expected, there was a strong seasonal pattern in survey catches. The seasonality was evident in time series of catches of individual species (such as bay anchovy and white perch) and in the multivariate analysis where water temperature proved to be the dominate factor in explaining the ordination of survey catches. In most cases the seasonal response evident in the data resulted from recruitment of juvenile fish to either the midwater or bottom trawls, as evidenced by both the bay anchovy and white perch data. The second most important factor explaining the distribution of catches was salinity, or river mile. Again, this should not be viewed as a surprising factor given the strong salinity gradients that characterize estuarine habitats.

Thirty-three different species of fish were collected during the survey overall. Species ranged from freshwater residents such as pumpinkseed sunfish (*Lepomis gibbosus*) to marine end members such as the harvest fish (*Peprillus alepidotus*). However, although the diversity was relatively high, the distribution of abundance was not even. In midwater trawl catches, the top ten species accounted for 99% of total
average catch per effort. Within this group, bay anchovy accounted for 81% of the average CPUE in the midwater trawl. Only white perch, which accounted for 10% of the remaining average CPUE was anywhere near as abundant. The eight other relatively abundant species were hogchoker, coraker, blue crab, spot, weakfish, striped bass and brown bullhead. The pattern was similar in the bottom trawl component of the survey, although less marked. In bottom trawl catches, the top ten species still accounted for 98% of the total average CPUE. However, the most dominant species in bottom trawl catches, white perch, only accounted for 58.1% of the total average CPUE. Bay anchovy accounted for an additional 21.5% of the total average CPUE – together combining for 79% of the total average CPUE. Hogchoker, Atlantic croaker, blue crab, spot, weakfish, striped bass and brown bullhead completed the top ten most abundant species in the bottom trawl survey.

We employed a complemented survey involving both a midwater trawl and a bottom trawl. The intent of using both gear was to fully capture the entire fish community in the River. In previous surveys where only a single gear had been used, concern had been expressed over gear avoidance. Concerns similar to these are what motivated McEarlean et al to use a bottom trawl, beam trawl and seine in their survey of the Patuxent River (McErlean et al. 1973). However, as can be seen by the summary provided above, the relative indices of community composition were not sensitive to the gear used. Thus, if one seeks only to develop a community metric to serve as an indicator of overall status a single gear will likely suffice.
We explored the application of general additive models to predict the distribution and abundance of individual fish species (Jensen et al. 2005). In general these models had relatively low predictive power. It is likely that the relatively linear nature of the Patuxent River system accounts for the lack of success of these applications, which have been successful elsewhere. GAMs were dominated by relatively linear salinity and temperature terms, reflective of the one dimensional nature of the environment. However, the results of the model also indicated the broad similarity of the samples in the midwater and bottom trawls.

We were more successful in using multi-modal size decomposition algorithms to provide estimates of the growth of the principal species collected in the survey. The approach used did not rely on directly ageing individual fish, but rather makes the assumption that the modal assignments remain constant through time, so that one may use the time different between samples, and modal means as surrogates for size at age. Using this assumption, our analysis showed the presence of two distinct cohorts of croaker recruiting to the Patuxent River in 2004. It is not clear whether this is a consistent feature of recruitment of croaker to the river or simple a feature of the pattern for 2004. However, it is known that the recruitment of croaker to the Chesapeake Bay system generally is tied to meteorology (Montane and Austin 2005), suggesting that the presence of multiple recruiting cohorts may be a common feature of the system. The growth rates of the two cohorts appeared to differ substantially. The first cohort grew at approximately 1 mm.day, whereas the later cohort appeared to have recruited to the river and ceased growing perhaps due to declining water temperatures. The modal size
analysis approach was also capable of estimating growth rates of different year classes in some species as well as in different cohorts. For example, in white perch we were able to identify three different age classes, age-0, age-1 and age 2+ as well as estimate growth rates for each year class. The youngest age class was growing most rapidly (g=0.231 /day), whereas the oldest age class had a very low growth rate (g=0.06 /d). These estimates are in line with what is known of the growth of this species.

The survey was designed to sample more often during times of rapid temperature change in the river, as it was suspected that this was when the community would be changing most rapidly. The sampling scheme did not appear to provide any advantage in terms of increased resolution in community structure. In part, this may have resulted from the vessel engine failure in the proposed PF04 survey in mid May. This survey may have provided a clearer pattern. However, it is more likely that the dynamics of the system are driven by the production arising during summer and early autumn than by changes in temperature per se. This would suggest that subsequent surveys concentrate more effort in the July – September period, reducing effort in the early spring months. During these early surveys catches and diversity were low and the effort did not provide much resolution of community structure. Investment of some of the effort expended in early cruises to increase the number of stations on individual cruises, or by adding additional cruises during the Autumn months would have been preferred.

In summary, we completed a complemented survey of the Patuxent River to collect data in support of ecosystem-based fisheries management. The survey was
capable of providing estimates of relative abundance of numerous fish species during a single calendar year. Estimates of absolute abundance could not be developed from the data. Additional survey work would be required to determine whether a single multispecies survey could replace the multitude of single species surveys currently employed by regional agencies in support of fisheries management. Of additional benefit, samples collected during the survey have been retained and are currently undergoing age and diet analyses. It is anticipated that these data will be available within the next 6-12 months, and they will provide additional useful information for parameterizing food-web based ecosystem models.
4.5. LITERATURE CITED

Literature Cited


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Secor DH, Houde ED (1995) Temperature effects on the timing of striped bass egg production, larval viability, and recruitment potential in the patuxent river (chesapeake bay). Estuaries 18:527-544


Table 4.1. Schedule of cruises conducted as a part of the PAXFIMS program

<table>
<thead>
<tr>
<th>Cruise</th>
<th>Dates</th>
<th>Number of Stations</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Beginning</td>
<td>Ending</td>
</tr>
<tr>
<td>PF0401</td>
<td>1/22/2004</td>
<td>1/22/2004</td>
</tr>
<tr>
<td>PF0404</td>
<td>Abandoned due to engine failure on vessel</td>
<td></td>
</tr>
<tr>
<td>PF0409</td>
<td>10/5/2004</td>
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<td>10/22/2004</td>
</tr>
<tr>
<td>PF0412</td>
<td>11/30/2004</td>
<td>12/2/2004</td>
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Table 4.2. Results of analysis of length frequencies of bay anchovy in the midwater trawl for each cruise. Modes are fitted by maximum likelihood methods

<table>
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<tr>
<th>Cruise D</th>
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<td></td>
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<td>61.560</td>
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Table 4.3. *Results of analysis of length frequencies of white perch in the bottom trawl for each cruise. Modes are fitted by maximum likelihood methods*

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<tr>
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<th>Weighted average length (mm)</th>
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</thead>
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<td></td>
<td></td>
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<td>Mean</td>
<td>Variance</td>
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Table 4.4. Results of PCA analysis of environmental data from midwater trawl

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<th>PCA 3</th>
<th>PCA 4</th>
<th>PCA 5</th>
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<tr>
<td>Standard deviation</td>
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<td>1.097</td>
<td>0.961</td>
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<td>Cumulative Proportion</td>
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Loadings:

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<th>PCA 3</th>
<th>PCA 4</th>
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Figure 4.1. Average seasonal temperature and salinity for the Patuxent River (1985 – 2001) based on CBP monitoring data.
Figure 4.2. Rate of change of temperature in the Patuxent River (data from Figure 1.) Sampling intensity shown in bottom panel – see text for details
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CHAPTER 5:

DISTRIBUTION AND DIET OF ATLANTIC CROAKER *MICROPOGONIAS UNDULATUS* IN CHESAPEAKE BAY

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5.1 INTRODUCTION

The relative effect of biotic and abiotic factors in determining the distribution and diets of organisms is a fundamental question of ecology. The distribution and abundance of an organism is ultimately determined by its ecological niche. Hutchinson (1957) was the first to describe and stress the importance of the multifaceted niche as the ecological space in which an organisms lives building on the works of Grinell (1917) and Elton (1927). While Grinell (1917) was the first to use the term "niche" to describe the geographic location of an organism in its environment, Elton (1927) emphasized food availability and predators in determining the ecological niche of a species. Hutchinson in a sense combined the ideas of these and other works and conceived the ecological niche as defined by many biotic and abiotic variables. As such he defined a niche as a multifaceted "hypervolume" or a multidimensional space occupied by an organism.

Estuaries are good places to study to understand the complexities of niche theory. These highly dynamic physio-chemical environments are influenced by energetic tidal flows and wind-induced turbulence with strong seasonal effects and variability in freshwater input (Kennish 1986, Mann and Lazier 1996). Because of their characteristic circulation patterns, there are strong gradients that provide the full spectrum of physical properties that might define an organisms' niche. For example, the full range of salinities are found in estuaries as freshwater rivers and tributaries flowing out of the estuary meet and mix with marine waters flowing into the estuary. Thus, physiological tolerances in defining the niche can be determined. However, estuaries introduce challenges in understanding an organism's niche because these systems are
not closed systems and have strong annual and seasonal changes in temperature, salinity, and even dissolved oxygen.

In estuarine environments three abiotic factors: temperature, salinity and dissolved oxygen, are likely the dominant regulators of fish distributions (Jung 2002, Lankford and Targett 1994, Rueda 2001) and their prey (Bottom and Jones 1990, Seitz and Schaffner 1995). These studies exemplify the rich body of research on abiotic factors that affect species distribution. Although temperature and salinity may influence population abundance and distribution based on the physiology of each species, substrate and habitat structure are also important for fish feeding and may influence distribution (Gibson and Robb 1992, Methratta 2006, Stoner et al. 2001). Such studies are important because they are informative at the scale on which a fishery operates and can be used in management decisions such as delineating essential fish habitat and marine reserves (Methratta and Link 2006). However, few studies exist that attempt to quantitatively delineate which biotic and abiotic factors influence species abundance and distribution.

Atlantic croaker *Micropogonias undulatus*, hereafter croaker, is a common, abundant bottom-associated fish species that is distributed in marine and estuarine systems from the Gulf of Mexico to Delaware Bay (ASMFC 1987). Numerous diet studies have been conducted on croaker. Adult croaker have been described as opportunistic bottom-feeders that occasionally eat small fishes (Murdy et al. 1997, Hildebrand and Schroeder 1928). Young of year (YOY) croaker rely heavily on polychaetes in their diets, but also consume other benthic food such as detritus, nematodes, insect larvae and amphipods (Homer and Boynton 1978, Nemerson 2002, Overstreet
and Heard 1978, Sheridan 1979). Croaker appear to change feeding habits as they get larger, relying more heavily on large organisms such as mysids and fish (Nemerson 2002, Overstreet and Heard 1978, Sheridan 1979). Hildebrand and Schroeder (1928) noted that of 392 fish whose stomach contents were examined only three contained fish. Studies also indicate strong ontogenetic patterns in diets. These data studies suggest less reliance on benthic prey than is typically expected of this demersal Sciaenid (Chao and Musick 1977). Despite many diet studies the trophic ecology of croaker, the ontogenetic, seasonal and spatial patterns in diet remain poorly understood. More significantly, the consequences of this variability have been completely ignored particularly with regard to the spatial distribution and abundance of croaker in the Chesapeake Bay estuary.

The objectives of this study were first, to describe the distribution and diet of croaker in the Chesapeake Bay and secondly, to understand how distribution and diet are related. In quantifying these patterns, I seek specifically to determine the role of abiotic and biotic factors in determining both aspects of croaker ecology. Quantification of the patterns and trends in diet is challenging from both a sampling and statistical view points (Cortes 1997, Tirasin and Jorgensen 1999). No single approach or technique fully captures the spatial and temporal diversity in dietary patterns. Accordingly, I used multivariate analyses to quantify seasonal, regional and inter-annual patterns in diet. Subsequently, I used a two-stage Generalized Additive Model (GAM) to determine biotic and abiotic factors that influence spatial distribution. The first stage of the model predicts the probability of occurrence based on environmental variables using presence/absence data as the response variable. The second stage of the GAM predicts the abundance of croaker using the same explanatory variables that were used in the first stage, but
only using stations where croaker were present. I have used GAMs to relate distribution and diet because they allow for linear and nonlinear relationships between explanatory and response variables. GAMs have been widely used to quantify distributions of estuarine organisms (Jensen et al. 2005, Jowett and Davey 2007, Stoner et al. 2001). However, few have attempted to connect diet and distribution using GAMs to elucidate the relative importance of environmental factors and the prey field to understand how each influences distribution. Using GAMs I hypothesize that 1) croaker presence/absence is determined by physiological tolerances to abiotic factors and, 2) that croaker abundance is influenced by availability of suitable prey. Accordingly, abiotic factors should be the most important factors describing croaker occurrence in the 1st stage of the GAM and biotic factors the most important in predicting croaker abundance in the 2nd stage of the GAM.

5. 2. METHODS

5.2.1. Data collection

Croaker and environmental data were collected from 1995-2005 as part of two fishery-independent sampling programs in the Chesapeake Bay. The Trophic Interactions in Estuarine Systems (TIES) program surveyed the fish community in Chesapeake Bay from 1995-2000 (Jung and Houde 2003). Subsequently, the Chesapeake Fishery-Independent Multispecies trawl survey (CHESFIMS) extended the TIES sampling protocols for the fish community from 2001-2005. In both programs, research cruises occurred over 5-7 day periods three times annually, the only difference being that cruises occurred in May, July, and October from 1995 to 2000 and in May, July, and September from 2001 to 2005. During both programs additional cruises supplemented the three annual cruises opportunistically. The survey design changed very little
during the eleven year time series. Trawl stations in the TIES program were located along 15 fixed transects spaced approximately 18.5 km (10 nm) apart from the head of the Bay to the Bay mouth to ensure bay wide coverage (Jung and Houde 2003). Within each season, 11 of the 15 transects were occupied. Transects were identified as falling within one of three strata: upper, middle, and lower Bay (Figure 5.1).

The individual strata have distinctive characteristics, and their boundaries broadly correspond to ecologically relevant salinity regimes. The upper Bay is generally shallow, with substantial areas less than 5 m in depth, and well mixed waters with high nutrient concentrations. The bottom topography in the mid Bay includes a narrow channel in the middle of the Bay with a stratified water column and broad flanking shoals. This region has relatively clear waters and experiences seasonally high nutrient concentrations and periods of hypoxia. The lower Bay has the clearest waters, greatest depths and lowest nutrient concentrations (Kemp et al., 1999). The strata volumes are 26,608 km$^3$ (Lower), 16,840 km$^3$ (Mid) and 8,664 km$^3$ (Upper). The CHESFIMS sampling design consisted of both fixed and random stations with stations proportionally allocated to strata according to strata volume. Some fixed stations from the TIES program were kept in CHESFIMS sampling for continuity. However, an additional number of stations were randomly allocated based on strata volumes were added to each survey, resulting in a complementary survey design.

Survey deployments throughout the 11-year time series followed the TIES trawling procedures (Jung and Houde 2003) with standardized 20-minute oblique, stepped tows conducted at each station using midwater trawls of the same design. Croaker was one of the
most frequently caught species caught in this time series. A midwater trawl with an 18-m² mouth-opening with 6-mm cod end was deployed to collect primarily pelagic and benthopelagic fishes. Oblique tows of the net were fished from top to bottom, and were 20 minutes in duration. The trawl was towed for two minutes in each of ten depth zones evenly distributed throughout the water column from the surface to the bottom, with minimum trawlable depth being 5 m. The section of the tow conducted in the deepest zone sampled epibenthic fishes close to or on the bottom. The remaining portion of the tow sampled pelagic and neustonic fishes. A minilog was attached to the float line of the net and measured depth, temperature, and time during each tow. The depth profile from the minilog was inspected after each tow to ensure that the trawl was deployed in the manner described above and that the net fished the bottom portion of the water column, important in the case of the demersal croaker. All tows were conducted between 18:00 and 7:00 Eastern Standard Time to minimize gear avoidance and to take advantage of the reduced patchiness of multiple target species at night. At each station, a CTD was deployed to measure dissolved oxygen, salinity, and temperature in the water column.

Catches at every station were identified, enumerated, measured and weighed onboard. For each species, all fish or for large catches a subsample of 50-100 fish were measured (total length in mm). Total weight of the catch of each species was measured. Croaker from the 2002-2005 cruises were collected from each tow when present and were frozen for subsequent processing in the laboratory. At each station, a CTD was deployed to measure dissolved oxygen, salinity, and temperature throughout the water column. Data from the CHESFIMS collections were used to map spatial distributions and describe diets. Data from the combined TIES and
CHESFIMS collections were used to develop two-stage GAM models to predict croaker distributions.

5.2.2. Spatial distribution

To visualize the spatial distribution of croaker, spatial maps of croaker were developed. I modeled adult croaker, defined as croaker greater than 100mm because of sporadic catch and abundance estimation of YOY croaker. There were many stations where no croaker were caught, causing the data to be zero-inflated. Thus, to adequately model the spatial distribution of croaker I used indicator kriging to map the probability of croaker occurrence in the mainstem of the bay. Indicator kriging changes abundance data into presence/absence data and does not require the data to meet the assumptions of normality or stationarity (Chica-Olmo and Luque-Espinar 2002). The abundance variables are transformed to categorical presence/absence variables before the kriging process by picking a threshold level, in this case an abundance equal to one fish. Points above this threshold are given a value of one and points below are given a value of zero. Thus, indicator kriging is robust to outliers (Journel 1983). This analysis provides maps of probability of occurrence, rather than spatial abundance estimates of Atlantic croaker.

Maps were developed for each of the three annual CHESFIMS cruises from 2002-2005 using the indicator kriging option in ArcMap using a spherical semivariogram in all cases. The semivariogram was adjusted by changing the number of nearest neighbors and geometry of the search sectors in ArcMap. By changing these parameters, the model with the lowest Root Mean Square (RMS) and lowest average standard error was chosen to represent croaker distribution. In most cases, the search geometry had four sectors with a 45° offset.
5.2.3. Diet analysis

Frozen croaker collected during the CHESFIMS cruises (2002-2005) were thawed and individual fish were weighed (wet weight, g), measured for total length (TL, nearest mm), and their otoliths and stomachs removed. To quantify diets, the preserved stomach was blotted dry and weighed with contents intact. The stomach contents were removed and the remaining stomach tissue reweighed. The dissected stomach contents were examined and quantified under a dissecting microscope at 10-40x magnification. Prey items were identified to the lowest taxon feasible. Each prey type was weighed and the number of individuals determined. Diet was quantified using percent composition by weight (%W). Mean proportional contribution of a prey type by weight was calculated for each experimental unit or station with a two-stage clustering scheme (Buckel et al. 1999, Cochran 1977). For each group, i, the total weight \( w_{ik} \), of prey item k was divided by the total weight of all identifiable prey items at the station, \( w_i \). Thus, the mean proportional contribution of a prey type \( W_k \) was calculated as:

\[
W_k = \frac{\sum M_i (w_{ik}/w_i)}{\sum M_i}
\]

where \( M_i \) is the number of fish >100mm caught at the station. This method was used to calculate %W for two clustering schemes, 1) where group (i) were equal to the year and strata and 2) where the group (i) was simply the cruise (or year and season).

I used simple graphic analyses and summary statistics to describe croaker diet composition by age, season, region and year. To quantify patterns in croaker diets more fully, I applied Canonical Correspondence Analysis (CCA) to analyze patterns in %W (ter Braak 1986). CCA is an ordination technique, but unlike ordination approaches such as principal components analysis, CCA does not seek to explain all the variation in the data, rather it seeks to explain only
that variation directly associated with specified factors. For my analyses I examined contributions of year, season, and strata of the bay. Analyses were conducted using the Vegan package (Version 1.8.8) in R (Oksanen et al. 2007).

To understand trends in croaker diet composition by size, two-stage clustering was not used and data was pooled from 2002-2005. Instead total weight of each prey item was divided by the total weight of all prey items to arrive upon %W for each individual fish. Subsequently, %W for each individual was averaged by 10mm length class and displayed graphically. To determine if the incidence of anchovy in croaker stomachs exhibited diel trends the average total weight (not %W) of anchovy in stomach was plotted against the time of capture for each season. The average weight of anchovy in stomachs was also compared between males and females using a non-parametric Mann-Whitney U test. Percent occurrence (%O) is also reported for each prey category for individual fish pooled from 2002-2005 and is calculated by dividing the number of stomach in which a prey item occurred by the total number of stomachs.

5.2.4. Effect of environmental variables and diet on croaker presence and abundance

To understand the biotic and abiotic factors that influence spatial distribution of adult croaker as illustrated in maps produced by indicator kriging, I developed two-stage Generalized Additive Models (GAMs). I chose four environmental parameters and two biotic parameters to include in Generalized Additive Models (GAM). The parameters selected were chosen to reflect parameters believed to influence the distribution of croaker. Salinity, temperature, and dissolved oxygen were averaged over the entire water column for each CTD cast at each station. Maximum depth was determined as the maximum depth from the CTD cast. Average grain size
was estimated using data from the Chesapeake Bay Program data collected from 1975-1981. Grain size was reported on log₂ (phi) scale where a value of 1 is the grain size for gravel and a grain size of 8 and above corresponds to clay. Most of the area of the Chesapeake Bay floor consists of sand (Phi ~0 to 4). The locations of stations at which sediment analyses were conducted differed from TIES and CHESFIMS stations. Therefore, a map of interpolated phi values for the entire Chesapeake Bay mainstem was created. Subsequently, I overlaid the TIES and CHESFIMS station locations on the interpolated grain size map and the appropriate interpolated values of phi were obtained using Hawth Tools (http://www.spatialecology.com/htools/) in ArcGIS 8.1 software.

Maximum depth and grain size are physical properties that may represent a habitat quality that croaker prefer. However, I have interpreted these variables as proxies for benthic food resources available to croaker. Anchovy biomass was also used as a biotic variable because it is a frequent food item in adult croaker stomachs. Anchovy biomass was log transformed so that the data would be normally distributed and values would be within an order of magnitude of the other variables in the model. The Pearson correlation coefficients among these variables were quantified to understand the relationships among biotic and abiotic parameters used in the model.

I first conducted a two stage GAM for data pooled over all years (1995-2005) and seasons to explore broad trends in distribution. The predictions from the two stage GAM using pooled data allowed evaluation of the method to predict croaker abundance. However, the
purpose of the two-stage GAM was to determine factors that influence distribution other than seasonal migrations as timing of seasonal migrations can be easily discerned from distribution maps. Therefore, I conducted three separate two stage GAMS for spring, summer, and fall to understand factors that influence croaker distribution on a smaller temporal scale.

To evaluate how important each factor was in predicting croaker presence and secondarily abundance I took 100 random samples of 79% of the data (n=1000), fit the GAM, and then tallied the number of times a parameter was significant. Those factors that were consistently significant in the GAMs were considered more important factors in determined croaker distribution. All statistical analysis was done in R (Version 2.4.1) using the mgcv package (Wood 2007). It should be noted that in the mgcv library the degree of smoothing is part of model fitting so rather than set the degrees of freedom a priori, the best model is chosen in part by changing the degrees of freedom. Model fits with more degrees of freedom indicate more "curviness" and the overall model fit is penalized by high degrees of freedom.
5.3. RESULTS

The incidence of croaker occurrence exhibits seasonal and annual variation (Figure 2). However, Atlantic croaker were consistently located in the lower to middle part of the Chesapeake Bay. As indicated by the overall low probabilities of occurrence in spring cruises, there are relatively few croaker in the Bay in the spring as adult croaker are just beginning to migrate into the Bay. In the summer months, there are higher incidences of occurrence with large aggregations of croaker in the low to mid section of the bay. However, in some years - notably 2002 and 2003, there is another aggregation of croaker in the Upper Bay.

Eleven categories of prey were recognized in croaker diets collected between 2002 and 2005 (Table 5.1). Overall, polychaetes were the dominant component of croaker by weight (61.5%) and by occurrence (83.6%). Anchovy (8.9%) and mysids (8.2%) followed polychaetes in importance by weight. However, in combination mysids, amphipods, and other benthic organisms were more common in croaker stomachs than anchovy. Detritus and miscellaneous pelagic prey were the least common food items and in many years were not recorded in stomachs at all. The diet of Atlantic croaker varied annually and seasonally (Figure 5.3). Croaker consumed more anchovies, fish, and mysids in the summer and fall of several years. In the summer, at least 20% of the diet of croaker consistently consisted of anchovies and fish. In particular, in the summer of 2002, about 50% of the diet of croaker by weight consisted of anchovy in the middle strata of the bay.
The CCA of croaker diet explained approximately 4.1% of the data, but reinforced annual and seasonal trends (Figure 5.4). Polychaetes and other organisms which were consistently present in croaker stomachs were located centrally in the ordination. Anchovy, fish, and detritus occurrence in diet was attributable to most of the explained variation on an interannual basis, as reflected by the strong coherence of these three prey categories and the year variable in the ordination. The presence of crabs in croaker diet was more strongly associated with season than with region, but the coherence was not strong. In general, it appears that bivalves were more frequently eaten in the upper part of the Bay and shrimp in the lower part of the Bay (Figure 5.3).

Correlations of environmental variables (temperature, salinity, dissolved oxygen, and grain size) with prey categories were tested, but all correlation coefficients were very low and only one comparison was significant at the P=0.001 level (Bonferoni adjustment, P=0.05/44=0.001). Proportion of amphipods in diets was positively correlated with salinity (r=0.246, P=0.001), indicating that amphipods are consumed in waters of higher salinity, perhaps in the lower Bay. Grain size and other benthic prey category were positively correlated (r=0.17, P=0.0248). Dissolved oxygen and %W of anchovy was weakly negatively correlated (r=-0.15, P=0.0468).

There was an ontogenetic change in croaker diets with small croaker eating small crustaceans, particularly amphipods (Figure 5. 5). As croaker got larger their diet seemed to become more diverse, but this may in part be a result of a greater number of individual stomachs examined in moderate size classes. Size classes were pooled for fish <100m and >390 because...
of small sample size. Larger croaker tended to have higher proportion of anchovies and fish in their diet. Polychaetes were the staple diet item in all size classes.

The weight of anchovy in the stomachs of croaker was highest following sunset in spring and summer (Figure 5.6). In the spring, the weight of anchovy in croaker stomachs was also high near sunrise. However, this trend was not seen in other seasons. In contrast, there did not appear to be any diel trend in polychaetes consumption.

Croaker occupied waters of the Bay exhibiting a wide range of temperatures, salinities, and dissolved oxygen (Figure 5.7). The log of croaker abundance was weakly, but significantly positively correlated with salinity and negatively correlated with grain size (Table 5.2). Croaker biomass was not significantly correlated with any other factors examined and appeared to be present and abundant at a wide range of values for all physical parameters examined (Figure 5.3). There were several correlations between variables used in the GAMs (Table 5.2). Salinity was negatively correlated with dissolved oxygen and grain size, but positively correlated with depth, croaker biomass, and anchovy biomass. The significant negative correlation with grain size can be explained by the estuarine gradients in both salinity and grain size from the freshwater input at the head of the estuary to the mouth of the bay. Grain size decreases from large to small grain sizes in general from the head to the mouth of the bay (Figure 5.8). Other correlations with salinity were relatively low. The correlation between dissolved oxygen and temperature was relatively high which can be explained by the decrease in oxygen solubility as temperature increases. Interestingly, salinity was correlated with both anchovy and croaker
biomass, reflecting the high abundance of croaker in the lower to middle parts of the Bay (Figure 5.2).

Bootstrapping each stage of the GAM with data pooled over all seasons indicated that of all the included main effects, croaker presence was most influenced by temperature and salinity when year and the interaction of temperature and salinity were not included in the model (Table 5.3). In 100 iterations, temperature was significant at the p=0.01 level 100% of the time and salinity 93% of the time. However, when year and the interaction of temperature and salinity were included, the main effects of both temperature and salinity were significant only 16 and 12% of the time in predicting croaker presence respectively. This suggests that the main effects of temperature and salinity are reflective of the seasonal migrations of croaker. Interestingly, anchovy biomass was a predictor of croaker presence in every run with or without year effects included in the model.

In the second stage of the model where croaker abundance was modeled, temperature and salinity were again important factors in the model when the effect of year or the interaction of temperature and salinity was not included (Table 5.3). In contrast to the first stage bootstrapping results, when year and the interaction of temperature and salinity were included in the model, the main effects of temperature and salinity remained the most important factors in predicting abundance. While anchovy biomass and grain size were frequently incorporated in the 1st stage GAM, these factors were rarely significant in predicting croaker abundance in the 2nd stage of the
GAM. Dissolved oxygen was never a significant factor for either the 1st or 2nd stage GAM. Depth was occasionally a significant factor in the 1st stage, but never in the 2nd stage.

After this bootstrapping exercise on 100 subsets of the data, a two stage GAM was run with all data (n=1258) to evaluate the predictive ability of the model. In the first stage, significant factors in predicting croaker presence were temperature, depth, grain size, anchovy biomass, year and the interaction of temperature and salinity (Table 5.4, Figure 5.9). The relationships of croaker occurrence with temperature, depth and year were curvilinear (Figure 5.10). The relationship appears dome shaped with depth and anchovy weight. In the second stage, temperature, salinity, grain size, year, and the temperature and salinity interaction were incorporated to predict croaker abundance (Figure 5.10). The relationship of croaker abundance predicted by the second stage of the GAM was curvilinear with temperature, dome shaped with grain size and year, and linear with salinity. Deviance explained in the second stage of the model was 43.2%, much higher than the deviance explained in the first stage of the model, 18.7%.

Predicted croaker abundance was calculated in two ways: 1) by the 2nd stage GAM itself using only stations where croaker were present and 2) by the product of the presence and abundance predicted by the 1st and 2nd stage models respectively. The explanatory variables from the original data were used in both cases and observed croaker biomass was compared to these predictions. The second stage of the two stage GAM alone predicted croaker abundance much better than the full two stage GAM (Figure 5.11). However, neither captured the range of
values of croaker biomass and the GAM seemed to dampen much of the variability in abundance that was observed.

To eliminate the effects of seasonal migrations, two stage GAMs were run for the spring, summer, and fall. Year and the interaction between temperature and salinity and Year were important factors in almost all of the seasonal models even though the data was separated by season (Table 5.4). The relationship of both croaker occurrence and abundance with year was highly curvilinear especially in the spring and fall (Figures 5.12-17). In general, croaker occurrence and abundance increased linearly or approached linearity with salinity. In the second stage of the seasonal GAMs, croaker abundance increases linearly with dissolved oxygen and depth in the Spring (Figure 5.13). Most other relationships of explanatory variables with croaker occurrence and abundance were curvilinear reflecting the patchiness in croaker distribution. The deviance explained and $R^2$ values were higher for the seasonal models than for the pooled model (Table 5.4). The seasonal two stage GAMs also predicted observed croaker abundance better than the pooled model, but again, the modeling approach dampened the range of croaker abundance estimates (Figure 5.18). The maximum observed croaker biomass was much higher than the maximum predicted value in both the pooled and seasonal models.
5.5 **DISCUSSION**

Croaker feeds on a wide variety of organisms, but in contrast to previous studies croaker were found to eat a substantial amount of anchovy during the summer months in Chesapeake Bay. Fish have been reported as small components of the diet of adult croaker in previous studies (Darnell 1961, Nemerson 2002, Overstreet and Heard 1978, Sheridan 1979). The work herein suggests that about 20% of the diet of croaker by weight consists of anchovy. While croaker still consistently feed on benthic portions of the food web, these results suggest that a substantial portion of their bioenergetic needs (as indicated by %W) are met by anchovy in the summer months and that croaker predation could influence both the benthic and pelagic portions of the food web.

Anchovy could be more common in croaker diets because of the effects of eutrophication on the ecosystem. Estuarine ecosystems worldwide are increasingly subject to anthropogenic stresses that have lead to eutrophication, which induces widespread alterations in the ecosystem (e.g. Kemp et al. 2005). De Levia Moreno et al. (2000) proposed that one of the effects of eutrophication was to increase the ratio of biomasses of pelagic to benthic associated fishes, indicative of general system wide change from benthic to pelagic production. Indeed in the Chesapeake Bay, the ratio of pelagic to benthic fishery removals increased from 1.90 to 2.66 between the 1960’s and the 1990s. Eutrophication and the change from a more pelagic to benthic ecosystem may cause alteration of diet patterns. Powers et al. (2005) found that the diet of Atlantic croaker shifted from clams to less nutritious food sources such as detritus and plant tissue after summer hypoxic events in the Neuse River estuary (NC, USA). Studies on other
benthic feeders in Chesapeake Bay illustrated that the ability of a benthic predator to prey upon clams was reduced during periods of even sporadic low dissolved oxygen events (Seitz 2003).

The earliest of croaker diet studies, that of Hildebrand and Schroeder (1928) reported less than 1% of the stomachs that were examined had fish in them. In contrast, this study and other studies since the 1970s report fish as a relatively small, but common part of croaker diet (Chao and Musick 1977, Nemerson 2002, Overstreet and Heard 1978, Sheridan 1979). The increase in fish reported in the diet of croaker might be a result of different sampling, but it might also reflect increasingly poor water quality in coastal areas where croaker live. There was no statistically significant correlation between dissolved oxygen and the amount of anchovy in croaker diet. However, croaker eat more anchovies in the summer when hypoxia is more common. In the summer of 2003 the middle and upper regions of the Bay experienced very low oxygen conditions, which is coincident with a high proportion of anchovy and fish in the diets of croaker in the same regions. However, the highest incidence of anchovy feeding was in 2002, when hypoxia was not as severe as 2003. Factors that influence diet were difficult to detect in this and other diet studies. Therefore, it is possible that a general shift from a benthic to a pelagic Chesapeake Bay ecosystem may explain the higher incidence of anchovy in present day croaker diets.

It is more likely that the incidence of anchovy and fish in the diet of croaker were higher in this study because croaker are crepuscular predators on anchovy. This crepuscular feeding was captured by sampling with a midwater trawl at night while other studies of croaker diet have used bottom trawls during the day. The only other diet study where samples were collected at
night probably did not capture this because it was conducted in shallow waters and there was a notable decrease in croaker catches at night presumably because croaker moved to deeper water at night (Homer and Boynton 1978). In this study, there was a higher weight of anchovy in croaker stomachs following sunset indicating crepuscular feeding behavior. The adjustment in sight and behaviors of many fish during the twilight period after sunset and before sunrise is thought to provide an opportunistic feeding time for some predators in aquatic environments. Indeed diel variations in diet have been detected in other studies (Clark et al. 2003, Johnson and Dropkin 1993). Taylor et al. (2007) also found that swimming speeds of bay anchovy were lower and less variable at night than during the day, which may enable a demersal fish such as croaker to feed upon prey that is much more mobile than its traditional benthic prey. While some consumption of anchovy could be from net-feeding in the midwater trawl, this is unlikely. The relative degree of digestion was recorded in 2004 and 2005 and all stages of digestion were present, indicating that the consumption of anchovy is not simply a result of net feeding.

Distribution of croaker varied seasonally and annually and is reflected in the maps of probability of occurrence and in the two stage GAMs. Croaker occurrence and abundance fluctuated annually so that the effect of year was included in all but two of all the first and second stage GAMs produced. Temperature and salinity and/or their interaction was also a consistent contributor to predict croaker distribution. We hypothesized that presence of croaker would be predicted by physical properties of the water column because the presence of croaker should be bounded by its tolerance to water chemistry. However, croaker was tolerant of a wide range of salinity, temperature, and dissolved oxygen. Furthermore, the prey field seemed to be
important in determining croaker occurrence. Anchovy was a consistent predictor of croaker occurrence in these models.

We secondarily hypothesized that croaker would be more abundant where prey resources were high. However, the second stage of the GAMs indicated that both abiotic and biotic factors were important in predicting abundance. In fact, anchovy biomass was not included in any of the second stage models and grain size was included only in the second stage GAM pooled over seasons. These results do not mean that prey field is not important in determining croaker distribution. Grain size was used as a proxy for benthic food resources, but it would have been better to use actual abundance estimates of benthic organisms upon which croaker frequently feed. Estimates of benthic biomass are available but do not overlap temporally with our sampling scheme. Furthermore, the estimates of grain size were obtained from the 1980s and there may have been changes in sediment characteristics since that time. However, the overall trends in grain size are probably similar. While anchovy was a consistent predictor of croaker presence it is possible that anchovy abundance is influenced by the same factors as croaker and these factors may or may not have been incorporated into the model.

While pooling data across all seasons provided a large number of data points to fit the GAMs, seasonal GAMs predicted the abundance of croaker much better. The two stage GAM did predict general trends in croaker abundance, but was unable to capture the wide range of estimates of croaker biomass. In particular, GAMs were unable to capture the number of stations with zero values. GAMs have been used to predict the spatial distribution in much of the marine ecology literature (Hedger et al. 2004, Jensen et al. 2005, Stoner et al. 2001). While it is possible
to create spatially explicit maps of croaker abundance based on abiotic and biotic factors, in this
application GAMs were used to identify factors that influence croaker presence and secondarily
abundance. GAMs allowed the incorporation of many possible explanatory variables, different
distributions of data (Poisson in the first stage and Gaussian in the second stage), and the ability
to fit curvilinear relationships to predict distribution, which is more biologically realistic.

Here, we have documented clear trends and levels of variability in the distribution and
diet of Atlantic croaker in Chesapeake Bay. While the patterns were clear, the consequences of
these patterns to the fitness of individual fish remain uncertain. For example, does the variability
in croaker diet observed at the regional and interannual levels have any fitness consequence for
the individual croaker? Specifically, does a higher proportion of anchovy in the diet confer a
growth advantage, or does it reflect changes in diet driven by exclusion of croaker from preferred
habitats, and therefore the presence of anchovy in croaker diets actually confers a fitness cost.
To explore these and other potential hypotheses, it would be necessary to assess the condition of
croaker with different observed diets. The challenge of such analyses will be matching the
temporal resolution of indices of condition with that of the diet. Dietary information derived
from analysis of stomach contents represents a "snapshot" of consumption, but do not necessarily
represent what a fish is consistently eating and more importantly assimilating. Similarly, indices
of condition also have characteristic response and latency times (Ferron and Leggett 1994,
Suthers et al. 1992). Thus, addressing the consequences of the patterns in distribution and diet
observed here will require additional studies that seek to match observations on diet and
condition at appropriate spatial and temporal scales.
Table 5.1: Description of prey categories used to describe croaker diet.

<table>
<thead>
<tr>
<th>Prey category</th>
<th>Description</th>
<th>%W</th>
<th>%O</th>
</tr>
</thead>
<tbody>
<tr>
<td>Polychaetes</td>
<td>Many unidentified species, but include trumpet worms <em>Pectinaria gouldi</em>, clam worms, <em>Neries spp.</em> and terebellid worms <em>Terebellidae</em></td>
<td>61.5%</td>
<td>83.6%</td>
</tr>
<tr>
<td>Anchovy</td>
<td>Mostly bay anchovy, <em>Anchoa mitchilli</em>, but may include striped anchovy <em>Anchoa hepsetus</em></td>
<td>8.9%</td>
<td>13.2%</td>
</tr>
<tr>
<td>Mysids</td>
<td>Mostly <em>Neomysis americanus</em>, but may include <em>Mysidopsis bigelowi</em></td>
<td>8.2%</td>
<td>36.5%</td>
</tr>
<tr>
<td>Amphipods</td>
<td>Many species including <em>Gammarus spp.</em>, <em>Leptocheirus plumulosus</em>, <em>Corophium lacustre</em>, <em>Monoculodes edwardsi</em></td>
<td>5.2%</td>
<td>21.0%</td>
</tr>
<tr>
<td>Other benthic</td>
<td>Hydroids, molluscs, gastropods, barnacles, cumaceans, isopods, <em>Cyathura spp.</em>, skeleton shrimp, other crustaceans, sea squirts, and ribbon worms</td>
<td>4.3%</td>
<td>20.2%</td>
</tr>
<tr>
<td>Bivalves</td>
<td>Unidentified bivalves, clams and seedling mussels</td>
<td>3.5%</td>
<td>12.7%</td>
</tr>
<tr>
<td>Fish</td>
<td>Unidentified fish and fish remains, and YOY weakfish <em>Cynoscion regalis</em></td>
<td>3.4%</td>
<td>12.3%</td>
</tr>
<tr>
<td>Crabs</td>
<td>Unidentified crab remains and white fingered mud crab <em>Rhithropanopeus harrisii</em></td>
<td>1.8%</td>
<td>4.5%</td>
</tr>
<tr>
<td>Shrimp</td>
<td>Unidentified shrimp remains, Caridean shrimps, <em>Pugeo spp.</em>, sand shrimp <em>Crangon septemspinosa</em>, and mantis shrimp <em>Squilla empusa</em></td>
<td>1.6%</td>
<td>6.5%</td>
</tr>
<tr>
<td>Detritus and macroalgae</td>
<td>Unidentified algae, inorganic matter, and plant matter</td>
<td>1.3%</td>
<td>11.4%</td>
</tr>
<tr>
<td>Other pelagic</td>
<td>Squids, sea nettles, insects</td>
<td>0.3%</td>
<td>1.1%</td>
</tr>
</tbody>
</table>
Table 5.2: Pearson correlations between explanatory variables used in the 1st stage of the GAM, all seasons and years combined. Pairwise comparisons were considered significant at the P=0.002 level to maintain an experiment-wise error rate of P=0.05 (Bonferroni adjustment P =0.05/21=0.002).

<table>
<thead>
<tr>
<th></th>
<th>Salinity</th>
<th>Temperature</th>
<th>Dissolved Oxygen</th>
<th>Depth</th>
<th>Grainsize</th>
<th>Log Anchovy Biomass</th>
<th>Log Croaker Biomass</th>
</tr>
</thead>
<tbody>
<tr>
<td>Salinity</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Temperature</td>
<td>0.099</td>
<td>0.0151</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dissolved Oxygen</td>
<td>-0.18344</td>
<td>-0.679</td>
<td>&lt;0.0001</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Depth</td>
<td>0.129</td>
<td>0.01934</td>
<td>-0.082</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Grainsize</td>
<td>-0.611</td>
<td>-0.06962</td>
<td>0.112</td>
<td>-0.082</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Log Anchovy Biomass</td>
<td>0.319</td>
<td>0.01038</td>
<td>-0.173</td>
<td>0.0075</td>
<td>-0.105</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Log Croaker Biomass</td>
<td>0.19928</td>
<td>0.075</td>
<td>-0.036</td>
<td>0.014</td>
<td>-0.134</td>
<td>0.0825</td>
<td></td>
</tr>
</tbody>
</table>

P-values are indicated for each correlation.
Table 5.3: The percentage of simulations (number out of 100 iterations obtained from bootstrapping) where each explanatory variable was significant in 1\textsuperscript{st} and 2\textsuperscript{nd} stage GAMS of data pooled over all seasons 1995-2005.

<table>
<thead>
<tr>
<th>Explanatory Variable</th>
<th>1st stage</th>
<th>2nd stage</th>
<th>1st stage</th>
<th>2nd stage</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No year effects</td>
<td>Year effect included</td>
<td>No year effects</td>
<td>Year effect included</td>
</tr>
<tr>
<td>Temperature</td>
<td>100</td>
<td>16</td>
<td>100</td>
<td>92</td>
</tr>
<tr>
<td>Salinity</td>
<td>93</td>
<td>12</td>
<td>100</td>
<td>99</td>
</tr>
<tr>
<td>Dissolved Oxygen</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Depth</td>
<td>3</td>
<td>9</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Grain size</td>
<td>69</td>
<td>75</td>
<td>4</td>
<td>5</td>
</tr>
<tr>
<td>Log Anchovy Biomass</td>
<td>100</td>
<td>100</td>
<td>13</td>
<td>4</td>
</tr>
<tr>
<td>Year</td>
<td>83</td>
<td></td>
<td>56</td>
<td></td>
</tr>
<tr>
<td>Temperature*Salinity</td>
<td>100</td>
<td></td>
<td></td>
<td>78</td>
</tr>
</tbody>
</table>
Table 5.4: Significant variables used in final two stage models for all seasons combined and then for each separate season.

<table>
<thead>
<tr>
<th>Explanatory Variable</th>
<th>All seasons</th>
<th>Spring</th>
<th>Summer</th>
<th>Fall</th>
<th>All seasons</th>
<th>Spring</th>
<th>Summer</th>
<th>Fall</th>
</tr>
</thead>
<tbody>
<tr>
<td>Temperature</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td>X</td>
<td></td>
<td></td>
<td>X</td>
</tr>
<tr>
<td>Salinity</td>
<td></td>
<td>X</td>
<td></td>
<td></td>
<td>X</td>
<td></td>
<td></td>
<td>X</td>
</tr>
<tr>
<td>Dissolved Oxygen</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>X</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Depth</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>X</td>
</tr>
<tr>
<td>Grain size</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>X</td>
</tr>
<tr>
<td>Anchovy Biomass</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Year</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>Temp*Salinity</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Deviance Explained</td>
<td>18.7%</td>
<td>36.60%</td>
<td>20.4%</td>
<td>24.3%</td>
<td>43.2%</td>
<td>65.4%</td>
<td>34.60%</td>
<td>46.6%</td>
</tr>
<tr>
<td>Adjusted R²</td>
<td>0.195</td>
<td>0.351</td>
<td>0.188</td>
<td>0.262</td>
<td>0.383</td>
<td>0.602</td>
<td>0.272</td>
<td>0.417</td>
</tr>
<tr>
<td>N</td>
<td>1258</td>
<td>396</td>
<td>415</td>
<td>447</td>
<td>446</td>
<td>120</td>
<td>122</td>
<td>204</td>
</tr>
</tbody>
</table>
Figure 5.1: An example of the TIES and CHESFIMS survey design using the stations from the spring of 2001. Fixed stations are indicated with stars. Random stations are indicated with circles. The three strata of Chesapeake Bay (Upper, Middle, and Lower Bay) are separated with horizontal lines and labeled accordingly.
Figure 5.2: Maps of the probability of occurrence of Atlantic croaker in Chesapeake Bay as estimated by indicator kriging for a) 2001, b) 2002, c) 2003 and d) 2004. Numbers in parentheses indicate the number of stations sampled in that particular cruise.
Figure 5.3: Diet of Atlantic croaker (proportion by weight) by year, season, and strata of the Bay a) 2002 Spring, b) 2002 Summer, c) 2002 Fall, d) 2003 Spring, e) 2003 Summer, f) 2003 Fall, g) 2004 Spring, h) 2004 Summer, i) 2004 Fall, j) 2005 Spring, k) 2005 Summer, and l) 2005 Fall. Panels where a figure is missing indicates that no croaker were collected in that sampling period.
Figure 5.4: Biplot from Canonical Correspondence Analysis of the factors influencing diet composition of Atlantic croaker. Arrows represent factors while labels in blue are centroids of scores for the prey species.
Figure 5.5: Diet composition by weight for each 10mm size class of Atlantic croaker examined 2002-2005.
Figure 5.6: Total weight (g) of polychaetes and anchovies in croaker stomachs by one hour time periods. X-axis labels represent the beginning of each time interval (i.e. 19:00 indicates the time period from 19:00-20:00). Arrows indicate sunset.
Figure 5.7: Relationship of the log of croaker biomass with explanatory variables used in the two stage GAMs.
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- For spring:
  \[ y = 0.399x + 1.1641 \]
  \[ R^2 = 0.4402 \]

- For summer:
  \[ y = 0.204x + 1.4667 \]
  \[ R^2 = 0.2299 \]

- For fall:
  \[ y = 0.2276x + 1.6185 \]
  \[ R^2 = 0.2428 \]
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CHAPTER 6

DESIGN EFFICIENCIES OF TRANSECT AND STRATIFIED RANDOM TRAWL SURVEYS

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6.1 ABSTRACT

Spatially overlapping transect and stratified random trawl surveys were conducted simultaneously in the Chesapeake Bay during spring, summer, and fall during 2002 and 2003 to quantify the relative abundance, diversity, distribution and trophic interactions of economically and ecologically important fish species. We evaluated the design efficiency of each survey with respect to the precision of relative abundance estimates for a given sampling effort. We used Kish’s design effects and effective sample sizes to assess the efficiency and cost-effectiveness of each survey with respect to estimates of relative abundance for selected species and overall. The empirical design effects suggested that the stratified random survey, with proportional allocation, was more effective than the transect sampling in estimating mean CPUE across species, and for most target species. However, for weakfish, trawling along transects appeared to be more effective than the stratified random survey. We developed a composite estimator to combine the estimates of mean CPUE from the two independent surveys within season for each year, using weights that are based on their respective effective sample sizes. The weights are optimized with respect to achieving minimum variance. Our method for combining estimates across surveys is robust to heterogeneous variances such as might be found when the means and variances are correlated, which is often the case for CPUE from marine trawl surveys. A similar approach, with possible modifications for gear differences, could also be used to combine multiple surveys to develop a composite index for use in stock assessments.

**Keywords:** Marine trawl surveys; Survey design; Design effect; Transect surveys; Effective sample size; Cluster-sampling; Intra-cluster correlation; Composite estimator.
6.1 INTRODUCTION

Fisheries-independent trawl surveys are widely used to provide estimates of relative abundance and other population parameters crucial for effective fisheries management (Gunderson, 1993). The average number of fish caught per area or volume swept has long been used as an index of relative abundance (Grosslein, 1969; Pennington, 1985, 1986; Smith, 2002). Standardized trawl surveys, coupled with appropriate allocation of stations, can provide reliable estimates of changes in abundance, if the catch efficiency of the survey gear remains approximately constant by depth and over time. However, given the expense of trawl programs, it is important to optimize the survey design so that the precision of key parameters is maximized for a fixed total survey cost.

The distribution of marine resources is generally highly patchy (cf. Seber, 1986), and often results in strong short-range spatial autocorrelation in measures of relative abundance (Polacheck and Vølstad, 1993; Kingsley et al., 2002). Accordingly, a considerable body of research has sought to determine survey designs appropriate for temporal and spatial variability with possible clustering. A classic example includes the application of stratification and sample allocation schemes that seek to increase inter-stratum variability while minimizing intra-stratum variability, thereby increasing the precision of parameter estimates for single species (Cochran, 1977; Gavaris and Smith, 1987; Harbitz et al., 1998). Designs for surveys that target multiple species are more complicated as distributions of the individual species are likely to vary at differing spatial and temporal scales. The recent interest in multispecies fisheries management will require development of multispecies, fishery-independent surveys. However, guidance on optimization of multispecies surveys is lacking.

The presence of biological and technical interactions among Chesapeake Bay fisheries (Miller et al. 1996) has motivated management agencies to establish a goal of implementing multispecies management in the Chesapeake Bay by 2007 (C2K agreement). To support the development of multispecies management in the Chesapeake Bay an international workshop recommended the development of coordinated, baywide surveys to estimate key species abundances and to provide biological data on both economically and ecologically important species that are currently lacking (Houde et al. 1998).
We conducted seasonal midwater trawl surveys in the Chesapeake Bay to evaluate the efficiency of different survey designs for a range of finfish species as a component of the Chesapeake Bay Fishery Independent Multispecies Survey (CHESFIMS). Information for the initial survey design came from an earlier research program to quantify ‘Trophic Interactions in Estuarine Systems’ (TIES). The TIES program included baywide midwater trawl surveys, conducted from 1995 - 2000 during spring, summer and fall (Jung and Houde, 2003). The TIES data demonstrated that baywide seasonal surveys are required to characterize the communities in the Bay because of the spatial and temporal variability in fish abundance and community structure (Jung and Houde, 2003).

Our goals for the design of CHESFIMS were to: (1) maintain the time series from the TIES program while improving survey efficiency (2) complement existing fishery-independent surveys and (3) expand survey coverage to ecologically important forage species to aid development of multispecies fisheries management in the Chesapeake Bay. We sought to develop a cost-effective design for the monitoring of abundance, diversity, distribution and trophic interactions of economically and ecologically important fish species in the Chesapeake Bay over broad spatial and temporal scales given limited resources. Accordingly, we conducted spatially and temporally overlapping transects and stratified random trawl surveys in the Chesapeake Bay during spring, summer, and fall in 2002 and 2003. Here we evaluate the efficiency of both survey designs for estimating relative abundance using design effects and effective sample sizes (Lehtonen and Pakinen, 1994; Kish, 2003). We also demonstrate how two survey indices of abundance can be combined to yield an overall index with minimum variance.

6.2. MATERIAL AND METHODS

6.2.1. Study area

The Chesapeake Bay is the largest estuary in the United States, with an area of approximately 6,500 km², a length of over 300 km, a mean depth of 8.4 meters, and a volume of 52,112 km³. Fisheries in Chesapeake Bay contribute significantly to U.S. catches at the national and regional levels. Fisheries statistics from the National Marine Fisheries Service (NMFS) shows that around 220,000 metric tons (t) of fish and shellfish were harvested in 2002 from
Chesapeake Bay waters, with a dockside value of more than $172 million. All exploited species in the Chesapeake Bay are currently managed and regulated on a single species basis.

Bay anchovy (*Anchoa mitchilli*) is the most abundant and ubiquitous fish in the Bay (Jung and Houde, 2004). Although not of commercial importance, bay anchovy has an important role in the ecosystem because it is a major prey of piscivores, including several economically important fishes (Baird and Ulanowicz, 1989; Luo and Brandt, 1993; Hartman and Brandt, 1995). Several anadromous species were also common in survey catches including white perch (*Morone americana*), and members of the Sciaenidae family such as Atlantic croaker (*Micropogonias undulatus*), and weakfish (*Cynoscion regalis*).

### 6.2.2. Survey methods

Standardized trawl surveys have been conducted during spring, summer, and fall in the mainstem of the Chesapeake Bay since 1995 using an 18-m² midwater trawl (MWT) with 3-mm codend mesh. MWTs are commonly used to survey pelagic fish including anchovy (*Anchoa japonica* – Komatsu et al. 2002), walleye pollock (*Theragra chalcogramma* – Wilson 2000), and Pacific whiting (*Merluccius productus* – Sakuma and Ralston 1997) and in commercial fisheries for many of these same species. The MWT employed in the Bay samples fish 30-256 mm total length of most species effectively, but appears to be less effective for Atlantic menhaden (*Brevoortia tyrannus*) of all sizes (Jung and Houde, 2003). Trawl stations in the TIES program were located along 15 fixed transects spaced approximately 18.5 km (10 nm) apart from the head of the Bay to the Bay mouth to ensure bay wide coverage (Jung and Houde, 2003). Within each season, 11 of the 15 transects were occupied. Transects were identified as falling within one of three upper, middle, and lower Bay strata (Figure 6.1). Individual strata have distinctive characteristics, and their boundaries broadly corresponding to ecologically relevant salinity regimes and depths above 5 m. The upper Bay is generally shallow, with substantial areas with depths less than 5 m, and has well mixed waters with high nutrient concentrations. The bottom topography in the mid Bay includes a narrow channel in the middle of the Bay with a stratified water column and broad flanking shoals. This region has relatively clear waters and experiences seasonally high nutrient concentrations and periods of hypoxia. The lower Bay has the clearest
waters, greatest depths and lowest nutrient concentrations (Kemp et al., 1999). The strata volumes are 26,608 km³ (Lower), 16,840 km³ (Mid) and 8,664 km³ (Upper).

CHESFIMS was initiated in 2001, employing the TIES trawling procedures, transect design and stratification, with 2-4 trawl stations sampled within 11 transects during spring, summer, and fall. Sampling was conducted from the University of Maryland Center for Estuarine and Environmental Science’s R/V ‘Aquarius. The \( m_i \) stations within the \( i^{th} \) transect were selected by restricted random sampling. Each transect was divided into \( m_i \) segments of equal size, with one station allocated randomly within each segment. For the transect surveys, the clustering of stations and variable transect lengths resulted in heterogeneous selection probabilities for stations within strata. Starting in 2002, the transect sampling was augmented with an independent, stratified random trawl survey in an effort to optimize the monitoring design. We were restricted to maintaining the transects used for monitoring and so chose stratified random sampling as an appropriate additional sampling design for optimizing the geographic distribution of sampling locations and as a counterpoint to the transect design. In the stratified random surveys, conducted simultaneously with the transect surveys, 20 stations covering the entire bay were allocated to the each stratum proportional to their volumes. Twenty new locations were chosen during each survey. Latitude and longitude of stations within strata were randomly generated. Weather precluded complete sampling of all 20 stations during some surveys. An example of the allocation of stations in the 2002 stratified random survey is shown in Figure 6.1.

Survey deployments followed the TIES trawling procedures (Jung and Houde, 2003), with standardized 20-minute oblique, stepped tows conducted at each station using the same midwater trawl. The trawl was towed for two minutes in each of ten depth zones distributed throughout the water column from the surface to the bottom, with minimum trawlable depth being 5 m. The section of the tow conducted in the deepest zone sampled epibenthic fishes close to or on the bottom. The remaining portion of the tow sampled pelagic and neustonic fishes. All tows were conducted between 19:00 and 7:00 Eastern Standard Time to minimize gear avoidance and to take advantage of the reduced patchiness of multiple target species at night. Catches were identified, enumerated, measured and weighed onboard.
6.2.3. Estimating mean catch per unit effort

To estimate the mean catch per unit effort (CPUE) and the associated variance, we treated the transect survey as a stratified, two-stage design, with primary sampling units of unequal size (e.g., Cochran, 1977; Wolter, 1985) to account for the variable transect lengths. For estimating purposes, we assumed that the $n_h$ primary sampling units (transects) were selected randomly from all possible transects within each stratum $h$ ($h = 1, 2, 3$). Let $\overline{y}_{hi}$ denote the mean CPUE for the $m_h$ stations within transect $i$ in stratum $h$, and let $l_{hi}$ denote the transect length. We applied a combined (across strata) ratio estimator for a two-stage survey (Cochran, 1977) to estimate the overall mean CPUE

$$\overline{y}_T = \frac{\sum_{h=1}^{3} \sum_{i=1}^{n_h} w_h l_{hi} y_{hi}}{\sum_{h=1}^{3} n_h}$$  \hspace{1cm} [6.1]

where, for stratum $h$,

$$\overline{y}_h = \frac{\sum_{i=1}^{m_h} l_{hi} y_{hi}}{\sum_{i=1}^{m_h} l_{hi}}$$

is the weighted mean CPUE across transects,

$$\overline{l}_h = \frac{1}{n_h} \sum_{i=1}^{m_h} l_{hi}$$

is the mean transect length within a stratum, and

$$w_h = \frac{V_h}{3 \sum_{h=1}^{3} V_h}$$  \hspace{1cm} [6.2]

is the stratum weight, with $V_h$ being the stratum size (volume). The transect-wise variation of mean CPUE as well as the variation in estimated mean transect length by stratum contributes the variance of Eq. 6.1. An approximate estimator of the variance of Eq. 6.1 is (see Sukhatme and Sukhatme, 1970, p. 307)
\[ \text{Var}(\bar{Y}_T) = \sum_{h=1}^{3} \lambda_h^2 \left\{ \frac{s_{hh}^2}{n_h} + \frac{1}{n_h^2} \sum_{i=1}^{n_h} \left( \frac{t_{hi}}{t_h} \right)^2 \frac{s_{hi}^2}{m_{hi}} \right\} \quad [6.3] \]

where

\[ \lambda_h = \frac{w_h t_h}{\sum_{h=1}^{3} w_h t_h} \]

is the proportion of second-stage units in stratum \( h \),

\[ s_{hh}^2 = \frac{1}{n_h-1} \sum_{i=1}^{n_h} (\bar{Y}_{hi} - \bar{Y}_h)^2 \]

is the between transect variance in CPUE for stratum \( h \), and

\[ s_{hi}^2 = \frac{1}{m_{hi}-1} \sum_{j=1}^{m_{hi}} (Y_{hij} - \bar{Y}_{hi})^2 \]

is the within transect variance in CPUE for transect \( i \) in stratum \( h \). We used SUDAAN (RTI 2001), a specialized software for the analysis of complex surveys and cluster-correlated data (Brogan, 1998; Carlson, 1998), to estimate the variance of \( \bar{Y}_T \) (Eq. 6.3).

In the stratified random surveys (STR), stations were allocated proportional to the volume of each stratum. We applied the standard estimators for the stratified mean and its variance (Cochran, 1977)

\[ \bar{Y}_{str} = \sum_{h=1}^{3} w_h \bar{Y}_{h,srs} \quad [6.4] \]

and

\[ \text{Var}(\bar{Y}_{str}) = \sum_{h=1}^{3} w_h^2 \text{Var}(\bar{Y}_{h,srs}) \quad [6.5] \]

where the weight for stratum \( h \) is based on its fraction of the total volume as in equation 6.2, \( \bar{Y}_{h,srs} \) is the ordinary mean CPUE for simple random sampling within stratum \( h \), and \( \text{Var}(\bar{Y}_{h,srs}) \) is the corresponding variance of the stratum mean CPUE. The spring survey in 2002, and the fall survey in 2003 had incomplete sampling coverage for logistical reasons. For these surveys we collapsed the strata and treated all stations as a simple random sample (SRS), and then used the ordinary estimators of the mean and variance.
6.2.4. Analytical evaluation of design efficiency

The efficiency of each survey design was evaluated by comparing the respective design-based variance of the estimated mean CPUE ($\bar{y}$) with the expected variance obtained under simple random sampling. Kish (1965; 1995; 2003) defined the “design effect” as the ratio of the two variances,

$$\text{deff} = \frac{\text{Var}_c(\bar{y}_c)}{\text{Var}_{srs}(\bar{y}_{srs})}$$ \hspace{1cm} [6.6]

where $\text{Var}_c(\bar{y}_c)$ is the expected variance based on the actual (complex) survey design, and $\text{Var}_{srs}(\bar{y}_{srs})$ is the expected variance under simple random sampling (SRS) for a sample of equal size. The design-based variance, $\text{Var}_c(\bar{y}_c)$, reflects the effects of stratification and, for the transect survey, clustering of stations. Kish (1995) and Potthoff et al. (1992) provide a general discussion on the calculation of design effects and effective sample sizes. We estimated $\text{Var}_c(\bar{y}_c)$ for mean CPUE for the stratified random survey from equation 6.5, while $\text{Var}_{srs}(\bar{y}_{srs})$ was estimated by treating the stations as a simple random sample from the total survey area. This estimate of the variance that would have been obtained under a simple random sample of the same size is justified because stations in general were allocated proportionally to the strata sizes.

The “effective sample size” for estimation of the mean CPUE ($\bar{y}$) using data from the complex survey design $C$ is defined as

$$n^* = n / \text{deff}$$ \hspace{1cm} [6.7]

The effective sample size $n^*$ is the number of stations selected by simple random sampling that would be required to achieve the same precision obtained with $n$ stations under the actual complex sampling design. If, for example, the design effect equals two for the estimated mean CPUE for a transect survey with 30 stations, then a simple random sample of 15 stations (the effective sample size) would have achieved the same precision.

To further evaluate the efficiency of the survey designs we also compared the lengths of the cruise track for a given sample size. We quantified the inter-station distance in our alternative survey designs based on actual and simulated sample selections, using ArcMap (v8.
ESRI Corp, Redlands, CA). To assess the impact of alternative designs, we increased the number of stations in the stratified random survey to levels comparable to the combined survey.

6.2.5. Development of a composite estimator

We used a composite estimator to take a weighted average of the mean CPUE for the independent stratified random and transect surveys (e.g., Korn and Graubard, 1999; Rao, 2003). The estimator for the combined mean is given by:

$$\bar{y}_{comb} = \phi \bar{y}_{STR} + (1 - \phi) \bar{y}_T \quad [6.8]$$

with the weight $\phi (0 \leq \phi \leq 1)$ being chosen to minimize the variance of $\bar{y}_{comb}$

$$Var(\bar{y}_{comb}) = \phi^2 Var(\bar{y}_{STR}) + (1 - \phi)^2 Var(\bar{y}_T) \quad [6.9]$$

where $Var(\bar{y}_{STR})$ and $Var(\bar{y}_T)$ are the design-based expected variances of the mean CPUE estimators for the stratified random and transect surveys, respectively. The optimum weight ($\phi_{opt}$), expressed as a function of the effective sample sizes for each survey ($n_{STR}^*, n_T^*$), is

$$\phi_{opt} = \frac{n_{STR}^*}{n_{STR}^* + n_T^*} = \frac{1}{1 + R}$$

where $R = n_T^* / n_{STR}^*$ (See appendix 6.1 for derivation). Thus, the optimal weight depends only on the ratio of the effective sample sizes $R$. We used the sample data to estimate the variances and the optimal weight $\phi_{opt}$ in equation 6.9.
6.3 RESULTS

Our comparisons of the transect and stratified random survey designs focused on mean catch per unit efforts for all species combined, and for bay anchovy, white perch, Atlantic croaker, and weakfish individually (Tables 6.1-6). The relative standard error (RSE), defined as the ratio of the standard error (SE) to the survey estimate (\( \overline{y} \)), was used as a measure of precision (Jessen, 1978). The comparison of design effects shows that stratified random sampling with proportional allocation generally is more effective than transect sampling for estimating the mean CPUE across all species in the mainstem of Chesapeake Bay. The transect survey resulted in less precise estimates of mean CPUE across species compared to the stratified random survey in each season, even though the former survey completed 55% to 81% more trawling stations.

The two independent surveys produced comparable estimates of mean catch per unit effort (CPUE) of all species combined (Figure 6.2) but differed for the individual species that were considered (compare Tables 6.1-2, and Tables 6.4-5). The combined estimates shows that bay anchovy was most abundant and widely distributed during all seasons in both years, but with significantly lower (p<0.5) summer abundance in 2003 as compared to 2002 (Tables 6.3 and 6.6). White perch dominated catches in the upper Bay, but was rare or absent in the mid and lower bay strata. In the mid and lower bay regions, weakfish and croaker were common. Overall, diversity of catches was highest at the northern-most and southern-most stations.

The respective design effects suggest that the stratified random survey consistently is more efficient than the transect survey for estimating mean CPUE in every season for all species combined (Figure 6.3), and for bay anchovy and white perch specifically (Tables 6.1-2, and 6.4-5). The relative standard errors of these estimates from the stratified random survey were on par, or lower than those from the transect survey, although the latter survey occupied from 55 % to 81% more stations. This supports the conclusion that transect sampling generally is less efficient than stratified random sampling for the system studied here. The effective sample sizes for estimating overall mean CPUE for the transect surveys were lower than the number of stations during all seasons, and similar to the number of transects during summer and fall. In contrast, the design effects suggested that transect sampling was at least as effective as stratified random sampling for estimating the abundance of weakfish during all three seasons (\( deff \leq 1 \)) (Tables
Here the effective sample sizes were larger than the actual number of stations for some seasons, especially for spring and fall. These design effects may be biased downwards because of the high frequency of zero catches within some strata. However, an inspection of the distribution of weakfish and the allocation of stations (Figure 6.1) confirms that transects effectively captured the spatial variability in abundance. For bay anchovy, in contrast, stations within transects had similar CPUE and thus did not capture both sources of the overall variance (Eq. 6.3). White perch were patchily distributed, but some locations appear to have persistent high density over time. Trawl stations along transects had significantly higher mean CPUE than the stratified random stations in both years (Tables 6.1-2, and 6.4-5). This suggests that white perch are highly patchy in distribution and that, while the deff was very poor, the fixed transects probably covered more of the patchy habitats that are favored by white perch, while the random stations missed these high-density areas by chance.

The inter-sample distances varied with the number of stations in the survey. The stratified random survey had the smallest sample size, involving approximately 20 stations in each survey. The average inter-station distance was 11.49 ±2.77 nm (mean ±SD). The fixed transect survey involved 28 stations, and had a corresponding longer inter-station distance of 7.86 ± 6.72 nm. When the two surveys were combined, the average inter-station distance was 5.65±0.411 nm. A stratified random survey with approximately 50 stations could be expected to have an average inter-station distance of 5.48 ± 0.94 nm, slightly shorter than the inter-station distance for the combined survey design. However, this difference was not significant. When all survey designs were compared, the average inter-station distance decreased as the number of stations in the survey increased (Fig. 6.5).

The composite estimator produced precise estimates of mean CPUE for all species combined, with relative standard errors (RSE) between 13% and 22% (Tables 6.3 and 6.6). The relative standard errors of the composite estimates of mean CPUE were 18% to 27% lower than the most precise individual component estimate. The combined estimates for white perch shows that the use of effective sample sizes to determine weights can yield more accurate results than the use of traditional weights based on the variances of each survey estimate. In the 2002 fall surveys, the stratified random trawl stations caught zero white perch (Table 6.1), compared to a
mean of 7.9 fish per tow for the transects. Weighting based on the variances would have assigned all the weight to the stratified random survey, resulting in a poor combined CPUE estimate of zero. The combined estimate (2.3 fish per tow) based on effective sample sizes is more reliable than the former.
Our approach to the use of the design effect is superior to using the relative standard error (RSE) for evaluating survey efficiency, as it is independent of the sample size $n$. Hence, it can be used to determine the sample size required to achieve an adequate level of precision in key estimates resulting from a given design. The efficiency of sampling along transects depends inversely on the homogeneity in catch per tow for clusters of stations within transects. Sampling at stations along transects is an efficient design if stations within each transect are as variable as those in the general population of trawling stations. In the transect surveys analyzed here, homogeneity is a common problem and so selecting an additional station from the same transect generally adds less new information than would a completely independent selection. With the exception of weakfish and croaker, results from the fixed transect surveys show that the design effect tends to be higher than unity. Hence, a simple random survey would generally be expected to produce more precise estimates for a similar survey effort. There was no evidence in our simulations of any systematic effect of the survey design on the expected inter-sample distance. Thus, in Chesapeake Bay, a stratified random survey with proportional allocation would be expected to achieve at least the same number of stations as the combined transect and stratified random survey for a fixed cost. A possible advantage of stratified random sampling over systematic sampling in open waters is that the former tends to result in a shorter sailing distance to occupy all stations (Harbitz and Pennington, 2004), and thus reduces survey cost for a fixed number of stations.

We treated transects and stations within transects as a two-stage cluster sampling design. In fact, the actual design was slightly more structured in the sense that transects were chosen so that spacing would be somewhat even. Such a design does not involve replication, and thus there is no unbiased design-based estimator of the variance of the mean CPUE. One reason for this allocation of stations in the TIES program was to ensure maximal spatial coverage over the bay. This is the same reasoning often used for taking systematic samples.

Effective estimation of means using complex survey designs requires estimators that fully account for the sampling design. Data collected from clustered samples often result in a
reduction in the effective sample size for estimating a statistic such as mean CPUE because of
the tendency of measurements collected within clusters to be more similar than measurements
taken between clusters (e.g., Pennington and Vølstad 1994; Williams 2000). For complex survey
designs, the estimation of the variance of the mean CPUE under the assumption of independence
between all observations will generally underestimate the true variance in the presence of
positive intra-cluster correlation. For complex surveys, we concur with Brogan (1998) and
recommend that specialized sample survey software such as SUDAAN be used for design-based
estimation of population parameters, descriptive analyses and analytical analyses. Alternatively,
a model-based approach such as geostatistical models could be used to determine the sampling
error in the form of the global estimation variance for a wide range of sampling designs (Petitgas
1999; Rivoirard et al. 2000; Christman et al., in preparation).

The effective sample size for the transect survey when estimating CPUE for all species
combined is closer to the number of transects than to the overall number of stations. This again
suggests that CPUE from stations within the same transect tend to be similar, while any two
observations from different transects are different.

The designated strata and proportional allocation of random stations did not substantially
reduce variability in CPUE between stations in the 2002 surveys, but generally resulted in higher
precision than for simple random sampling in the 2003 surveys. Thus, the relative efficiency of
the stratified random and transect sampling vary across years. However, the stratified random
design appears to be robust to variations in the spatial distribution of different species and hence
is recommended over simple random sampling.

For stratified random sampling the theoretical optimum allocation (Neyman allocation) of
a given number of hauls is to sample each stratum in proportion to its standard deviation
multiplied by the stratum size (Cochran, 1977). However, in practice it may be better to allocate
stations proportional to stratum size since the standard deviation only can be approximated from
previous surveys, and the spatial distribution of fish exhibits temporal variability. Stratification
with proportional sampling nearly always leads to gain in precision (Cochran, 1977), with the
largest gains being achieved when the strata means exhibit large variation.
This study suggests that a composite estimator with weights based on the effective sample sizes of individual survey estimates can yield more accurate results than weights based on variances. For trawl surveys, patchy distributions can result in zero catch even though some habitats have high densities. If an estimate from a simple random survey with zero catch is combined with another survey estimate with mean and variance greater than zero, then the commonly used weighting based on their respective variances will produce a poor combined estimate of zero. In this case, weights based on the variances would clearly yield an inappropriate estimate of the mean if both surveys employ simple random surveys with equal sample sizes. Our method of assigning weights based on their respective effective sample sizes, in contrast, will yield a more equitable combined estimate because the number of stations will determine the weight of the simple random survey. In the simplest case of combining two independent surveys with simple random sampling, our weights would appropriately yield the same estimate as the simple mean for the pooled samples. The composite estimator is unbiased as long as the variances are independent of the means. For trawl surveys, catch per tow tend to have a skewed distribution because of patchiness of fish populations, and the variance thus is likely related to the mean (Seber, 1986; Pennington and Vølstad, 1991). This is a serious problem when combining two surveys if the weight used in equation (1.8) is based on the variances obtained from the two surveys. Since we are using the effective sample sizes which depend on both the variance and the sample size for each survey, the differences are greatly attenuated. For example, had we used the variance weighting for the fall 2003 white perch data, the weight would have been 0.000079 and hence the transect results would have dominated the combined estimator. Instead, the use of effective sample size provided a weight of 0.46 and so both $\bar{y}_{STR}$ and $\bar{y}_{T}$ contribute to $\bar{y}_{comb}$ almost equally.

Our analysis suggest that the variances of the mean CPUE for the transect survey were relatively high because the stations were clustered, and not because the means were higher than for the stratified random (except for white perch). For a series of combined surveys, we recommend that the weight be fixed to eliminate bias caused by the dependence between the variance and the mean. The maximum reduction of 50 % in the variance of the combined mean CPUE is achieved when the two surveys have equal effective sample sizes. However, the precision of the combined estimate is robust to deviation from the optimal ratio ($R$) of effective
sample sizes; a change to $R$ from unity to 6 does not significantly increase the variance of the composite estimator (Rao, 2003, p. 58). In practice, hence, the use of a fixed weight across years should not appreciably increase the variance of combined estimates.

Acknowledgements
This study (Contribution No XXX of the University of Maryland Center for Environmental Science) was funded by the National Marine Fisheries Service, through a grant from the Chesapeake Bay Stock Assessment Committee (Grant NA07FU0534). This research would not have been possible without the help of the students and technicians at CBL who participated in the research cruises. In particular, we thank Kiersten Curti, Chris Heyer, and Dave Loewensteiner who served as chief scientists on CHESFIMS cruises. We appreciate comments from John Hoenig (VIMS) that helped improve this manuscript.
6.5. LITERATURE CITED


Table 6.1

Mean catch-per-unit-effort (CPUE) and measures of precision and design effects for the 2002 stratified random surveys.

<table>
<thead>
<tr>
<th>Season</th>
<th>Species</th>
<th>deff</th>
<th>N</th>
<th>n_eff</th>
<th>$\overline{y}_{STR}$</th>
<th>SE</th>
<th>RSE</th>
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Table 6.2
Mean catch-per-unit-effort and measures of precision and design effects for the 2002 transect surveys. The design effects ($deff$) are obtained from SUDAAN.

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<th>$\bar{y}_r$</th>
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<th>RSE</th>
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</table>
Mean catch-per-unit-effort and measures of precision and design effects for the 2002 combined stratified random and transect surveys. The estimates are obtained by using the optimal weights ($\phi_{opt}$) in eqs. 1.8 and 1.9. The ratio $r$ is the RSE for the composite estimate divided by the smaller RSE for the individual survey estimates.

<table>
<thead>
<tr>
<th>Season</th>
<th>Species</th>
<th>$deff$</th>
<th>$n$</th>
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<th>$\bar{y}_C$</th>
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<th>RSE</th>
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<td>0.67</td>
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<td>0.66</td>
<td>0.73</td>
<td>0.77</td>
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<td>0.33</td>
<td>0.38</td>
<td>0.73</td>
</tr>
<tr>
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<td>Weakfish</td>
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Table 6.4.

Mean catch-per-unit-effort (CPUE) and measures of precision and design effects for the 2003 stratified random surveys.

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<th>n_{eff}</th>
<th>\bar{Y}_{STR}</th>
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<th>RSE</th>
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<td>22</td>
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<td>0.1</td>
<td>0.55</td>
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<tr>
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<td>9</td>
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Table 6.5.

Mean catch-per-unit-effort and measures of precision and design effects for the 2003 transect surveys. The design effects ($deff$) are obtained from SUDAAN.

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<tr>
<th>Season</th>
<th>Species</th>
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<th>$N$</th>
<th>$n_{eff}$</th>
<th>$\bar{y}_T$</th>
<th>SE</th>
<th>RSE</th>
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</tr>
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</tr>
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<td>22.2</td>
<td>0.22</td>
</tr>
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<td>All Species</td>
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<td>31</td>
<td>6</td>
<td>223.2</td>
<td>108.9</td>
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</tr>
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<td>20</td>
<td>8</td>
<td>1,412.7</td>
<td>529.8</td>
<td>0.38</td>
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</tbody>
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Table 6.6.

Mean catch-per-unit-effort and measures of precision and design effects for the 2003 combined stratified random and transect surveys. The estimates are obtained by using the optimal weights ($\phi_{opt}$) in eqs. 1.8 and 1.9. The ratio $r$ is the RSE for the composite estimate divided by the smaller RSE for the individual survey estimates.

<table>
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<tr>
<th>Season</th>
<th>Species</th>
<th>$deff$</th>
<th>$n$</th>
<th>$n_{eff}$</th>
<th>$\overline{Y}_C$</th>
<th>SE</th>
<th>RSE</th>
<th>$\phi_{opt}$</th>
<th>$r$</th>
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<td>51</td>
<td>59</td>
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<td>0.50</td>
<td>0.9</td>
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<td>48</td>
<td>402.6</td>
<td>96.1</td>
<td>0.24</td>
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<td>18</td>
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<td>295.2</td>
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<td>0.49</td>
<td>0.8</td>
</tr>
<tr>
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<td>Croaker</td>
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<td>59</td>
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<td>0.9</td>
<td>0.37</td>
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<td>75</td>
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<td>0.49</td>
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<tr>
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<td>51</td>
<td>51</td>
<td>0.5</td>
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<td>0.27</td>
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<td>347.8</td>
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</table>
Figure 6.1. Stratification of the Chesapeake Bay mainstem (Lower, Mid, and Upper Bay), and an example of station allocation for the transect survey (●) and stratified random survey (○) and the distribution of relative abundance of (a) Bay anchovy and (b) weakfish during fall 2002.
Figure 6.2. Seasonal design-based estimates of mean catch per unit effort (cpue) across all species, and the combined estimates across surveys based on the composite estimator. Error bars represent ± SE.
Figure 6.3. Design effects for estimating seasonal mean catch per unit effort (CPUE) across all species by survey. The combined estimate is based on the composite estimator.
Figure 6.4. Design effects for estimating seasonal mean catch per unit effort (CPUE) of weakfish by survey. The combined estimate is based on the composite estimator.
Figure 6.5. Estimated inter-station distances for the fixed transect and stratified random surveys designs, and for combined surveys for actual and simulated sample selections.
Appendix 6.1

The optimum weight, obtained by minimizing equation Error! Reference source not found. with respect to \( \phi \) is a function of the expected variances of the mean CPUE under each design,

\[
\phi_{opt} = \frac{\text{Var}(\bar{Y}_T)}{\text{Var}(\bar{Y}_{STR}) + \text{Var}(\bar{Y}_T)}
\]

when the two surveys are independent (Rao, 2003). By definition, the expected variance of the estimated mean CPUE from each survey can be expressed by dividing the population variance of CPUE under simple random sampling, \( \sigma_{SRS}^2 \), with the effective sample size,

\[
\text{Var}(\bar{Y}_T) = \frac{\sigma_{SRS}^2}{n_T^*} \quad (A.1)
\]

and

\[
\text{Var}(\bar{Y}_{STR}) = \frac{\sigma_{SRS}^2}{n_{STR}^*} \quad (A.2)
\]

where \( n_T^* \) and \( n_{STR}^* \) are the effective sample sizes for the transect and stratified random surveys, respectively. Replacing \( \text{Var}(\bar{Y}_T) \) and \( \text{Var}(\bar{Y}_{STR}) \) in \( \phi_{opt} \) with their equivalents from (A.1) and (A.2) yield the desired result.