

ABSTRACT

Title of Document: AN EVALUATION OF THE
SYNCHRONIZATION IN THE DYNAMICS
OF BLUE CRAB (*CALLINECTES SAPIDUS*)
POPULATIONS IN THE WESTERN
ATLANTIC

Amanda R. Colton, Master of Science, 2011

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Marine, Estuarine, and Environmental Sciences

Blue crab populations along the east coast of the United States are known to fluctuate in size annually. Previously, the degree of coherence in abundance between these populations was unknown. My research used a combination of fishery-dependent and fishery-independent data to quantify the amount of synchrony among blue crab populations and to determine the mechanisms that drive abundance fluctuations. This was done by first fitting catch-survey models to time series of survey abundance and catch to obtain absolute abundance estimates. Subsequently, I used multivariate techniques to quantify the extent and pattern of synchronization. I found that a latitudinal pattern among blue crab populations exists among all the regions except Chesapeake Bay, which appeared to be anomalous. A combination of larval mixing in the coastal ocean and a Moran effect appear to be drivers of the synchrony among blue crab populations although more investigation into these mechanisms is needed.

AN EVALUATION OF THE SYNCHRONIZATION IN THE DYNAMICS OF
BLUE CRAB (*CALLINECTES SAPIDUS*) POPULATIONS IN THE WESTERN
ATLANTIC

By

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Chapter 1: Introduction

Understanding the processes by which animal and plant populations are regulated has been and continues to be a central question in ecology (Real & Brown 1991). Initial views held that populations were regulated internally. In a series of classic experiments Gause (1934) demonstrated that inoculations of *Paramecium* attained an equilibrium abundance, suggesting internal regulation of population growth. In particular, he showed that the rate of population growth was linearly dependent on population size. When present, the mechanisms responsible for regulation include density-dependent changes in mortality (e.g., due to predation or cannibalism) and density-dependent changes in fecundity (e.g., due to changes in resource availability). Such mechanisms act to decrease population abundance when the population is above its equilibrium abundance, or carrying capacity, and increase it when it is below carrying capacity. In contrast, others have argued that populations are impacted largely by density-independent factors (Andrewartha & Birch 1954). In this view, populations are not internally regulated, but rather their abundances vary in response to abiotic environmental factors, such as temperature. Although density-independent processes cannot regulate population abundance, it has been argued that they can control or limit population abundance. The debate between these two views of how population sizes are controlled was one of the foundational issues in ecology (Real & Brown 1991) and interest in the topic continues today.

Much of the literature exploring how and the extent to which populations are regulated has focused on interactions between populations. Much of this work has focused on models of predation and competition. For example, classic Lotka-Volterra predator-prey dynamics assume density-dependent mortality in the prey and

density-dependent production in the predator (May 1972). Such models predict the presence of equilibria for both predators and prey. Depending on the parameterization of the model, a range of dynamics can be generated including synchronized abundance patterns in predators and prey with the predator dynamics following the prey with a $\frac{1}{4}$ phase shift lag from the prey (May 1972). Similarly, models of interspecific competition imply density-dependent response changes in the vital rates of one species due to the abundance of the other and can also introduce correlations in abundances of interacting species.

The idea that the fluctuations of two or more populations can be correlated through time is called synchronization. Yet, the presence of synchrony need not imply the presence of density-dependent processes, as density-independent processes have also been shown to induce synchronization in different populations. For example, Fromentin & Planque (1996) reported that the abundances of two zooplankton species, *Calanus finmarchicus* and *C. helgolandicus* are negatively correlated with a one-year lag (Figure 1.1). These authors show that the correlation is caused by a common response to an index of oceanic climate, the North Atlantic Oscillation (NAO). More generally, in such cases the synchronization occurs because of either exchange of individuals among populations in a metapopulation (Cowen et al. 2006) or because of a common response of vital rates, such as growth and fecundity, to broad regional-scale environmental conditions (Liebhold et al. 2004; Moran 1953; Stenseth et al. 2002; Walther et al. 2002). Liebhold et al. (2004) have termed such patterns spatial synchrony under the idea that populations that overlap

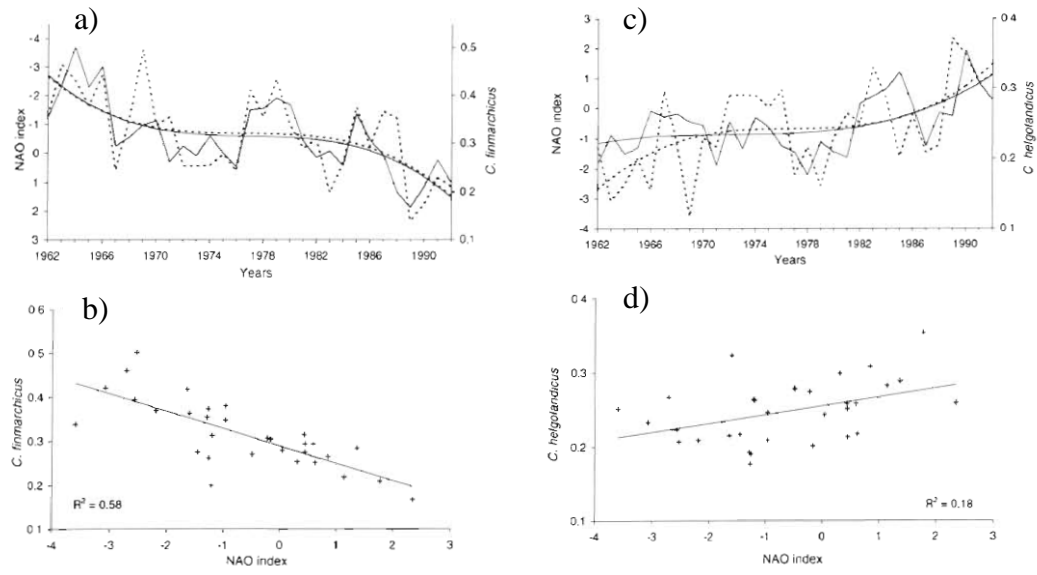


Figure 1.1. Relationship between NAO and two species of zooplankton in the North Sea where a) and c) demonstrate the time series of *Calanus finmarchicus* and *Calanus helgolandicus* (solid lines) respectively and NAO (dashed line) with a 3rd order polynomial smoother. Note the NAO scale is reversed in a). Linear regressions between NAO and b) *C. finmarchicus* and d) *C. helgolandicus* show opposite relationships between the two species and the NAO. A one year lag can be seen in the response of *C. helgolandicus* abundance to the NAO index. Figure taken from Fromentin & Planque 1996.

exactly would be perfectly synchronized and that the degree of synchrony decreases the further apart the populations get from one another.

Moran (1953) was one of the first to study the cause of spatial synchronization when he analyzed the synchronization of variation in the abundance of Canadian lynx, *Lynx canadensis*, and snowshoe hare, *Lepus americanus*, populations. Previous research had suggested that predator-prey dynamics were responsible for the observed pattern of synchronization (Volterra 1931). In contrast, Moran suggested that the dominant factor inducing the observed synchronization was a common response of both populations to temperature oscillations occurring at a larger, regional-scale. Owing to his seminal work, the density-independent synchronization of populations based on environmental processes became termed the Moran effect.

The Moran effect has been documented in many different ecosystems. The El Niño Southern Oscillation (ENSO) was found to correlate with instances of synchrony of damselfish species on the Great Barrier Reef (Table 1.1; Cheal et al. 2007) and three rodent species in Chile (Lima et al. 2001; Lima et al. 2002). The NAO may induce synchronization of zooplankton species in the northeastern Atlantic (Figure 1.1, Fromentin & Planque 1996), the timing of flowering of plants in Norway (Post & Stenseth 1999), phenotypic and demographic fluctuations in ungulates in North America and northern Europe (Post & Stenseth 1999), fluctuations in Canadian lynx populations (Stenseth et al. 1999), and breeding variations in European birds and amphibians (Forchhammer et al. 1998).

In cases of spatial synchrony, it is expected that the degree of synchrony should be negatively correlated with the distance separating the populations at the

Table 1.1. Response of damselfish populations in three reefs off of Queensland, Australia to patterns in summer El Niño Southern Oscillation and hard coral cover. Bold values indicate a significant effect of environmental variables on damselfish population size. Table taken from Cheal et al. (2007).

Species	Cooktown/Lizard Island			Cairns			Townsville		
	Effect size	95% CI	<i>P</i>	Effect size	95% CI	<i>P</i>	Effect size	95% CI	<i>P</i>
ENSO									
<i>P. lepidogenys</i>	-8.1	-18.4-2.2	0.12	13.9	6.1-21.7	0.0006	9.7	2.1-17.2	0.012
<i>P. moluccensis</i>	-7.0	-15.6-1.5	0.10	15.9	8.4-23.3	0.0001	3.2	-1.7-8.2	0.18
<i>P. wardi</i>	-3.4	-18.9-12.1	0.64	13.2	3.6-22.7	0.008	0.1	-7.3-7.4	0.99
<i>P. bankanensis</i>	-4.2	-23.1-14.7	0.69	6.8	2.4-11.2	0.003	6.6	-1.9-15.1	0.11
<i>P. brachialis</i>	-5.5	-16.9-5.9	0.32	21.6	10.8-32.4	0.0002	ND	ND	ND
<i>P. philippinus</i>	-0.3	-7.1-6.5	0.92	6.9	-0.9-14.7	0.07	3.6	-0.8-8.0	0.10
<i>P. amboinensis</i>	-2.6	-10.6-5.4	0.50	29.7	7.2-52.2	0.06	ND	ND	ND
<i>P. nagasakiensis</i>	5.3	-5.6-16.1	0.27	35.3	14.0-56.6	0.031	ND	ND	ND
<i>P. adelus</i>	-1.9	-5.8-2.0	0.31	5.2	-2.2-12.6	0.15	ND	ND	ND
Coral									
<i>P. lepidogenys</i>	0.8	-1.1-2.8	0.44	2.2	-0.8-5.1	0.19	2.2	0.4-4.0	0.024
<i>P. moluccensis</i>	0.9	-3.3-5.1	0.75	1.5	-0.8-3.7	0.17	0.7	-0.2-1.7	0.10
<i>P. wardi</i>	1.4	-10.1-13.0	0.85	-1.9	-4.4-0.7	0.15	-1.6	-3.5-0.4	0.17
<i>P. bankanensis</i>	2.7	-6.2-11.6	0.58	-1.7	-3.7-0.4	0.33	4.7	0.6-8.8	0.027
<i>P. brachialis</i>	0.3	-6.2-6.8	0.93	0.7	-2.5-3.9	0.66	ND	ND	ND
<i>P. philippinus</i>	1.5	-0.4-3.4	0.17	0.1	-3.0-3.3	0.95	0.1	-0.9-1.1	0.91
<i>P. amboinensis</i>	6.0	2.4-9.6	0.007	2.1	-18.4-22.6	0.85	ND	ND	ND
<i>P. nagasakiensis</i>	2.1	-4.4-8.7	0.59	-3.1	-25.7-19.4	0.80	ND	ND	ND
<i>P. adelus</i>	-1.2	-3.7-1.3	0.33	2.0	0.3-3.7	0.026	ND	ND	ND

scale of the environmental driver (Moran 1953) or at the scale of dispersal (Ranta et al. 1998). Aphid populations in the United Kingdom exhibited correlated dynamics at scales of 350-400km, owing to the broad scales at which the NAO influenced their dynamics (Saldana et al. 2007). Saether et al. (2007) reported that the spatial scale of correlation differed between populations of two common European birds: the great tit, *Parus major*, and the blue tit, *Cyanistes caeruleus*, partly due to the scale of the environmental forces acting on each population. Spatial correlations among blue tit populations declined substantially at scales >100km whereas great tit populations showed a high degree of coherence across the entire study range (800km) suggesting a more widespread environmental component influencing fluctuations of great tit populations than for blue tit populations (Figure 1.2). Ranta et al. (1998) examined how the rate of dispersal and the dispersal distance of individuals can influence fluctuations in the degree of synchrony of two populations through both space and time (Figure 1.3a). Higher dispersal rates and dispersal distances lead to a higher degree of synchrony and an increase in the scale over which synchronization occurs. Supporting this pattern, Myers et al. (1997) reported that recruitments of freshwater fishes were correlated at scales of up to 50km whereas marine species exhibited correlations at scales of up to 500km, which is a direct reflection of how the dispersal ability further increases the likelihood of synchronization. The presence of a Moran effect strengthens these relationships between dispersal and synchronization (Ranta et al. 1998; Figure 1.3b).

Detecting the effects of density-dependent and density-independent processes in marine organisms is particularly challenging because of the large dispersal

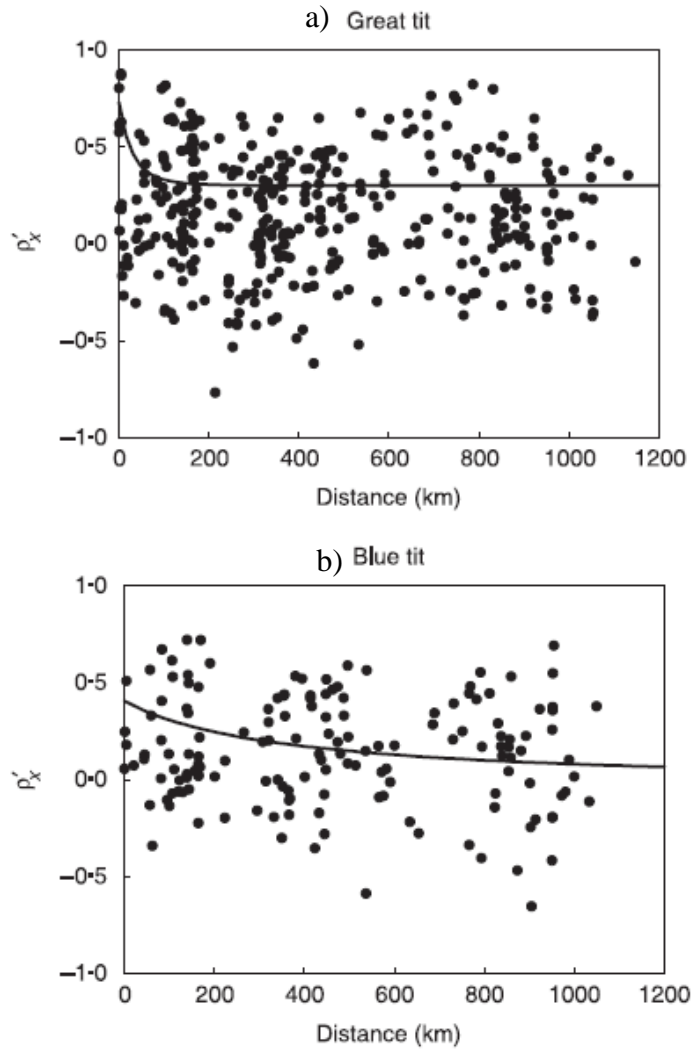


Figure 1.2. Correlation of a) great tit and b) blue tit populations with distance. Solid line represents the 50% bootstrap-distributions of the correlations. Figure taken from Saether et al. 2007.

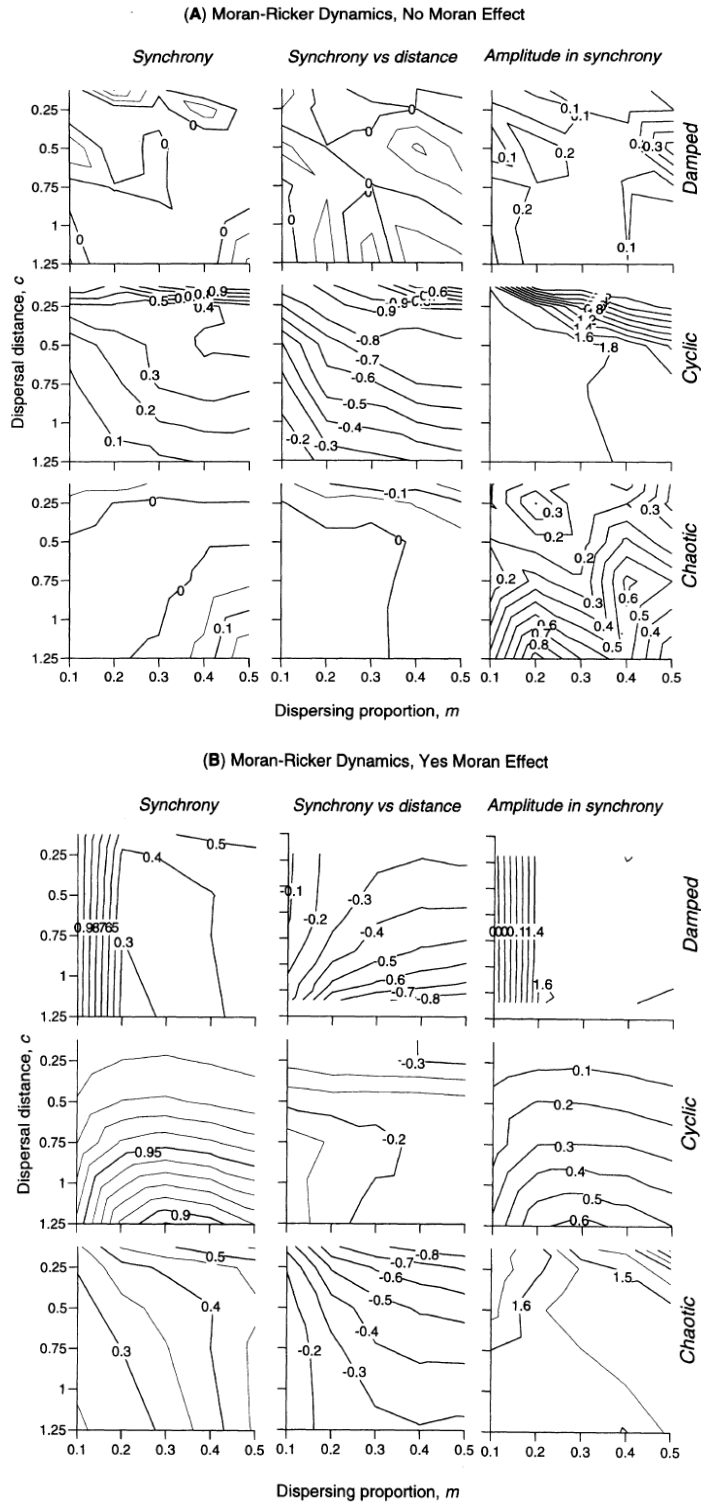


Figure 1.3. Effect of dispersal rate and dispersal distance on the synchrony in population dynamics, the distance over which synchrony occurs, and the scale of temporal fluctuation in synchrony in the a) absence and b) presence of the Moran effect. Figure taken from Ranta et al. 1998.

distances and open nature of marine populations. Many marine organisms are broadcast spawners, releasing gametes directly into the ocean where they are fertilized externally. The resultant offspring are susceptible to ocean currents and mixing which determine the pattern of offspring dispersal and how much inter-population exchange occurs. As a result, reproduction in marine species often becomes decoupled spatially from the recruitment of new individuals into the population, further complicating the quantification of regulation in marine species (Webster 2003). Adults of many species can also disperse large distances which can make it challenging to distinguish one population from another.

Populations of blue crab, *Callinectes sapidus*, occur in estuarine and coastal ecosystems in the western Atlantic commonly ranging from Cape Cod to northern Argentina, although they can be found as far north as Nova Scotia during warm conditions (Williams 1974). Throughout its range, blue crab is an important component of the ecosystem, often coupling benthic and pelagic food webs (Baird & Ulanowicz 1989; Hines 2007). In addition, the species supports important commercial fisheries in many areas. However, over the past two decades blue crab populations have been declining in several prominent Atlantic estuarine ecosystems in the United States (Miller et al. 2005). If these declining populations are synchronized, then the declines might be explained by a common natural factor in addition to or separate from a common response to over-exploitation. However, the extent to which blue crab populations in different regions are synchronized is currently unclear. Also, the mechanisms that might account for such synchronization, if present, are unexplored.

A consideration of the blue crab life history would suggest the potential for both direct exchange of individuals between neighboring populations and a common response to environmental forcing. The blue crab exhibits a complex life history wherein mature females release larvae near the mouths of estuaries and bays and these larvae are subsequently transported out into the coastal ocean (Figure 1.4). Larvae undergo several molts before returning to estuarine and coastal systems as megalopae (Hines 2007). The distribution of larvae in the coastal ocean and their subsequent ingress into estuarine nursery habitats is influenced by oceanic conditions (e.g. tides and currents – Roman & Boicourt 1999) and by wind stress (van Montfrans et al. 1995; Johnson & Hess 1990). Lunar phase has also been implicated in larval ingress, presumably through its effect on the tide (van Montfrans et al. 1995). Once in the estuary, temperature cycles can play a role in growth rates, as the intermolt period of blue crab depends on the water temperature (Brylawski & Miller 2006). Intriguingly, Hurt et al. (1979) suggested that blue crab landings, and therefore presumably abundance, may be influenced by tidal variation resulting from Earth-Moon-Sun interactions and sunspot cycles, as blue crab landings in Chesapeake Bay correlated with these cycles fairly well.

Given the blue crab's complex life history, understanding the coastal current systems in the western Atlantic can provide insight into the proportion of surviving larvae that will be retained in the parent estuary versus exported to a neighboring estuary. Retention of larval blue crab in Delaware Bay has been well- studied and it has been concluded that, due to the oceanographic conditions of the region, most surviving larvae released from Delaware Bay are either returned to the parent estuary

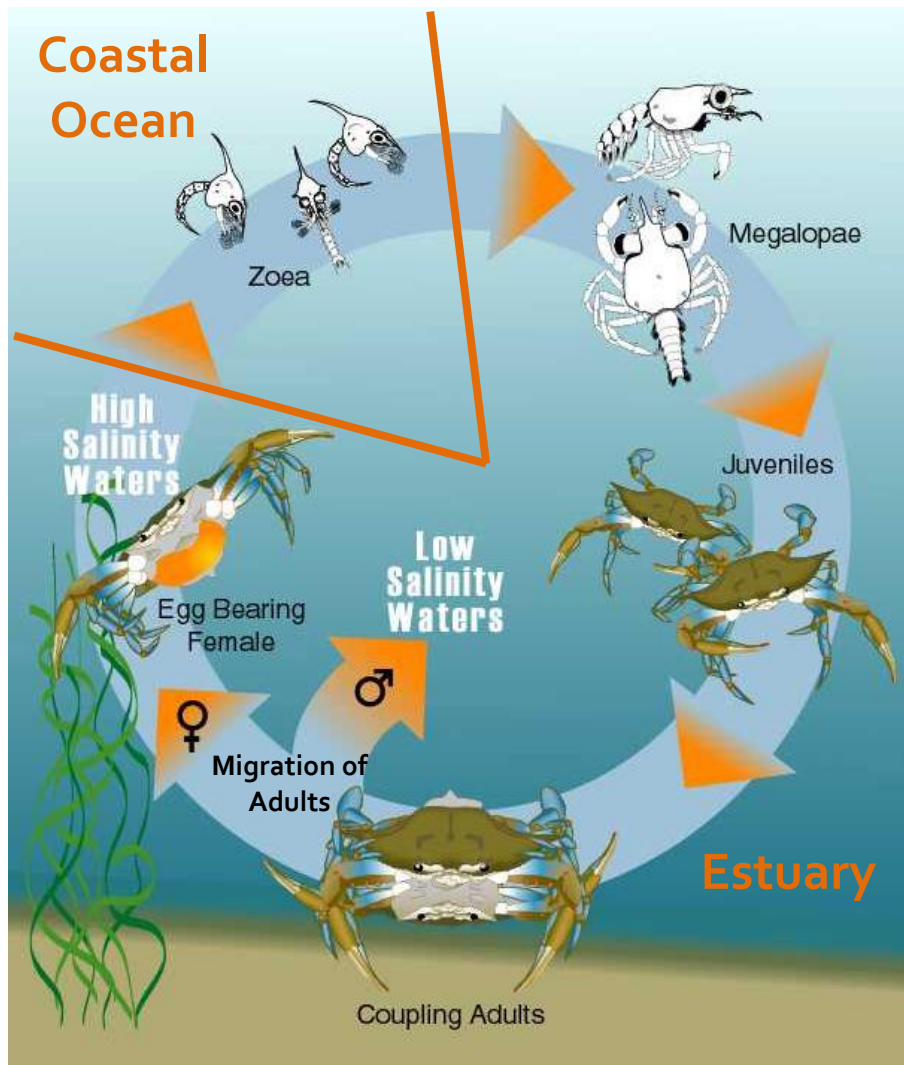


Figure 1.4. Conceptual diagram of blue crab life history adapted from Cheney (2002). Original credit for figure to Chip Cheney.

or transported southward in the coastal current (Tilburg et al. 2009; Epifanio et al. 1989; Little & Epifanio 1991; Garvine et al. 1997). Collectively, these studies indicate that there is likely not much import of blue crab larvae from other estuaries into Delaware Bay because of the oceanographic structure of the region. Together, these findings suggest that any synchronization due to mixing between Delaware Bay and other estuaries would have to be driven by the export of Delaware Bay larvae. Larval retention in other estuaries along the east coast of the United States has remained largely unexplored, but a few preliminary studies have been conducted. Roman and Boicourt (1999) have quantified dispersal of blue crab from the Chesapeake Bay. Limited work has begun in North Carolina. Reyns et al. (2007) found that blue crab recruitment in Pamlico Sound, NC was driven by both wind and tidal forces, as neither mechanism alone could be used to accurately simulate the distribution of crabs in this area. A study in the Newport River estuary, NC looked at the settlement of a number of species of crabs, including blue crab, and concluded that larval behavior may be the main mechanism influencing megalopal distribution in this particular estuary (Ogburn & Forward 2009). Even less is known about the dispersal of blue crab larvae in other estuaries. However, the patterns from those estuaries that have been studied suggests that exchange among estuaries is limited geographically and that there is unlikely to be a “common” offshore pool of potential recruits.

Genetic evidence provides further support that physically-driven exchange may be geographically restricted. McMillen-Jackson et al. (1994) and McMillen-Jackson & Bert (2004) quantified the genetic diversity in blue crab from United

States estuaries in the western Atlantic and in the Gulf of Mexico under the hypothesis that more diversity would indicate more mixing of populations. They found genetic diversity was extremely high throughout the entire study area. However, haplotype diversity decreased slightly as latitude increased, with New York populations being slightly less diverse, suggesting the potential of more limited gene flow in northern estuaries. This indicates that blue crab dispersal may be reduced along the northwestern Atlantic although it is not likely to have a measurable effect on synchrony because this difference in haplotype diversity with latitude is very small compared to the overall genetic diversity exhibited in blue crabs. If the interpretation of this genetic pattern is valid, we would expect higher variability in the dynamics within and among northern populations and higher synchrony in abundance among the southern populations. Preliminary work at the Institute of Marine and Environmental Technology (IMET) suggests that the diversity in blue crabs is too large to be able to distinguish between populations. This diversity is likely the result of a high gene mutation rate, but may also be indicative of mixing which would refute the findings of the McMillen-Jackson et al. work (A. Place, IMET, pers. comm.).

Traditionally, blue crab populations in the western Atlantic have been managed individually under the assumption that each population has unique dynamics. Yet, as suggested above, neighboring populations may be synchronized either through larval exchange or a common response to regional environmental conditions. If environmental conditions, such as ocean climate, are determined to be the primary mechanism driving synchronization, evidence from patterns of environmental covariates could be used to predict *a priori* the degree of

synchronization among populations. Further, if populations are coupled as a result of common climatic forcing, i.e., a Moran effect, then the coherence between pairs of populations should decrease as the distance between populations increases. Other mechanisms that link populations may also exist. Regardless of mechanism, if such regional coherence exists management strategies may need to be implemented on regional scales rather than on the state by state basis as is currently practiced.

Because of the economic importance of blue crab fisheries throughout the western Atlantic, the management jurisdictions have sought to monitor the status of the blue crab in each of their jurisdictions. Generally, each state has kept records of commercial catch and participation in the fishery for many years. For example, commercial landings data are available for the Chesapeake Bay from as early as 1880. These fishery-dependent data may provide a useful index of abundance in each system, even though there is evidence that fishery-dependent data are not always fully reliable as indices of abundance (Walters & Martell 2004). For the majority of these systems, relevant management agencies have also supported fishery-independent surveys that are more likely to provide reliable indices of abundance. However, in most jurisdictions the survey time series don't go back as far in time as landings data. In combination, these fishery-dependent and fishery-independent data provide a foundation to assess the extent to which blue crab populations are synchronized in the western Atlantic.

Objectives

The overall goal of my thesis research was to analyze fishery-independent (i.e. surveys) and fishery-dependent (i.e. harvest) data from blue crab populations in the

western Atlantic, from New York to Florida, to determine the extent and pattern of coherence in the time series of abundance for these populations. I quantified patterns in the spatial structure of coherence among time series to assess if synchronization was occurring. Also, I assessed whether and which environmental covariates could explain any coherence found in population fluctuations. All of the necessary fishery-independent and fishery-dependent data was obtained from the appropriate state agencies along the Atlantic coast from New York to Florida. I identified two specific objectives to structure my research.

Objective 1: *Employ catch-survey assessment models to generate absolute abundance estimates for each state.*

For this objective I used a simple, structured assessment model to estimate time series of absolute abundance. Fishery-independent survey indices were estimated using generalized linear models (Delta-GLM function in R v.2.11.1). A variety of environmental and survey design parameters were taken into account when creating these indices. I then fit a catch-survey model (CSA, Collie and Sissenwine 1983) to fishery-independent survey data and landings data for each region from Delaware Bay to Florida to estimate time series of absolute abundance.

I address this objective in Chapter 2 of the thesis. Chapter 2 is prepared as a draft of a manuscript to be submitted for publication in *Estuaries and Coasts* as Colton, Wilberg and Miller.

Objective 2: *Use standardized fishery-dependent data and absolute abundance estimates from catch survey models for each state to identify patterns of spatial coherence in abundance both among regions and in comparison with environmental factors.*

For this objective, I used both fishery-dependent estimates of landings (a possible index of relative biomass) from New York to Florida and estimates of absolute abundance from the catch-survey models obtained in Objective 1 to identify whether and the degree to which blue crab populations in the western Atlantic are synchronized. Harvest data were available from all reporting jurisdictions from New York to Florida. At least one survey was available for all regions except New York so all regions except New York had a time series of estimated absolute abundance.

Time series of landings and absolute abundance were examined using two multivariate approaches, principal component analysis (PCA) and dynamic factor analysis (DFA; Zuur et al. 2003a), to identify patterns of coherence in populations in the western Atlantic and to determine if a Moran effect is acting on blue crab populations.

I address this objective in Chapter 3 of the thesis. Chapter 3 is prepared as a draft of a manuscript to be submitted for publication in Marine Ecology Progress Series as Colton et al.

Chapter 2: Stock assessments for blue crab populations along the U.S. Atlantic coast

Abstract

Blue crab, *Callinectes sapidus*, is important both biologically and economically in coastal ecosystems of the western Atlantic. It is difficult to compare the dynamics of blue crab from different populations throughout this range because either stock assessments have not been conducted for all populations in the western Atlantic or because, when such assessments have been conducted, they have used methods that differ from population to population. For this study, I used a combination of fishery-dependent (i.e. landings) and fishery-independent (i.e. surveys) data from each region to estimate time series abundance for each population using a Collie-Sissenwine catch-survey model. Absolute abundances for adult and recruit blue crabs were successfully estimated by the model for each region. I found that my results were significantly correlated to the existing abundance estimates from the Delaware Bay, Chesapeake Bay, and Florida stock assessments, suggesting the model I applied to each state was robust. My results suggest that five of the seven regions for which I conducted assessments experienced declines in abundance when comparing the 2008 abundance to that of the first year of their survey. Only Delaware Bay and North Carolina witnessed an increase. This pattern suggests that blue crab populations in the western Atlantic may be demonstrating coherent changes in abundances, caused either by similar but potentially independent stressors, such as exploitation, or similar responses to a common factor affecting abundance.

Introduction

Management agencies typically collect and analyze two categories of data to better understand the status of exploited populations. The first category is fishery-dependent data, most often in form of landings and effort data. Such data are collected from fishermen or dealers and are used to quantify how much weight of the target species or how many individuals are being taken from the population each year as well as to understand the economics of the fishery. Although extremely valuable to fishery managers, a reliance on fishery-dependent data is not without concern. Most prominent among these concerns is that the catch in the fishery may not be linearly related to abundance. Important departures from linearity can be caused by changes in the efficiency of the capture gear resulting from new technologies, and changes in the distribution of the underlying exploited population that can make it more or less vulnerable to the fishery (Walters 2003). An additional concern affecting the utility of fishery-dependent data as a proxy for abundance is that management actions, through the implementation of new reporting policies, protocols, etc., have the potential to cause seemingly large increases or decreases in landings that do not necessarily reflect the underlying trends of abundance (Fogarty & Miller 2004).

The second category of data collected by management agencies is fishery-independent data. Fishery-independent data, which generally come from surveys, are collected externally to the fishery in order to implement unbiased, statistically-valid sampling methods that obtain reliable information on the relative abundance of a given population. There is an extensive literature on the design and use of fishery-

independent data in management (Rozas & Minello 1997; Smith & Tremblay 2003; Rotherham et al. 2007). These data are important for monitoring and assessing the status of aquatic resources, particularly in fisheries for which fishery-dependent data are known to be misreported or concentrated in a few areas (Cook 1997; Rotherham et al. 2007).

Most often both fishery-dependent and fishery-independent data are combined in stock assessments to assess the status and trends in abundance and exploitation of targeted species. Such assessments often aid fishery managers in establishing management reference points, such as target abundance and fishing mortality, that will ensure sustainability. Several different categories of stock assessments have been developed that differ in the degree to which they disaggregate the population, the extent to which they resolve independent sources of mortality, and the extent to which they represent sources of uncertainty in both the observed data and the population processes they represent. Experience suggests that because the different assessments weigh population processes and observations differently, they often produce different stock histories (Polacheck et al. 1993; Hollowed et al. 2000). Thus, if one wishes to compare the importance of processes among exploited populations, it is important that inferences are drawn from populations assessed under the same assessment framework.

Blue crab, *Callinectes sapidus*, populations exist in coastal bays and estuaries from Argentina to Massachusetts (Williams 1974). Understanding the dynamics of individual blue crab populations is of interest for both biological and economical reasons. Blue crabs function as important links in estuarine ecosystems, often

connecting benthic and pelagic food webs (Baird & Ulanowicz 1989; Hines 2007). Economically, blue crab support important commercial and recreational fisheries in many Atlantic estuaries (Bunnell et al. 2010). As a result, management agencies along the eastern United States have collected fishery-independent and fishery-dependent data on crabs within their corresponding jurisdictions over a long period of time. The fisheries within each jurisdiction are managed independently. However, the potential remains that neighboring populations may covary because of either inter-population exchanges (Roman & Boicourt 1999) or a common response to an environmental driver (Brylawski & Miller 2006; Hurt et al. 1979) which may suggest management should be applied on a broader scale.

Several management jurisdictions along the U.S. Atlantic coast have conducted stock assessments of the blue crab population within their jurisdiction (Wong 2009; Miller et al. 2011; Eggleston et al. 2004; Harris 2000; Murphy et al. 2007). These assessments reconstruct the historical trajectory of abundance in each of their jurisdictions. These reconstructions could form the basis of an analysis to evaluate the degree of synchrony among neighboring populations. Three deficiencies currently preclude such an analysis. First, not all jurisdictions along the Atlantic coast have conducted assessments. For example, the blue crab populations in the coastal bays of Maryland and Virginia and in Georgia have yet to be assessed. Additionally, the assessment frameworks used in these jurisdictions differ. For example, the blue crab population in Delaware Bay is currently assessed using a catch-survey analysis (Wong 2009), that in the Chesapeake Bay using a sex-specific catch multiple survey analysis (Miller et al. 2011), and that in North Carolina using

both a surplus production model and a catch-survey model (Eggleston et al. 2004). Finally, not all assessments that have been conducted have been updated recently. Thus, the periods for which absolute abundance estimates are available differ.

Catch survey models (CSA) can be used to incorporate both fishery-independent and fishery-dependent indices of abundance in order to obtain an annual absolute abundance estimate. These models were originally developed by Collie & Sissenwine (1983) and are useful because they do not require age structure as an input into the model, making them ideal for modeling species such as crustaceans where the age structure is difficult to measure and largely unknown. CSA models have been applied to yellowtail flounder and haddock in New England (Collie & Sissenwine 1983), northern shrimp in the Gulf of Maine (Cadrin et al. 1999), and blue crab in both Delaware Bay (Kahn & Helser 2005; Wong 2009) and in Chesapeake Bay (Miller et al. 2005).

There is flexibility in how CSA models are structured. For example, Cadrin et al. (1999) were able to separate mortality into six month intervals based on the timing of the fishery in relation to the timing of the survey. The 2005 Chesapeake Bay blue crab stock assessment was able to modify the catch survey model so that multiple surveys could be incorporated into the CSA (Miller et al. 2005). In addition to considering alterations in the structure of the CSA model, Cadrin et al. (1999) and Mesnil (2003) suggest that bootstrapping may be required to avoid inflated variances, which can result from minimization routines performed by the model.

As a preliminary step to an analysis of the synchrony of blue crab populations, here I conduct stock assessments of all the principal blue crab populations along the

U.S. Atlantic coast using the same assessment approach: New York, Delaware Bay, Chesapeake Bay, the coastal bays of Maryland and Virginia, North Carolina, South Carolina, Georgia, and Florida (Figure 2.1). Fishery-dependent and fishery-independent data were obtained from relevant management jurisdictions. I interviewed managers from each region to understand potential changes in survey design that may have affected fishery-independent indices and reporting changes that may have affected commercial data. I conducted intervention analyses to account for known reporting changes in each commercial catch time series (Fogarty and Miller 2004). Subsequently, I developed a common CSA for each region. I note that insufficient fishery-independent data were available for New York, and thus no assessment could be conducted for this jurisdiction. Here, I provide brief descriptions of the fishery-independent surveys that obtain blue crab information and are conducted by states within my study range. Next, I analyze and summarize patterns in commercial data. Subsequently, I present results of the application of CSA to each management jurisdiction. The pattern in abundances of blue crab in the different regions derived from the CSA models can be used to assess the degree of synchrony among the different regions. Specifically, in the absence of synchrony, I would expect to find no correlation among the abundance of blue crab in the different regions.

Methods

Fishery-independent data

Delaware Bay Surveys

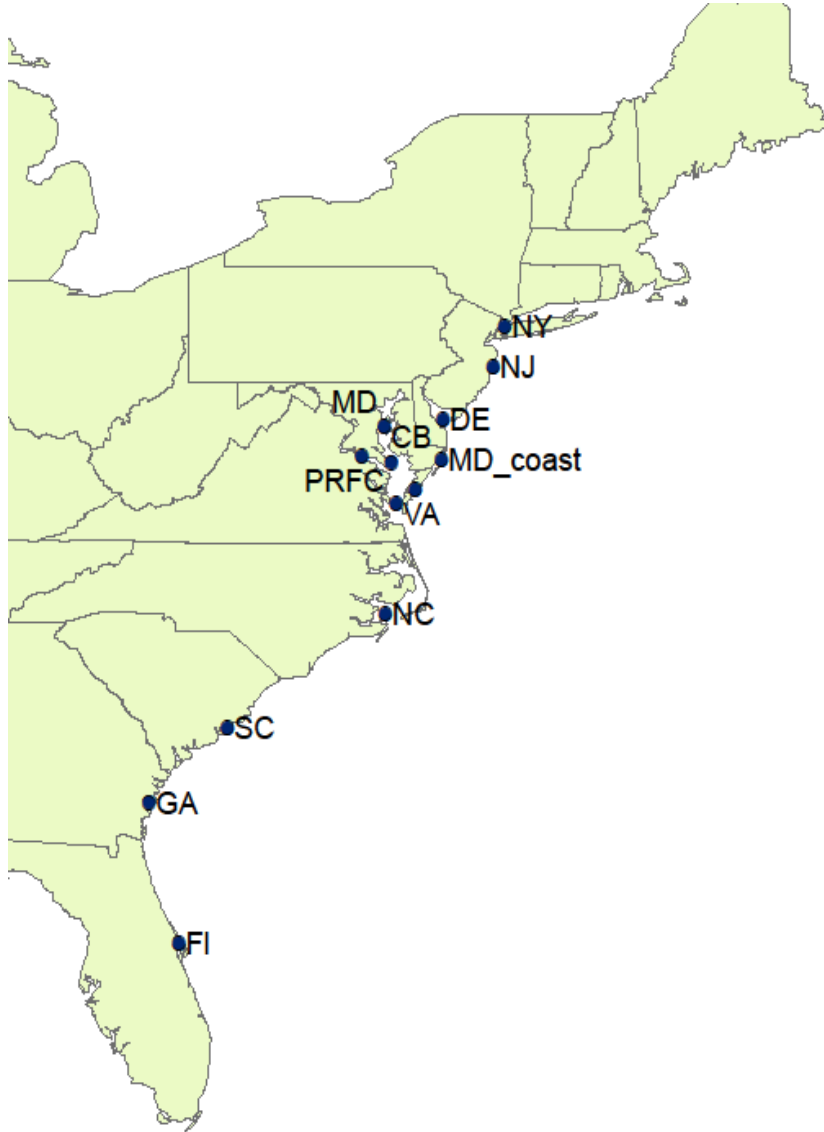


Figure 2.1. Map of the east coast of the United States. Each jurisdiction is labeled at the point that was estimated to be the center of landings.

Two surveys are available as fishery-independent data for Delaware Bay. The Delaware Division of Fish & Wildlife has conducted a trawl survey since 1978 using a trawl with a 16' footrope. Ten-minute tows are conducted at fixed stations in the western portion of Delaware Bay up into the Delaware River monthly from April through October (Figure 2.2). Crabs from each tow are counted, sexed, and classified by size into 5mm length bins. Wong (2009) determined that the lower 26 stations should be used when creating indices because they have been sampled the most continuously. Wong (2009) also recommended using data from September and October when creating indices for age-0 (<60mm) crabs.

The Bureau of Marine Fisheries within the New Jersey Department of Environmental Protection has conducted a finfish trawl survey since 1991 that is used to develop abundance estimates and analyze the status of a variety of species in the region (Normant & Hearon 2010). Eleven fixed stations on the eastern side of Delaware Bay are sampled monthly from April through October using an otter trawl with a 16' footrope (Figure 2.3). Ten-minute tows run against the tide are conducted at each station. Blue crabs are counted, sexed, and up to 50 randomly chosen individuals are measured for each sample. Blue crab is one of the five most abundant species caught in the survey. Depth, salinity, water temperature, and, in more recent years, dissolved oxygen are recorded for each tow. Between 1991 and 1996 sampling frequency of each station was inconsistent due to a combination of limited manpower and weather.

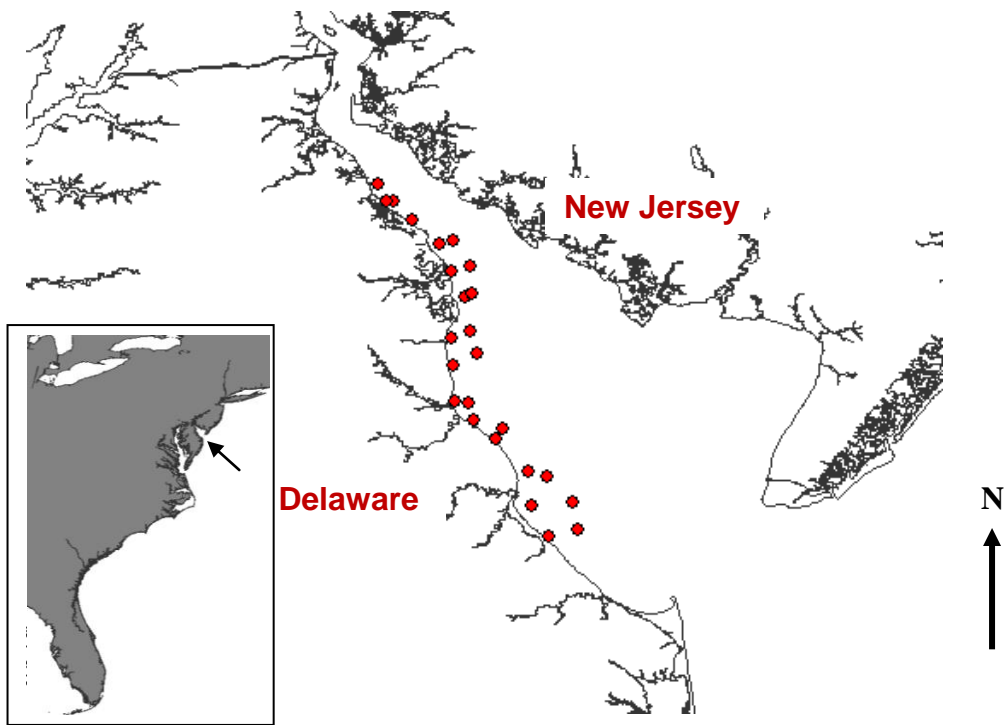


Figure 2.2. Map of survey stations for the Delaware trawl survey. Note that only the 26 core stations that were used for analysis are depicted here.



Figure 2.3. Map of survey stations for New Jersey trawl survey.

Chesapeake Bay Surveys

The Chesapeake Bay has abundant fishery-independent data available with a variety of surveys that contain information about the blue crab population in the Bay. Of the surveys available, I deemed four were appropriate for my study. The Virginia Institute of Marine Science (VIMS) trawl survey is the longest-standing survey in the region with a time series beginning in 1955 and samples the southern portion of Chesapeake Bay (Figure 2.4). The Maryland Department of Natural Resources (MDNR) trawl survey samples stations on the eastern shore and tributaries of the Maryland portion of Chesapeake Bay and has been conducted for the last 28 years (Figure 2.4). The primary survey for sampling blue crabs baywide is the winter dredge survey, which began in the winter of 1989/1990 (Figure 2.4). These first three surveys were used in the two most recent Chesapeake Bay blue crab assessments (Miller et al. 2005, 2011). However, an additional survey is also available. The Chesapeake Bay Multispecies Monitoring and Assessment program (ChesMMAAP), is a baywide trawl survey that was instituted in 2002 (Figure 2.4).

The VIMS juvenile finfish and blue crab trawl survey began in 1955 in the southern portion of Chesapeake Bay with the purpose of monitoring trends in abundance for species in the area. The survey has expanded over the years from sampling only the York River to covering seven strata ranging from the mouth of Chesapeake Bay to the Virginia/Maryland border and including the freshwater tributaries of the York, James, and Rappahannock River (Figure 2.4a). In total, about 60 stations are sampled monthly and these stations are chosen in both a random and fixed manner. Crabs caught in the trawl are counted, measured, and sexed. A few

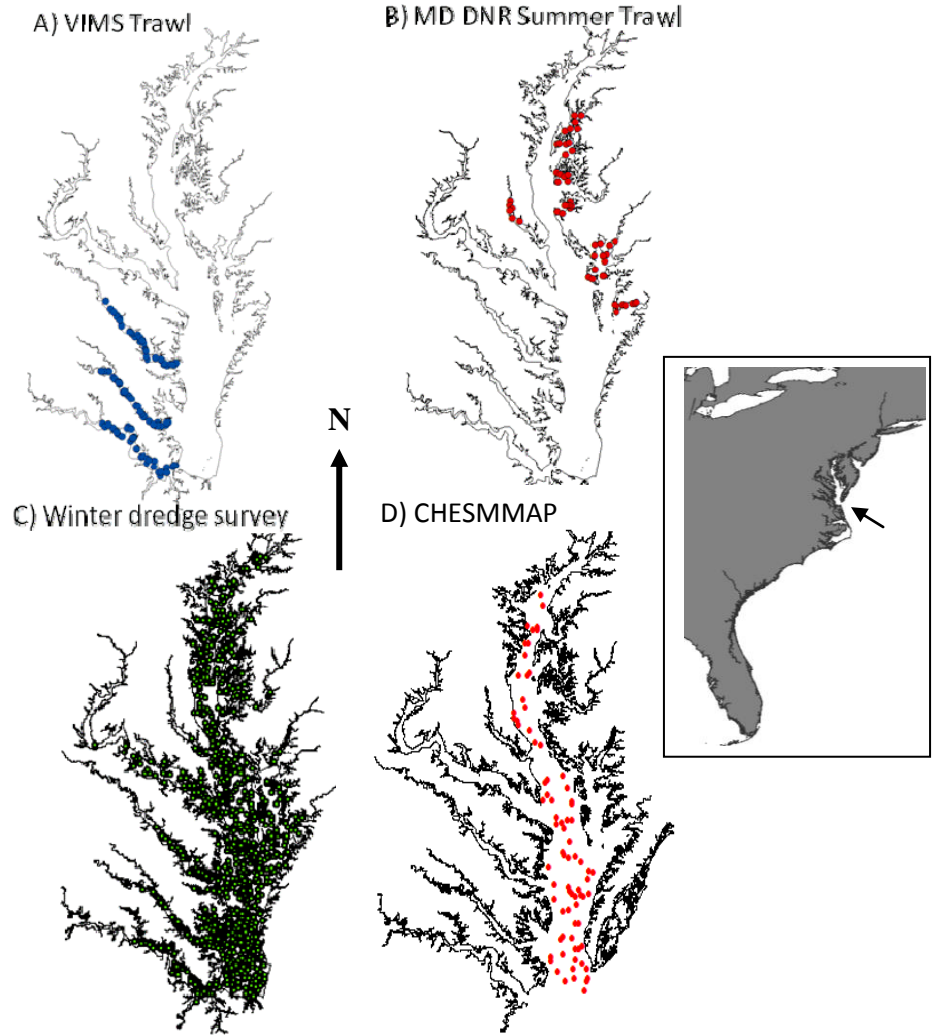


Figure 2.4. Map of survey stations used in analyses for a) the VIMS trawl b) the MD trawl c) the baywide winter dredge and d) one sampling period of the CHESMMAP trawl.

important changes have occurred throughout the duration of the survey. A tickler chain and net liner were added to the gear in 1973 and 1979 respectively. Calibration factors can be used to account for these changes (Hata 1997). Based on the findings in the 2011 stock assessment (Miller et al. 2011) data from the spring are most useful for creating age-0 crab indices due to the fact that in the fall age-0 crabs are continuously recruiting and therefore the cohort size will be constantly changing through the season. Adults should also be indexed from the spring survey because in the fall migration to the overwintering areas begins, which may influence abundance estimates. Because of inconsistencies in the length of the sampling period for each stations of the survey, data from the three tributaries (York, James, and Rappahannock) should be used to create indices (Miller et al. 2011).

The MDNR trawl was instituted in 1977 to sample both the bay portion and the tributaries on the eastern shore of Maryland. Some western shore tributaries were added in 1984 and more eastern shore areas were included in the survey beginning in 2003. The survey is conducted from May – November at fixed stations although coverage is inconsistent both temporally and spatially (Figure 2.4b). An otter trawl with a 16' footrope has been used throughout the entire duration of the survey. A change in how crabs were recorded occurred in 1989. Originally, crabs were counted and binned into size categories for age-0, age-1, and age-2⁺ crabs. Beginning in 1989, individual crabs were measured. Data for month, strata, water temperature, salinity, and water depth have also been recorded throughout the duration of the survey.

When water temperature falls below $\sim 10^{\circ}\text{C}$ growth ceases and blue crabs become dormant for the winter, burying into sediments (Brylawski & Miller 2006; Bauer & Miller 2010). This period of dormancy is an ideal time to conduct a baywide abundance survey. The baywide winter dredge survey has been conducted annually since the winter of 1989/1990 and is a cooperative effort between Maryland and Virginia. The survey is designed as a stratified random sampling scheme. These strata were created based on area, sediment, and depth for the first two years, but in all other years there have been three regional strata: upper Bay, mid-Bay, and lower Bay. About 1200 stations are sampled every year in waters deeper than 1.5m (Figure 2.4c). A 6' wide crab dredge has been used throughout the survey. Crabs are measured, counted, and sexed for each tow. Depth, temperature, and salinity have been measured at each station throughout the survey.

The ChesMMAP survey began in 2002 and is conducted by VIMS. The survey uses a stratified random design, dividing the bay into five strata with 80 sample sites within each of these strata (Figure 2.4d). It is conducted bimonthly from March through November each year using a two-bridle, four seam bottom trawl with a 45' footrope. The net is towed for 20 minutes at each site and blue crabs are counted and measured. Water temperature, salinity, and dissolved oxygen at both the surface and bottom of the water column are recorded at each site. This survey was designed to sample a variety of priority fish species for the Chesapeake Bay. Blue crab is not one of the target species, but data have been collected and indices are calculated each year. Survey indices for blue crab are calculated by taking month,

region, and depth strata into account and using a geometric mean catch per area swept approach (Bonzek et al. 2010).

Maryland Coastal Bays Surveys

Since 1972, the MDNR has conducted a trawl and seine survey for a variety of species in the coastal bays located on the ocean side of the eastern shore of Maryland. The trawl portion of the survey occurs monthly from April through October and samples 20 fixed stations with a semi-balloon trawl with a 16' footrope (Figure 2.5). The seine survey has 19 fixed stations that are sampled in June and September each year with a 50' bag seine (Figure 2.5). Crabs in these surveys are counted, sexed, and measured. A variety of environmental data are collected at each site for both surveys including depth, wind speed, temperature, and salinity. Area swept is also recorded for the trawl survey. Data prior to 1989 is generally considered to be unreliable due to the lack of a standard protocol before this sampling year (Barkman 2011).

North Carolina Survey

The North Carolina Department of Marine Fisheries instituted an estuarine trawl survey in 1971 to identify nursery areas and create recruitment indices for important species in the state, including blue crabs. Two major changes in survey design occurred in 1978 and 1989. In 1978 tow length was set to one minute and in 1989 an effort was made to make the survey more efficient, which led to the identification of 104 core stations that are sampled in May and June (and in some

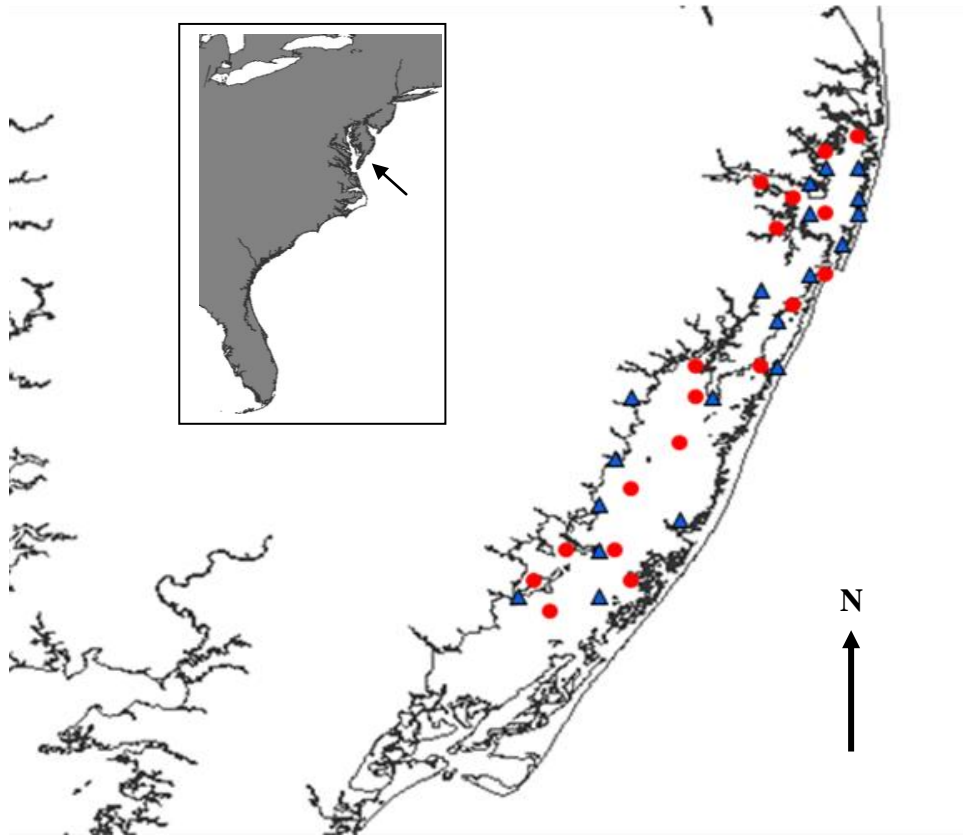


Figure 2.5. Map of survey stations for the Maryland coastal bays seine (blue triangles) and trawl surveys (red circles).

years July in order to survey weakfish, *Cynoscion regalis*, and spotted seatrout, *Cynoscion nebulosus*, rather than year round (Figure 2.6). This change in protocol also led to the use of only one gear type, a 10.5' head rope trawl with tickler chain. Data from 1978 through the current year are considered to be valid for use in studying blue crab populations. A number of environmental parameters are recorded at each site, including bottom composition, sediment size, secchi depth, water depth, water temperature, salinity, and dissolved oxygen (since 1997). Blue crabs are counted, sexed and up to 60 individuals are measured at each station.

South Carolina Survey

The Crustacean Management Section of the South Carolina Department of Natural Resources initiated a trawl survey in 1979 to sample its blue crab population. Fifteen-minute tows are conducted at each station. Seven areas are sampled monthly in Charleston Harbor and 27 other stations in seven of South Carolina's other estuaries are sampled in March, April, June, August, October, and December (Figure 2.7). Water temperature and salinity are recorded at each sample site. Crabs are counted, sexed, and measured for each tow.

Georgia Survey

The Coastal Resources Division of the Georgia Department of Natural Resources initiated an ecological monitoring trawl survey in 1976 (Belcher & Jennings 2009). Sampling is conducted using a stratified fixed station design, with strata determined by the estuary (Wassaw, Ossabaw, Sapela, St. Simons, St. Andrew,

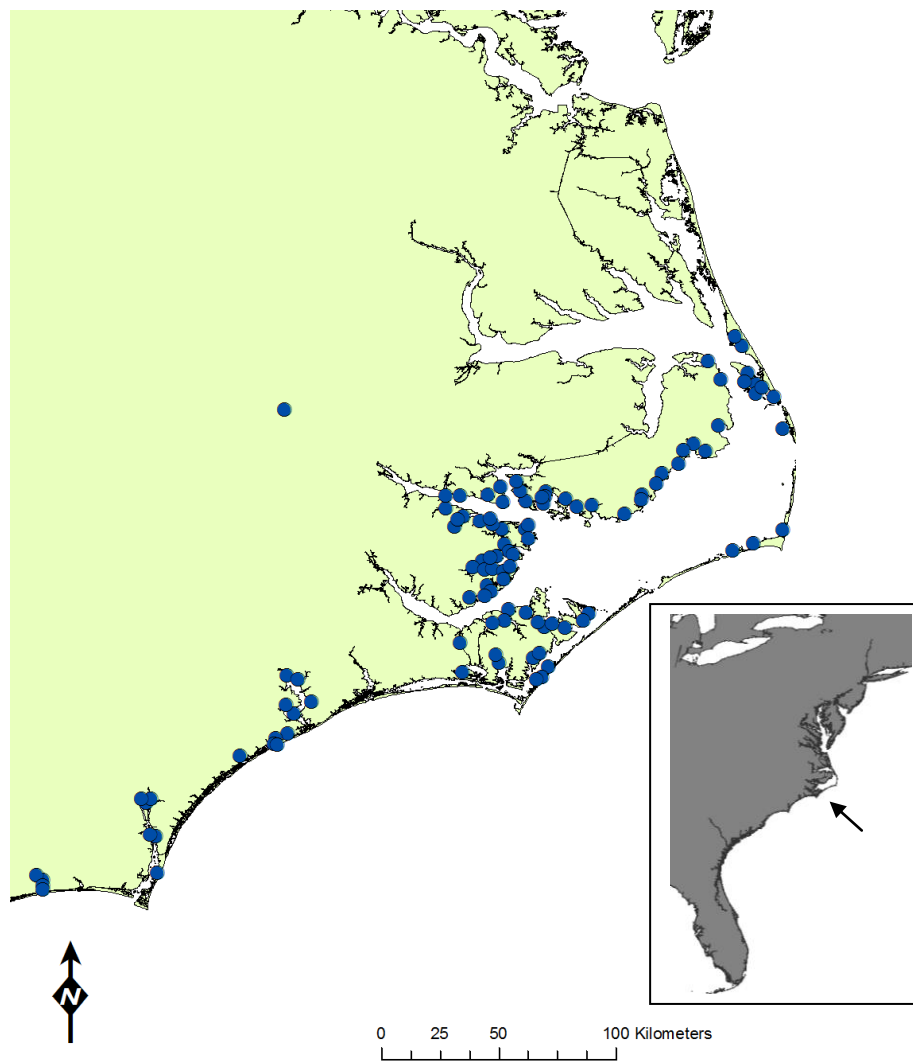


Figure 2.6. Map of survey stations for the North Carolina trawl survey.

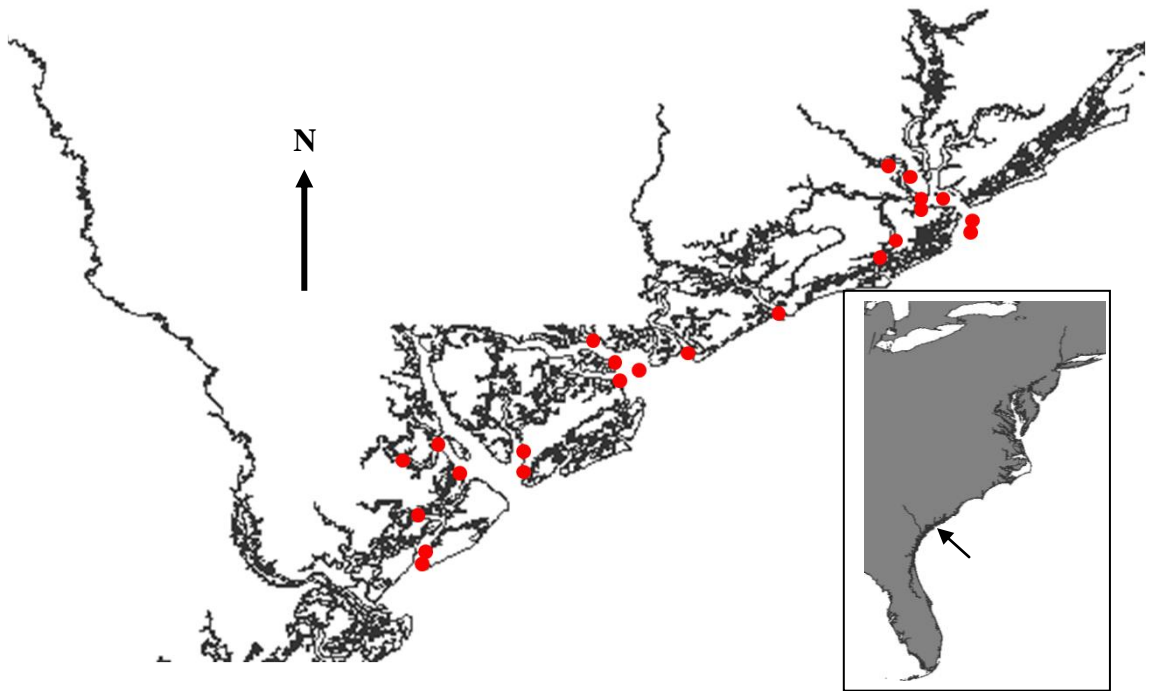


Figure 2.7. Map of survey stations for the South Carolina trawl survey. Note some stations are very close together geographically and in these cases separate points were not plotted on the map.

and Cumberland) and area (river, sound, offshore). Until 2005, two fixed stations in each stratum were sampled monthly leading to a total of 36 stations. Seven more sites were added in 2005, bringing the total number of stations up to 43 (Figure 2.8). The gear for the survey is an otter trawl with a 40' footrope, which is towed for 15 minutes at each station. Temperature, salinity, dissolved oxygen, and depth are recorded at each station. Blue crabs caught in each tow are counted, sexed, measured and weighed. Prior to 1985, the survey varied temporally from year to year before sampling was conducted consistently each month for the remainder of the time series.

Florida Survey

The Florida Fish and Wildlife Commission (FWC) Fishery Independent Monitoring (FIM) program conducts a series of monthly surveys on the Atlantic coast of Florida (Murphy et al. 2007). The extent of coverage for this survey has been extended over time and currently there are three regions surveyed each year. North Indian River Lagoon (IRM) has been sampled since 1990, South Indian River Lagoon (TQM) has been surveyed since 1997, and northeast Florida was added in 2001 (JXM). The survey is a stratified random design, with the strata determined based on depth, shore type, and bottom vegetation. Over 200 sites are sampled each year (Murphy et al. 2007; Figure 2.9). Three gear types are used for these surveys. The first is a 70' bag seine that can be set from the beach or from a boat and is good at catching smaller crabs. The second is a 20' otter trawl with tickler chain and the third is a 600' bag seine that is set from a skiff. Blue crabs caught at each site are counted,

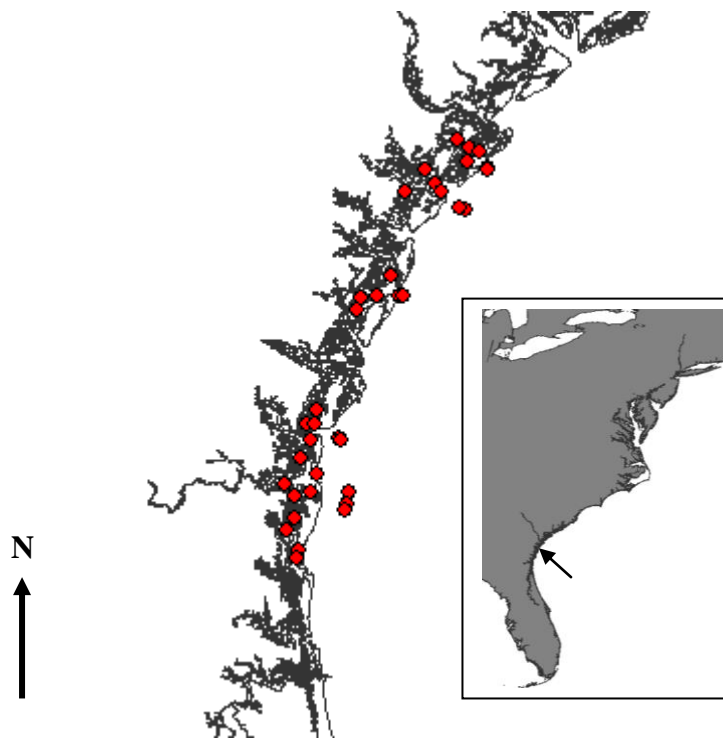


Figure 2.8. Map of survey stations for the Georgia trawl survey.

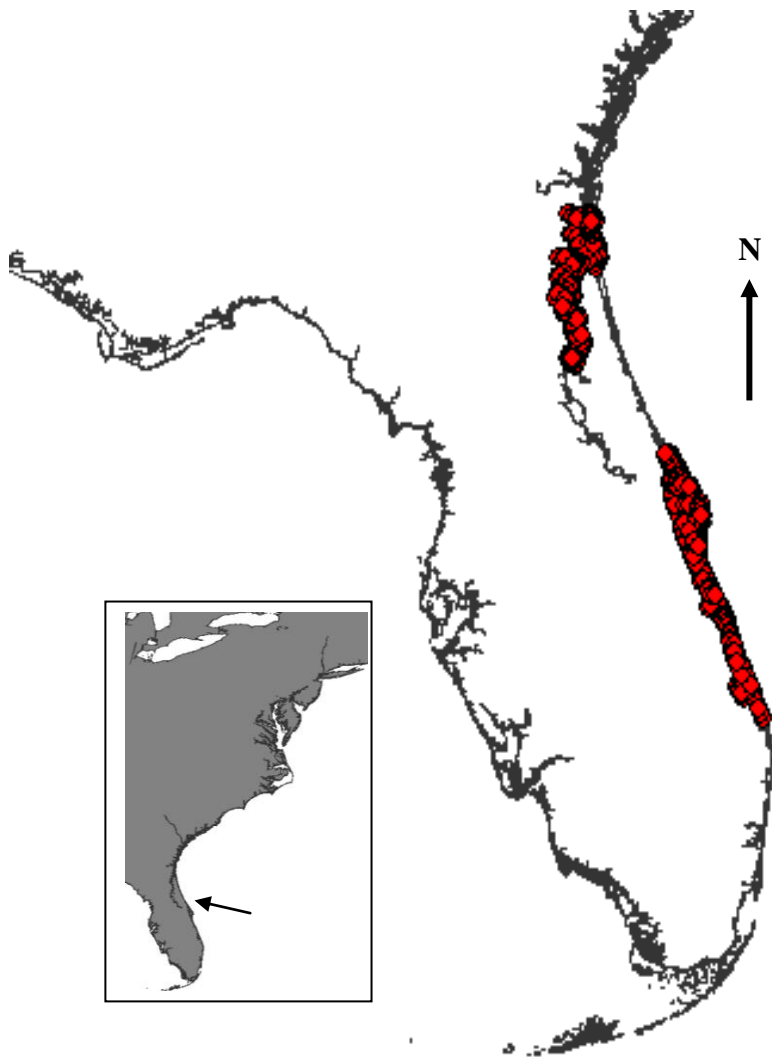


Figure 2.9. Map of Florida survey stations from the 2008 survey.

sexed, and up to 20 individuals are measured from each size class (young-of-the-year <80mm and exploited >127mm)

Fishery-independent indices

As summarized above, all states in the study area except New York have fishery-independent survey data available for their respective blue crab fishery. For each survey, I obtained raw data for every sample including sample number, date, station, and environmental data (depth, temperature, and salinity in most cases). For samples with blue crabs present I acquired total counts as well as individual length data for each crab caught (note: some states measure a subsample of large catches). I determined which years and months of the survey to include in my analyses based on information from the state agencies and from previous stock assessments for the different regions (Table 2.1). If no information was available I used the entire data set to develop indices.

I determined the estimated size cutoff between age-0 and age-1+ blue crabs either from inspection of breaks in a frequency histogram of lengths (Table 2.1) or by talking to state crab biologists. Counts from each sample were then summed up by age class for each jurisdiction. For states that took subsamples of large catches of crabs, I used the measured percentage in each age class at that station to assign categories to the unmeasured crabs at that same station except when states only took a subsample of small crabs in which case I assigned all unmeasured crabs to the age-0 category. Crabs in the age-0 category are termed recruits and those in the age-1⁺

Table 2.1. Summary of survey data used in the catch-survey analyses.

Survey	Age-0			Age 1+		
	Size	Years Used	Month	Size	Years Used	Month
Delaware Trawl	< 60mm	1978 - 2008	Sep - Oct	> 60mm	1978 - 2008	April - Oct
New Jersey Trawl	< 60mm	1991 - 2008	April - Oct	> 60mm	1991 - 2008	April - Oct
Maryland Trawl	< 50mm	1977 - 2008	Sep - Oct	> 50mm	1977 - 2008	June - Oct
VIMS Trawl	< 70mm	1968 - 2008	May-June	> 70mm	1968 - 2008	May - June
Winter Dredge	< 60mm	1990 - 2008	Dec - March	> 60mm	1990 - 2008	Dec - March
ChesMMAP Trawl		Not Applicable		> 60mm	2002 - 2008	March, May, July, Sep, Nov
coastal Maryland Seine	< 60mm	1989 - 2008	June & Sep	> 60mm	1989 - 2008	June & Sep
coastal Maryland Trawl	< 60mm	1989 - 2008	April - Oct	> 60mm	1989 - 2008	April - Oct
North Carolina Trawl	< 70mm	1978 - 2008	May - June	> 70mm	1978 - 2008	May - June
South Carolina Trawl	< 70mm	1979 - 2008	Jan - Dec	> 70mm	1979 - 2008	Jan - Dec
Georgia Trawl	< 70mm	1976 - 2008	Jan - Dec	> 70mm	1976 - 2008	Jan - Dec
Florida IRM	< 80mm	1990 - 2008	Jan - Dec	> 80mm	1990 - 2008	Jan - Dec
Florida JXM	< 80mm	2001 - 2008	Jan - Dec	> 80mm	2001 - 2008	Jan - Dec
Florida TQM		Not Applicable		> 80mm	1997 - 2008	Jan - Dec

category are considered adults and I will refer to them as such throughout this chapter.

Due to the nature of how surveys are conducted, a number of statistical properties must be taken into account when dealing with survey data. Surveys tend to have many observations where no crabs were caught, which causes the data to be zero-inflated. Count data can also be problematic because they are often not normally distributed. In addition, each state has a different protocol for how they conduct their survey, including how stations were chosen, what gear was used, and how long the station is sampled for. To account for these properties and differences among surveys I applied a standardization technique to each survey and obtained a time series of indices of abundance that were used subsequently in the stock assessment models. These standardized indices for age-0 and age-1⁺ blue crabs in each jurisdiction were calculated by using the Delta-GLM function in R (v. 1.7.2, developed by E.J. Dick at NOAA's Southwest Fisheries Science Center). This function conducts a set of two generalized linear models (GLMs), the first of which uses a binomial distribution to estimate the probability of a positive observation (i.e. catching at least one crab in a sample) and the second estimates the mean response when a positive observation occurs (i.e. how many crabs there are if at least one crab was caught in the tow) using a gamma error distribution (Stefansson 1996).

A variety of factor and continuous variables can be used as explanatory variables to develop survey indices within Delta-GLM. Akaike's Information Criterion (AIC) values are used to determine which combination of these explanatory factors is best for developing indices. The explanatory variables used to improve the

model do not need to be the same for the two stages of the model. For all surveys I used combinations of year, month, temperature, and salinity to develop indices. Depth was included for all states except South Carolina, as this state did not record depth data. Wind speed was also used as a variable for the two coastal Maryland surveys and tidal stage was used in the Georgia survey. Area swept, gear type, and/or effort were included in every run of the Delta-GLM models if data hadn't been corrected for these variables before I received the data. The final general formula for the GLM is:

$$f(N_t) = b_0 + \text{Year} + b_1 * \text{env}_{1,t} + b_2 * \text{env}_{2,t} + \dots + b_n * \text{env}_{n,t} + \epsilon_t \quad [\text{Eq. 2.1}]$$

where t refers to time, N is the estimated fishery-independent index, the b 's are individual regression parameter estimates, the env_i are separate environmental parameters and ϵ is an error term. The final indices that are produced by the model are the products of back-transformed year effects of the two stages of the model. A jackknife routine was used on the selected models to estimate the variance for the indices. Sample code for the Delaware survey is provided Appendix A. Code for the other surveys was similar, with only the variables included changing depending on the data available for that survey.

The best Delta-GLM model for each survey varied for each state (Table 2.2a-1). For the VIMS trawl survey I was not able to obtain environmental data so a geometric mean catch tow^{-1} was calculated for each of the three tributaries and the weighted (for area) average of these three indices was used as the final index (Miller

Table 2.2. Summary of the AIC values for the Delta GLM analysis to calculate indices of abundance for a) NJ trawl b) DE trawl c) MD trawl d) winter dredge e) coastal MD seine f) coastal MD trawl g) NC trawl h) SC trawl i) GA trawl j) FL IRM survey k) FL JXM survey l) FL TQM survey. The best model is indicated in **bold**.

a) New Jersey

Age 0							
	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models							
	+	+	+	+	+	+	1344.05
	+	+	+		+	+	1343.94
	+	+	+		+		1345.98
	+	+	+				1344.06
	+	+	+			+	1341.98
	+	+	+	+			1343.95
	+	+					1445.02
	+		+				1571.13
Abundance models							
	+	+	+	+	+	+	5736.05
	+	+	+		+	+	5743.31
	+	+	+		+		5754.39
	+	+	+				5753.72
	+	+	+			+	5741.77
	+	+	+	+			5746.35
	+	+					5850.09
	+		+				5923.70
Age 1 ⁺							
	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models							
	+	+	+	+	+	+	1531.66
	+	+	+		+	+	1538.07
	+	+	+		+		1540.78
	+	+	+				1539.62
	+	+	+			+	1537.34
	+	+	+	+			1531.89
	+	+					1598.18
	+		+				1656.08
Abundance models							
	+	+	+	+	+	+	3990.88
	+	+	+		+	+	3989.39
	+	+	+		+		3994.28
	+	+	+				3993.00
	+	+	+			+	3987.98
	+	+	+	+			3994.54
	+	+					4058.46
	+		+				4061.80

b) Delaware

Age 0							
	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	1131.57
	+	+	+		+	+	1130.41
	+	+	+		+		1140.15
	+	+	+				1140.01
	+	+	+			+	1129.68
	+	+	+	+			1140.96
	+	+					1655.97
	+		+				1178.45
Abundance							
models	+	+	+	+	+	+	10739.25
	+	+	+		+	+	10750.63
	+	+	+		+		10787.42
	+	+	+				10787.70
	+	+	+			+	10749.19
	+	+	+	+			10777.53
	+	+					11093.90
	+		+				10820.13
Age 1 ⁺							
	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	5717.30
	+	+	+		+	+	5715.91
	+	+	+		+		5724.73
	+	+	+				5730.61
	+	+	+			+	5722.14
	+	+	+	+			5731.59
	+	+					7004.77
	+		+				6159.21
Abundance							
models	+	+	+	+	+	+	19574.07
	+	+	+		+	+	19578.07
	+	+	+		+		19577.23
	+	+	+				19575.90
	+	+	+			+	19576.62
	+	+	+	+			19571.88
	+	+					20230.53
	+		+				19699.93

c) MD trawl

Age 0

	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models	+	+	+	+	+	+	2030.81
	+	+	+		+	+	2046.60
	+	+	+		+		2044.75
	+	+	+				2044.48
	+	+	+			+	2046.46
	+	+	+	+			2028.25
	+	+					2631.41
	+		+				2073.94
Abundance models	+	+	+	+	+	+	5522.57
	+	+	+		+	+	5553.56
	+	+	+		+		5552.23
	+	+	+				5551.43
	+	+	+			+	5553.23
	+	+	+	+			5519.77
	+	+					5862.95
	+		+				5550.53

Age 1⁺

	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models	+	+	+	+	+	+	2065.28
	+	+	+		+	+	2063.39
	+	+	+		+		2064.61
	+	+	+				2062.86
	+	+	+			+	2063.12
	+	+	+	+			2064.67
	+	+					2211.09
	+		+				2184.73
Abundance models	+	+	+	+	+	+	20126.88
	+	+	+		+	+	20126.32
	+	+	+		+		20138.36
	+	+	+				20172.21
	+	+	+			+	20173.83
	+	+	+	+			20171.62
	+	+					20537.64
	+		+				20442.67

d) winter dredge

Age 0

	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	19890.15
	+	+	+		+	+	20969.89
	+	+	+		+		23099.72
	+	+	+				26561.51
	+	+	+			+	21882.89
	+	+	+	+			25093.94
	+	+					29929.14
	+		+				26672.56
Abundance							
models	+	+	+	+	+	+	60456.45
	+	+	+		+	+	63343.71
	+	+	+		+		68555.76
	+	+	+				80130.13
	+	+	+			+	66013.81
	+	+	+	+			76230.00
	+	+					80461.47
	+		+				80142.27

Age 1⁺

	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	20508.21
	+	+	+		+	+	21847.24
	+	+	+		+		24238.45
	+	+	+				27379.12
	+	+	+			+	22736.81
	+	+	+	+			25741.54
	+	+					27898.70
	+		+				27432.82
Abundance							
models	+	+	+	+	+	+	52849.30
	+	+	+		+	+	56242.90
	+	+	+		+		64387.70
	+	+	+				72092.71
	+	+	+			+	72092.71
	+	+	+	+			67788.46
	+	+					72222.15
	+		+				72113.40

e) coastal MD seine

Age 0

	Year	Month	Strata	Wind speed	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models								
	+	+	+	+	+	+	+	491.10
	+	+	+		+	+	+	489.15
	+	+	+			+	+	487.17
	+	+	+	+				491.09
	+	+	+			+		485.58
	+	+	+					489.10
	+	+	+				+	490.68
	+	+	+		+			491.04
	+	+						608.57
	+		+					588.78
Abundance models								
	+	+	+	+	+	+	+	4899.48
	+	+	+		+	+	+	4911.10
	+	+	+			+	+	4913.11
	+	+	+	+				4914.26
	+	+	+			+		4924.62
	+	+	+					4923.51
	+	+	+				+	4911.56
	+	+	+		+			4920.86
	+	+						5032.43
	+		+					5224.77

Age 1⁺

	Year	Month	Strata	Wind speed	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models								
	+	+	+	+	+	+	+	557.69
	+	+	+		+	+	+	556.43
	+	+	+			+	+	555.21
	+	+	+	+				557.91
	+	+	+			+		556.97
	+	+	+					556.58
	+	+	+				+	554.50
	+	+	+		+			557.64
	+	+						653.47
	+		+					591.48
Abundance models								
	+	+	+	+	+	+	+	4246.03
	+	+	+		+	+	+	4247.67
	+	+	+			+	+	4248.68
	+	+	+	+				4264.94
	+	+	+			+		4260.17
	+	+	+					4265.22
	+	+	+				+	4252.03
	+	+	+		+			4265.85
	+	+						4341.90
	+		+					4306.97

f) coastal MD trawl

Age 0

	Year	Month	Strata	Wind speed	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models	+	+	+	+	+	+	+	1603.45
	+	+	+		+	+	+	1609.53
	+	+	+			+	+	1609.50
	+	+	+	+				1602.84
	+	+	+			+		1611.33
	+	+	+					1609.51
	+	+	+				+	1607.54
	+	+	+		+			1609.29
	+	+						2359.85
	+		+					1877.38
Abundance models	+	+	+	+	+	+	+	16959.36
	+	+	+		+	+	+	16966.10
	+	+	+			+	+	16964.32
	+	+	+	+				16958.39
	+	+	+			+		16963.30
	+	+	+					16963.93
	+	+	+				+	16964.69
	+	+	+		+			16965.60
	+	+						17644.18
	+		+					17521.94

Age 1⁺

	Year	Month	Strata	Wind speed	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models	+	+	+	+	+	+	+	1545.03
	+	+	+		+	+	+	1553.06
	+	+	+			+	+	1553.85
	+	+	+	+				1581.74
	+	+	+			+		1593.00
	+	+	+					1591.01
	+	+	+				+	1552.42
	+	+	+		+			1589.34
	+	+						1986.33
	+		+					2210.15
Abundance models	+	+	+	+	+	+	+	16248.83
	+	+	+		+	+	+	16261.42
	+	+	+			+	+	16261.96
	+	+	+	+				16299.98
	+	+	+			+		16309.94
	+	+	+					16313.67
	+	+	+				+	16267.23
	+	+	+		+			16313.30
	+	+						16629.81
	+		+					17188.33

g) North Carolina

Age 0

	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	5796.726
	+	+	+		+	+	5805.091
	+	+	+		+		5813.062
	+	+	+				5812.505
	+	+	+			+	5804.759
	+	+	+	+			5804.228
	+	+					7467.877
	+		+				5810.92
Abundance							
models	+	+	+	+	+	+	22870.31
	+	+	+		+	+	22874.64
	+	+	+		+		22883.56
	+	+	+				22902.37
	+	+	+			+	22893.16
	+	+	+	+			22898.27
	+	+					24794.64
	+		+				22958.01

Age 1⁺

	Year	Month	Strata	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	7048.582
	+	+	+		+	+	7051.116
	+	+	+		+		7067.114
	+	+	+				7066.821
	+	+	+			+	7050.978
	+	+	+	+			7064.353
	+	+					8022.747
	+		+				7132.142
Abundance							
models	+	+	+	+	+	+	12800.6
	+	+	+		+	+	12802.71
	+	+	+		+		12805.92
	+	+	+				12814.9
	+	+	+			+	12811.69
	+	+	+	+			12812.74
	+	+					13406.99
	+		+				12905.42

h) South Carolina

Age 0

	Year	Month	Strata	Salinity	Temperature (°C)	AIC
Occurrence models	+	+	+	+	+	5205.52
	+	+	+	+		5203.53
	+	+	+			5206.00
	+	+	+		+	5207.97
	+	+				5959.18
	+		+			5593.86
Abundance models	+	+	+	+	+	14262.53
	+	+	+	+		14261.44
	+	+	+			14294.02
	+	+	+		+	14295.33
	+	+				15185.71
	+		+			14604.79

Age 1⁺

	Year	Month	Strata	Salinity	Temperature (°C)	AIC
Occurrence models	+	+	+	+	+	3537.93
	+	+	+	+		3542.61
	+	+	+			3568.61
	+	+	+		+	3562.75
	+	+				4281.80
	+		+			4146.76
Abundance models	+	+	+	+	+	26799.00
	+	+	+	+		26811.82
	+	+	+			26815.80
	+	+	+		+	26802.35
	+	+				27321.54
	+		+			27301.34

i) Georgia

Age 0

	Year	Month	Strata	Tide	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models	+	+	+	+	+	+	+	6009.39
	+	+	+		+	+	+	6015.61
	+	+	+			+	+	6013.73
	+	+	+	+				6063.23
	+	+	+			+		6021.72
	+	+	+					6066.35
	+	+	+				+	6058.26
	+	+	+		+			6068.29
	+	+						7456.14
	+		+					8002.41
Abundance models	+	+	+	+	+	+	+	9122.84
	+	+	+		+	+	+	9126.29
	+	+	+			+	+	9135.76
	+	+	+	+				9138.76
	+	+	+			+		9134.65
	+	+	+					9141.79
	+	+	+				+	9142.61
	+	+	+		+			9132.94
	+	+						9476.84
	+		+					9289.89

Age 1⁺

	Year	Month	Strata	Tide	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence models	+	+	+	+	+	+	+	9265.47
	+	+	+		+	+	+	9267.29
	+	+	+			+	+	9265.33
	+	+	+	+				9417.12
	+	+	+			+		9267.18
	+	+	+					9415.66
	+	+	+				+	9413.71
	+	+	+		+			9417.57
	+	+						12544.52
	+		+					11016.51
Abundance models	+	+	+	+	+	+	+	36100.35
	+	+	+		+	+	+	36098.54
	+	+	+			+	+	36096.69
	+	+	+	+				36183.95
	+	+	+			+		36128.95
	+	+	+					36182.09
	+	+	+				+	36148.51
	+	+	+		+			36183.80
	+	+						36929.26
	+		+					36529.69

j) Florida IRM

Age 0

	Year	Month	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence						
models	+	+	+	+	+	5456.502
	+	+		+	+	5464.029
	+	+		+		5463.563
	+	+			+	5464.615
	+	+	+			5456.781
	+	+				5464.844
Abundance						
models	+	+	+	+	+	4566.133
	+	+		+	+	4577.28
	+	+		+		4579.695
	+	+			+	4575.301
	+	+	+			4566.05
	+	+				4577.963

Age 1⁺

	Year	Month	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence						
models	+	+	+	+	+	8167.301
	+	+		+	+	8168.646
	+	+		+		8194.061
	+	+			+	8225.953
	+	+	+			8258.803
	+	+				8258.706
Abundance						
models	+	+	+	+	+	7843.744
	+	+		+	+	7845.918
	+	+		+		7844.581
	+	+			+	7844.183
	+	+	+			7840.935
	+	+				7842.772

k) Florida JXM

Age 0

	Year	Month	Zone	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	7144.90
	+	+	+		+	+	7180.69
	+	+	+		+		7180.47
	+	+	+				7212.16
	+	+	+			+	7212.40
	+	+	+	+			7172.41
	+	+					7267.99
	+		+				7210.31
Abundance							
models	+	+	+	+	+	+	5260.36
	+	+	+		+	+	5262.66
	+	+	+		+		5261.30
	+	+	+				5259.34
	+	+	+			+	5260.70
	+	+	+	+			5256.89
	+	+					5309.19
	+		+				5261.59

Age 1⁺

	Year	Month	Zone	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	10213.92
	+	+	+		+	+	10245.18
	+	+	+		+		10247.41
	+	+	+				10283.09
	+	+	+			+	10280.87
	+	+	+	+			10246.64
	+	+					10298.32
	+		+				10319.34
Abundance							
models	+	+	+	+	+	+	13205.49
	+	+	+		+	+	13226.51
	+	+	+		+		13235.87
	+	+	+				13248.05
	+	+	+			+	13239.31
	+	+	+	+			13224.18
	+	+					13306.69
	+		+				13284.09

l) Florida TQM

Age 1⁺

	Year	Month	Zone	Depth (m)	Salinity	Temperature (°C)	AIC
Occurrence							
models	+	+	+	+	+	+	2262.34
	+	+	+		+	+	2292.47
	+	+	+		+		2300.47
	+	+	+				2311.86
	+	+	+			+	2302.37
	+	+	+	+			2279.85
	+	+					2328.97
	+		+				2382.06
Abundance							
models	+	+	+	+	+	+	2074.71
	+	+	+		+	+	2083.81
	+	+	+		+		2091.38
	+	+	+				2092.31
	+	+	+			+	2084.51
	+	+	+	+			2082.74
	+	+					2121.15
	+		+				2119.89

et al. 2011). The ChesMMAAP survey indices were calculated at VIMS using the method in the survey description above. These time series of age 0 and age-1⁺ blue crab indices were used as input in the catch survey analyses (Table 2.3, Figure 2.10a-m). Delta-GLM indices for many of the surveys are consistently under the mean due to how Delta-GLM calculates indices, but since they are relative they can be considered acceptable indices.

Fishery-dependent data

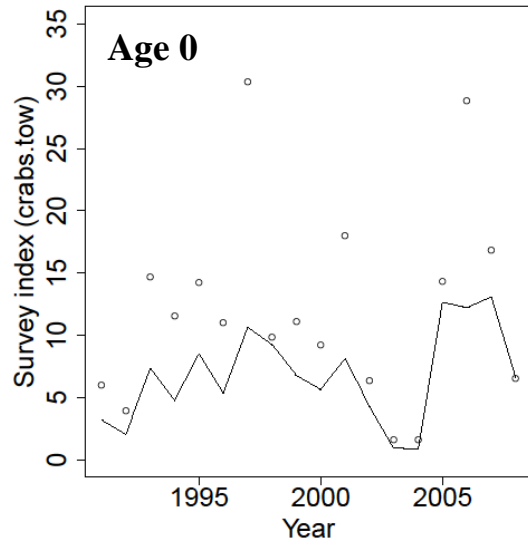
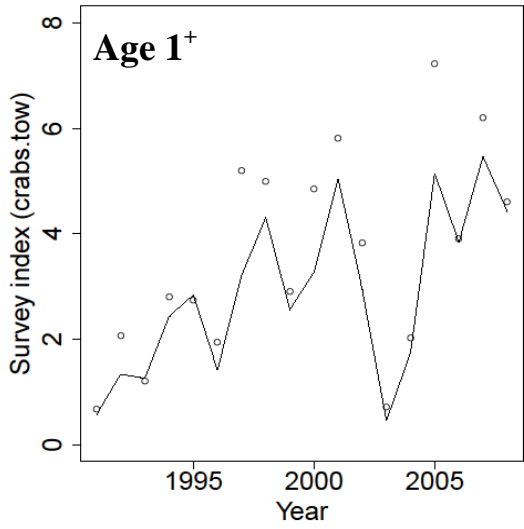
I obtained records of annual landings from blue crab management agencies covering New York, New Jersey, Delaware, Maryland, the Potomac River, Virginia, North Carolina, South Carolina, Georgia, and Florida. Each agency was also asked to provide insights into the history of the blue crab fishery in their jurisdiction, including a chronology of any changes in commercial catch reporting protocols, gear regulations, seasonal closures, or data compilation. Maryland and Virginia were each split into Chesapeake Bay landings and coastal bay landings, as it was thought that the two systems likely experience different population dynamics and thus may express different trends in their landings.

Landings data were available from all states, but for different durations. The earliest consistent year for which data are available is 1929 in Maryland and Virginia. The shortest time series are from coastal bay landings for Maryland and Virginia and New York landings, which have only been consistently recorded from 1985, 1971, and 1974 respectively. Before this, landings for Maryland and Virginia were reported as state-wide which included both the Chesapeake Bay and coastal bay landings. To account for the starting points of the different time series, I conducted analyses for the

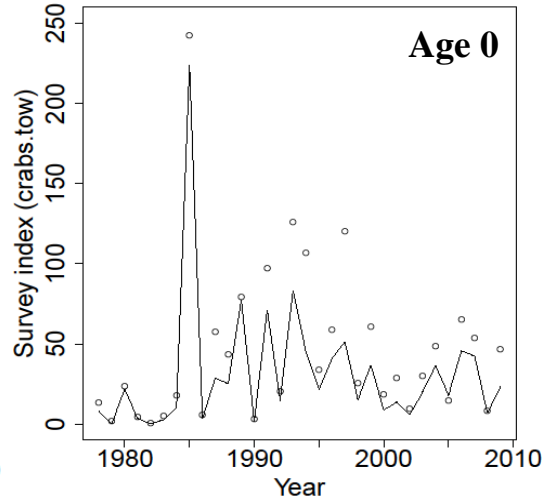
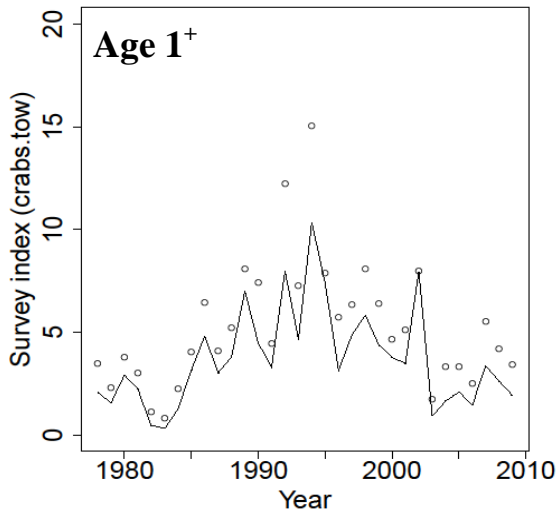
Table 2.3. Indices for each survey from the Delta-GLM analysis.

Year	DE		NJ		NJ		VIMS		MD trawl		MD trawl		dredge		ChesMMAP		coastal seine		coastal seine		coastal trawl		NC		SC		GA		FLIRM		FLJXM		FLTQM			
	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit	adult	recruit				
1968					3.12	0.67																														
1969					1.65	22.01																														
1970					7.85	8.04																														
1971					10.91	84.52																														
1972					5.7	8.42																														
1973					1.54	7.03																														
1974					1.77	3.49																														
1975					1.55	7.96																														
1976					1.61	1.61																														
1977					2.49	3.9			29.29	0.6																										
1978	2.09	8.13			1.79	3.07			3.83	0.21													0.91	2.53												
1979	1.58	0.42			5.47	6.42			2.01	0.29													1.53	2.88	9.46	1.42										
1980	2.88	21.35			3.68	2.26			1.76	0.7													1.15	3.37	6.15	1.88										
1981	2.24	3.54			12.93	37.77			14.96	0.78													2.19	5.84	13.58	2.61										
1982	0.47	0.21			11.7	12.15			8.62	0.36													1.90	5.42	5.23	1.16										
1983	0.32	2.61			11.73	45.6			16.08	1.94													1.40	5.00	5.11	1.53										
1984	1.28	10.47			3.9	49.35			16.84	6.27													1.61	5.58	9.23	1.08										
1985	3.14	223.73			10.09	24.66			26.69	2.57													2.13	5.95	11.46	3.43										
1986	4.79	3.83			5.81	11.72			26.34	4.13													1.51	2.94	21.16	5.77										
1987	3.00	28.36			4.67	15.09			20.48	1.92													1.37	5.14	24.82	4.75										
1988	3.77	25.15			6.79	11.78			14.24	5.23													1.46	5.62	17.10	4.03										
1989	6.98	77.27			8.07	14.1			29.35	3.79													0.74	2.76	10.08	2.64										
1990	4.44	1.42			20.9	40.24			14.93	14.73													11.00	0.74	2.76	10.08	2.64									
1991	3.27	71.05			9.62	4.26			28.42	1.32													6.30	1.83	3.76	14.89	2.86									
1992	7.95	14.56			3.97	3.04			11.84	10.62													6.87	9.86	6.47	5.37										
1993	4.64	83.22			3.1	8.14			23.88	4.92													11.93	11.40	6.32	7.08										
1994	10.33	44.16			2.43	4.73			20.77	1.16													8.00	19.42	7.34	15.39										
1995	7.35	21.28			8.48	3.03			9.05	1.88													8.05	14.30	10.03	20.37										
1996	3.10	40.55			4	10.35			32.73	2.7													8.40	10.71	11.10	16.01										
1997	4.84	50.97			2.98	5.04			22.75	0.93													13.11	8.58	12.83	12.12										
1998	5.81	14.96			4.35	4.72			9.55	2.02													8.06	7.95	7.16	10.97										
1999	4.35	36.46			2.6	17.56			17.56	4.75													5.75	15.28	5.43	8.03										
2000	3.75	8.90			2.46	2			10.27	1.78													7.07	15.84	8.42	9.66										
2001	3.48	13.96			4.12	4.46			10.93	2.62													8.34	11.57	9.96	6.44										
2002	0.94	6.17			4.1	2.61			11.35	2.53													5.19	10.07	7.92	13.16										
2003	0.94	19.96			0.93	1.61			6.79	1.93													6.10	8.67	10.38	8.05										
2004	1.67	36.03			1.75	0.87			8.2	6.77													7.80	8.94	10.54	8.19										
2005	2.06	17.91			5.14	12.64			13.2	6.34													8.18	9.95	11.89	10.86										
2006	1.46	45.53			3.83	12.20			1.43	11.3													5.98	8.39	3.13	2.57										
2007	3.34	42.37			5.45	13.07			2.42	1.69													6.91	8.80	0.89	1.79										
2008	2.59	7.19			4.42	6.60			11.48	5.25													5.85	5.67	0.57	0.29										

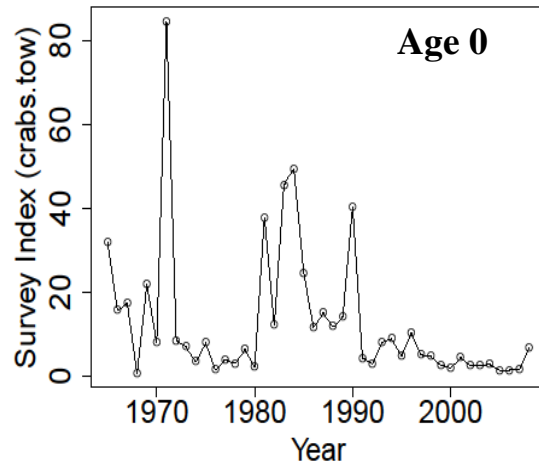
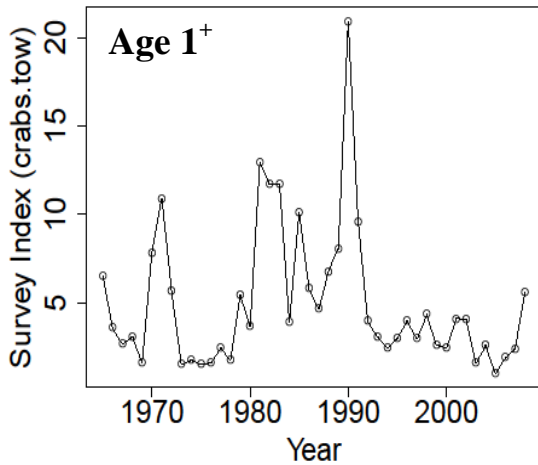
a) New Jersey



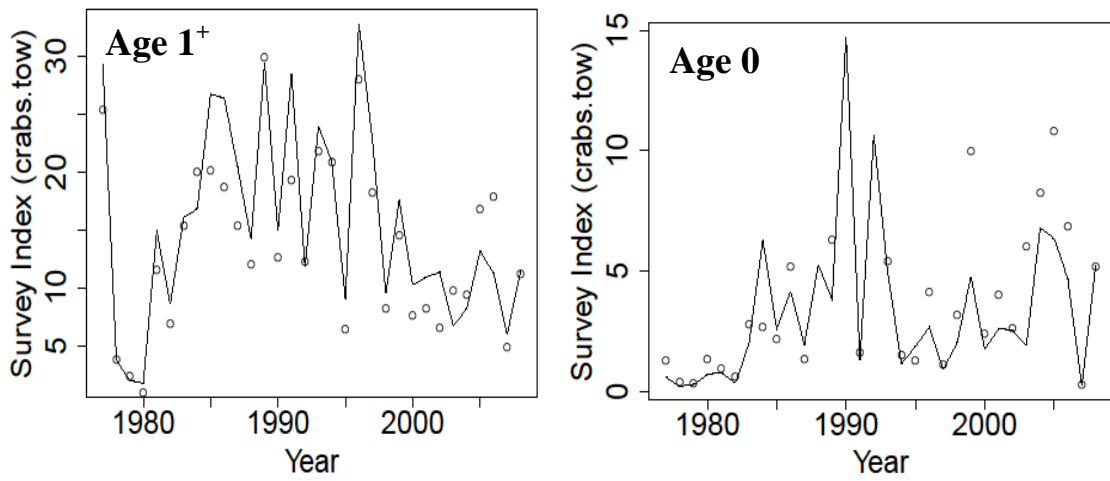
b) Delaware



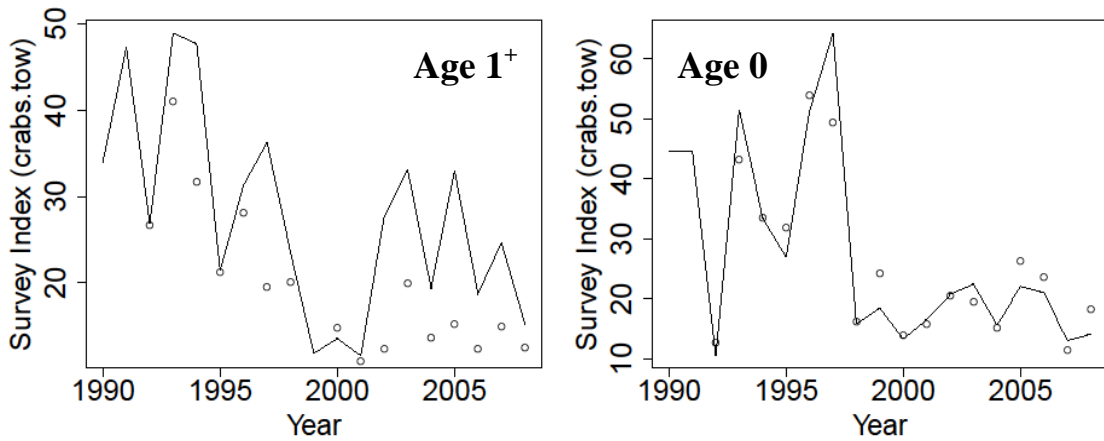
c) VIMS



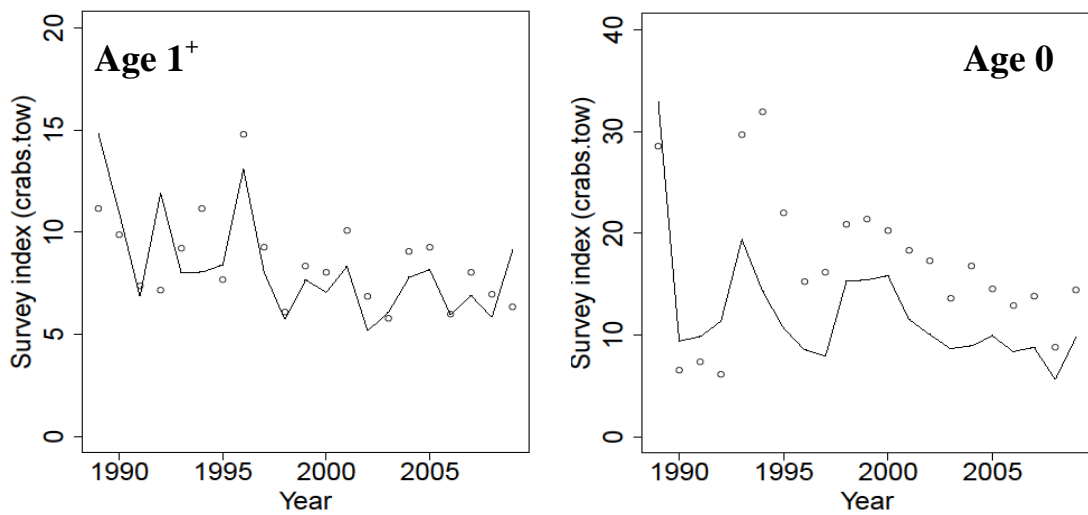
d) MD trawl



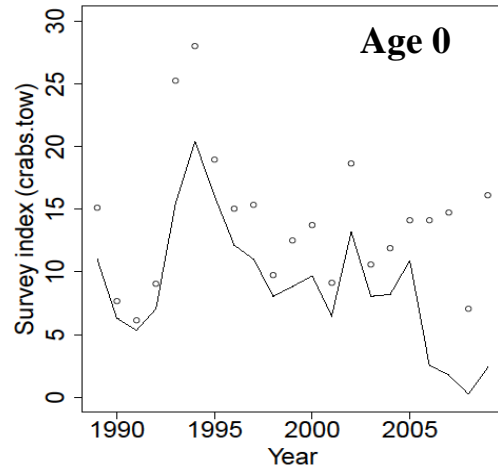
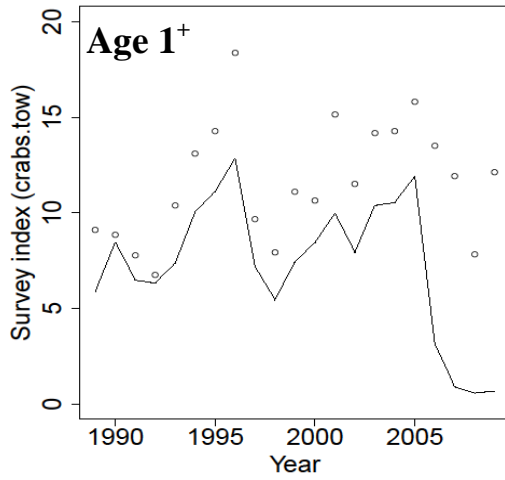
e) winter dredge



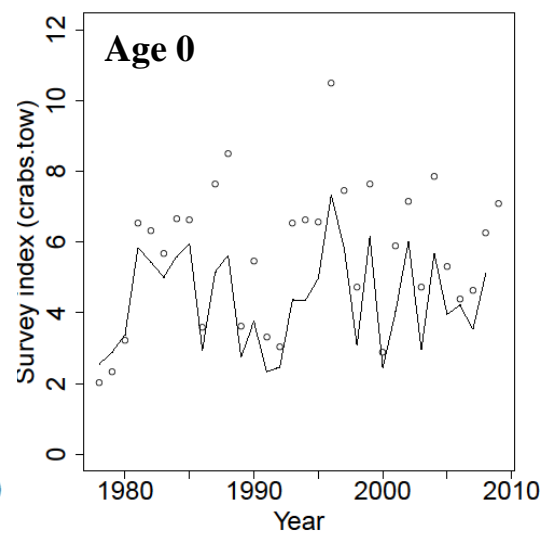
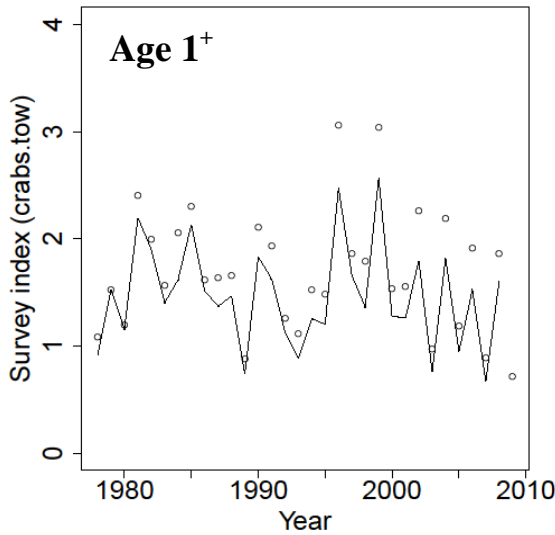
f) coastal MD seine



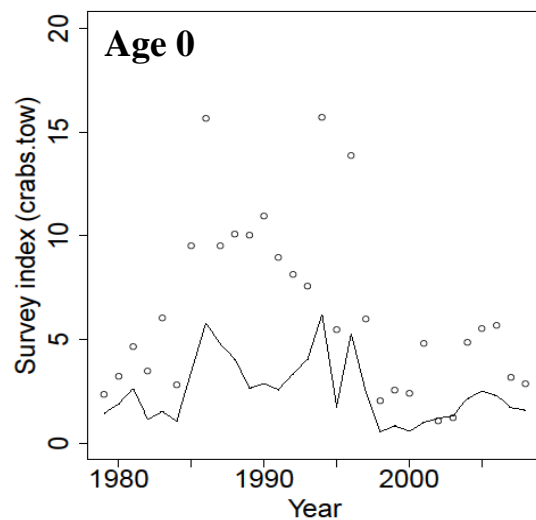
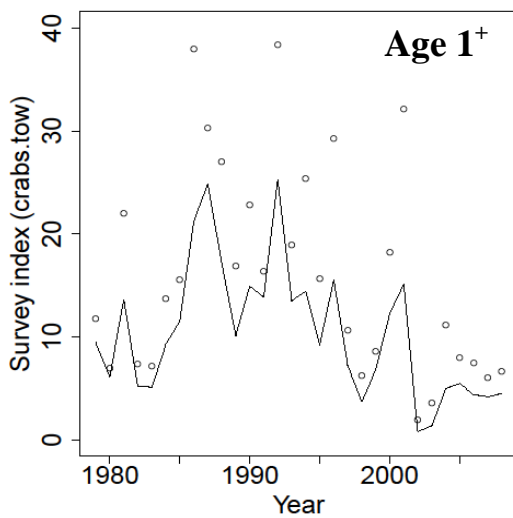
g) coastal MD trawl



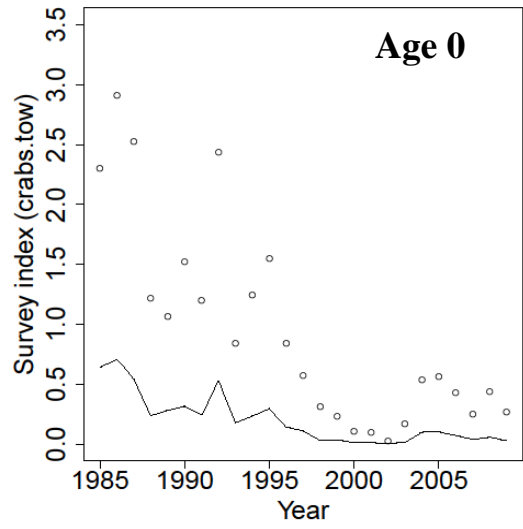
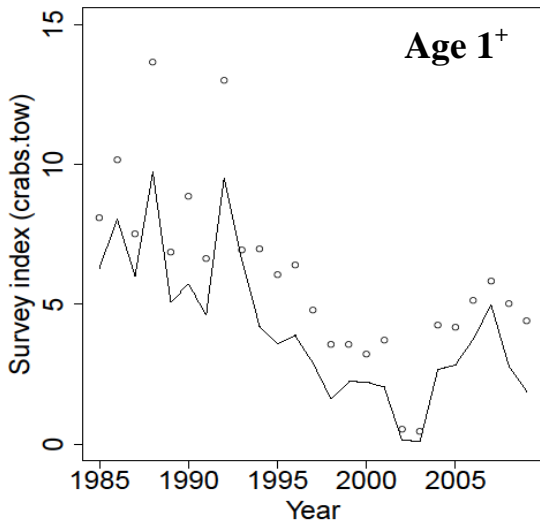
h) North Carolina



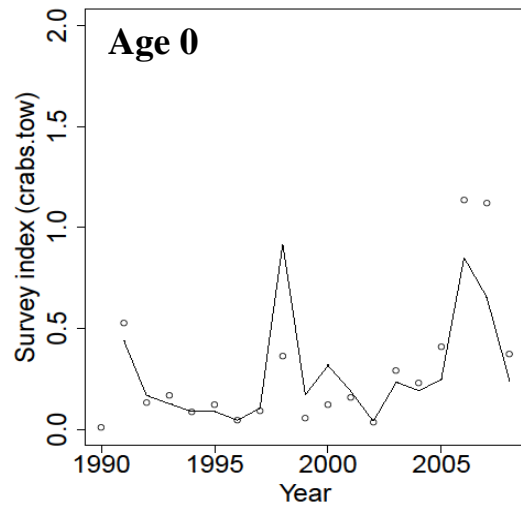
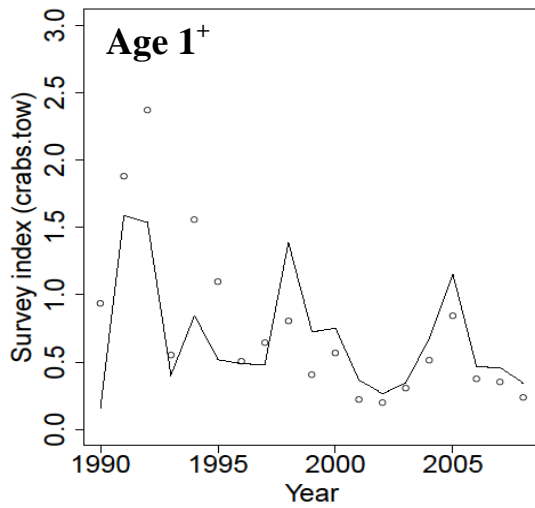
i) South Carolina



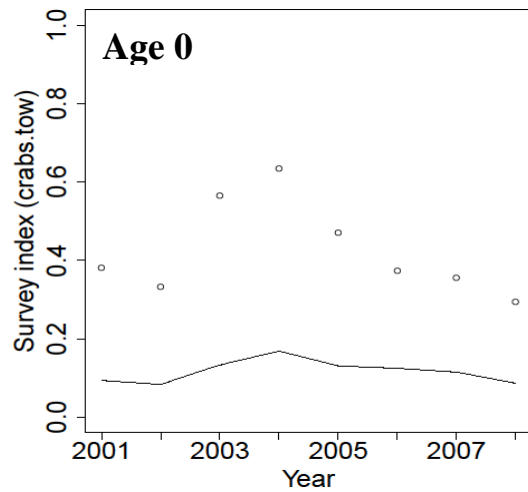
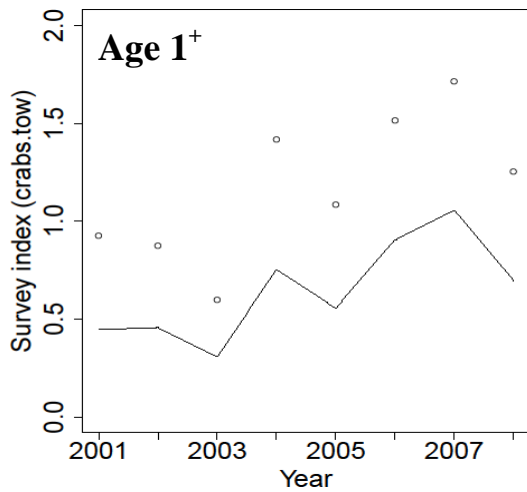
j) Georgia



k) FL IRM



l) FL JXM



m) FL TQM

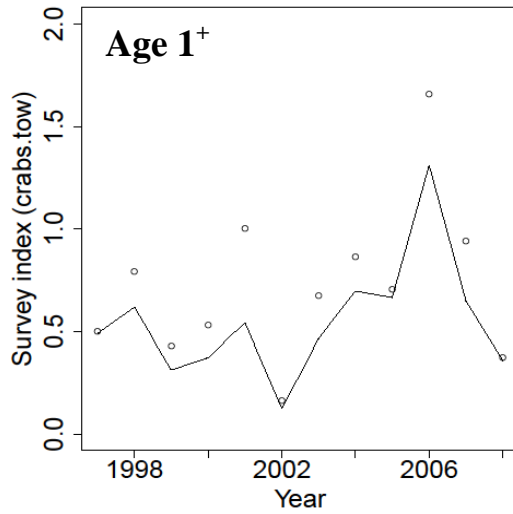


Figure 2.10. Plots of survey indices that were calculated using the Delta-GLM function for a) NJ trawl b) DE trawl c) VIMS trawl d) MD trawl e) winter dredge f) coastal seine g) coastal trawl h) NC trawl i) SC trawl j) GA k) FL IRM l) FL JXM m) FL TQM. The left panel of each set of graphs represents the age-1+ crabs and the right panel represents the age-0. Points represent the simple mean and the line represents the indices.

period 1974-2008, a period for which data were available for all but the Maryland coastal bays. Raw time series of landings in each state for this period are given in Table 2.4 and shown in Figure 2.11. To estimate data for the earlier years for the Maryland coastal bays, I evaluated two back-estimation procedures: a proportional and a regression approach. For the proportional approach I calculated the average percentage of coastal bay landings relative to total state landings for years where landings were separated into coastal bays and Chesapeake Bay landings and applied this percentage to years when there were no categorized landings data. The regression analysis was done by running a regression analysis between coastal bay landings and total landings and applying the regression equation to all years without separated coastal bay landings data. I determined that the proportional approach should be used because the regression approach led to all data points falling on or very close to the mean of the time series, which caused substantially reduced levels of variability. I chose to take this approach rather than starting all of my analyses in 1985 because I wanted to avoid the loss of 11 years of data for only one region and the proportional approach produced reasonable results for the projected period.

Two different approaches are available to address reporting changes in landings data when present. The first is to consider the fishery-dependent data as two separate time series – that up to the reporting change, and that after the reporting change. The second is to try to adjust for the reporting change. There are several alternatives available to detect breakpoints or interventions in time series of catch data. Statistical process control approaches using cumulative sum (CUSUM) control charts have been used in the fisheries literature to identify breakpoints (Mesnil &

Table 2.4. Raw time series for each of the twelve jurisdictions in millions of pounds and thousands of metric tons.

Ches. Bay Virginia		coastal Virginia		North Carolina		South Carolina		Georgia		Florida	
Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)
38.3851	17.4112	3.2751	1.4856	12.5406	5.6883	7.5475	3.4235	10.1311	4.5954	7.4718	3.3892
31.9876	14.5093	3.5855	1.6263	10.4704	4.7493	6.3803	2.8941	8.8652	4.0212	4.1859	1.8987
23.8550	10.8205	0.5950	0.2699	10.2092	4.6308	5.7401	2.6037	5.8727	2.6638	4.0244	1.8254
36.1004	16.3749	1.7720	0.8038	11.3812	5.1624	7.3333	3.3263	7.7215	3.5024	3.4245	1.5533
33.1503	15.0367	3.5097	1.5920	22.3233	10.1257	9.3969	4.2624	10.6285	4.8210	3.8109	1.7286
37.4425	16.9836	3.4437	1.5620	25.5663	11.5967	7.7297	3.5061	11.3377	5.1427	3.4932	1.5845
34.0127	15.4279	4.3114	1.9556	33.3911	15.1459	6.2162	2.8196	10.0601	4.5632	4.6021	2.0875
40.5879	18.4103	2.0392	0.9250	37.5350	17.0256	6.1134	2.7730	13.0386	5.9142	3.4838	1.5802
45.4965	20.6368	1.5702	0.7122	37.4818	16.9788	6.3128	2.8634	12.5496	5.6924	5.3935	2.4464
42.1723	19.1290	4.6715	2.1190	33.7533	15.3102	5.5931	2.5370	11.1100	5.0394	6.9907	3.1709
45.3798	20.5839	5.0541	2.2925	32.0135	14.5211	4.2260	1.9169	10.2530	4.6507	6.7377	3.0562
39.1316	17.7498	2.7732	1.2579	29.0104	13.1589	4.4493	2.0182	8.3368	3.7815	3.7123	1.6839
34.6714	15.7267	3.6086	1.6368	23.4547	10.6389	5.9509	2.6993	6.6368	3.0104	3.4587	1.5688
30.0599	13.6350	3.7794	1.7143	31.9904	14.5106	5.3968	2.4479	6.2902	2.8532	7.9246	3.5945
34.3778	15.5935	2.9754	1.3496	34.9435	15.8501	6.8657	3.1142	8.4503	3.8330	4.8360	2.1936
41.5859	18.8631	2.9727	1.3484	34.2744	15.5466	5.7019	2.5863	7.3340	3.3266	4.6065	2.0895
51.5071	23.3632	0.5362	0.2432	37.8096	17.1501	5.2064	2.3616	7.1378	3.2376	7.0718	3.2077
44.8486	20.3430	0.0266	0.0120	41.5058	18.8267	5.4861	2.4885	6.9567	3.1555	4.5992	2.0862
23.8472	10.8169	0.0194	0.0088	40.2902	18.2753	7.2243	3.2769	8.7429	3.9657	6.8131	3.0904
52.6511	23.8821	0.7671	0.3480	43.5551	19.7563	6.1341	2.7824	8.1580	3.7004	3.9546	1.7938
34.7213	15.7493	1.5471	0.7018	52.7906	23.9454	7.1362	3.2369	8.8891	4.0320	5.4532	2.4736
33.1049	15.0161	2.1667	0.9828	46.0834	20.9031	6.9400	3.1479	9.3475	4.2400	3.4757	1.5765
34.4866	15.6429	1.7838	0.8091	66.6723	30.2421	5.8821	2.6681	5.8532	2.6550	5.6094	2.5444
38.9838	17.6827	2.7915	1.2662	55.6560	25.2451	6.1478	2.7886	6.9019	3.1306	5.8114	2.6360
34.5031	15.6503	2.8100	1.2746	61.4019	27.8514	7.4534	3.3808	5.1211	2.3229	4.5901	2.0820
32.4725	14.7293	2.3115	1.0485	57.1687	25.9313	6.5206	2.9577	3.9532	1.7932	4.6075	2.0899
30.6350	13.8958	2.4173	1.0965	40.3137	18.2860	5.6700	2.5719	3.2640	1.4805	4.8448	2.1976
26.6819	12.1027	2.3300	1.0569	31.7904	14.4199	5.4302	2.4631	2.7388	1.2423	2.7373	1.2416
28.1142	12.7524	2.3016	1.0440	37.3077	16.9225	4.4786	2.0315	3.2227	1.4618	2.3214	1.0530
21.1373	9.5877	2.0066	0.9102	42.3674	19.2175	4.3323	1.9651	1.8802	0.8528	2.0736	0.9406
25.5070	11.5698	2.7786	1.2604	33.8999	15.3768	4.6124	2.0921	3.0968	1.4047	3.8117	1.7290
24.3338	11.0376	2.5935	1.1764	25.3344	11.4915	4.3678	1.9812	4.4171	2.0036	4.2032	1.9065
20.8333	9.4498	1.7371	0.7879	25.2603	11.4579	4.1543	1.8844	4.0948	1.8574	3.2740	1.4851
17.3808	7.8838	1.9082	0.8656	21.3491	9.6838	4.0761	1.8489	4.4519	2.0193	4.2575	1.9312
16.7265	7.5870	1.9099	0.8663	32.8126	14.8835	4.4345	2.0114	4.2283	1.9179	3.4996	1.5874

Year	New York		New Jersey		Delaware		Ches. Bay Maryland		coastal Maryland		PRFC	
	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)	Pounds (lbs * 10 ⁶)	Metric Tons (MT*10 ³)
1974	0.0032	0.0015	2.8706	1.3021	1.7854	0.8098	25.5748	11.6005	1.2300	0.5579	1.6689	0.7570
1975	0.0160	0.0073	2.9088	1.3194	3.3752	1.5309	25.0301	11.3535	1.2354	0.5604	2.0790	0.9430
1976	0.0523	0.0237	2.7860	1.2637	3.6467	1.6541	20.1872	9.1568	1.0869	0.4930	1.9886	0.9020
1977	0.0128	0.0058	0.3954	0.1794	1.0770	0.4885	20.5925	9.3406	1.1189	0.5075	2.9939	1.3580
1978	0.0014	0.0006	0.9167	0.4158	0.2923	0.1326	16.8610	7.6480	0.9852	0.4469	2.2201	1.0070
1979	0.0566	0.0257	0.8844	0.4012	0.5252	0.2382	24.8989	11.2939	1.4909	0.6762	2.9167	1.3230
1980	0.1984	0.0900	1.9010	0.8623	1.8849	0.8550	25.5455	11.5873	1.2869	0.5837	3.4745	1.5760
1981	0.0329	0.0149	1.5872	0.7199	0.8040	0.3647	57.6505	26.1498	1.8836	0.8544	5.2294	2.3720
1982	0.0458	0.0208	0.8023	0.3639	0.9187	0.4167	42.1671	19.1267	1.3777	0.6249	4.1734	1.8930
1983	0.1331	0.0604	1.1977	0.5433	1.0175	0.4615	50.6728	22.9848	1.6556	0.7510	4.8987	2.2220
1984	0.1341	0.0608	1.7144	0.7776	1.0591	0.4804	47.1000	21.3642	1.5389	0.6980	3.9749	1.8030
1985	0.2801	0.1270	2.4072	1.0919	2.4402	1.1069	55.5272	25.1867	0.8897	0.4036	6.0407	2.7400
1986	0.1439	0.0653	2.7001	1.247	2.7503	1.2475	46.4136	21.0529	0.9258	0.4200	5.8621	2.6590
1987	0.3102	0.1407	2.9238	1.3262	3.4472	1.5636	42.6477	19.3447	1.2265	0.5563	4.7906	2.1730
1988	0.2054	0.0931	5.1103	2.3180	3.5351	1.6035	41.6734	18.9027	1.3213	0.5993	4.9692	2.2540
1989	0.6547	0.2970	5.6802	2.5765	4.6629	2.1151	42.3523	19.2107	0.9166	0.4157	5.3220	2.4140
1990	0.5127	0.2326	4.8396	2.1952	6.5769	2.9832	45.0945	20.4545	1.7439	0.7910	5.2250	2.3700
1991	0.8175	0.3708	4.9716	2.2551	5.0082	2.2717	47.4907	21.5414	1.1370	0.5157	7.2245	3.2770
1992	0.7656	0.3473	6.5296	2.9618	4.5412	2.0599	30.8579	13.9969	0.4951	0.2246	5.8092	2.6350
1993	1.2148	0.5510	7.7404	3.5110	5.9944	2.7190	56.8210	25.7736	0.8043	0.3648	7.5486	3.4240
1994	0.8868	0.4023	5.6041	2.5420	5.5815	2.5317	44.2430	20.0683	1.3035	0.5912	5.9723	2.7090
1995	1.7431	0.7907	7.6970	3.4913	6.3794	2.8936	41.1733	18.6759	0.9891	0.4487	4.0499	1.8370
1996	0.0957	0.0434	3.3477	1.5185	4.3952	1.9936	37.0206	16.7923	0.6808	0.3088	5.6879	2.5800
1997	0.7831	0.3552	4.3691	1.9818	4.5904	2.0822	40.1599	18.2162	1.1465	0.5200	9.0610	4.1100
1998	0.8124	0.3685	6.2092	2.8165	4.6517	2.1100	25.6776	11.6472	0.5413	0.2455	5.2867	2.3980
1999	1.3341	0.6051	5.7673	2.6160	5.0094	2.2722	31.5700	14.3199	0.5612	0.2546	5.2889	2.3990
2000	1.4817	0.6721	5.0683	2.2990	4.1962	1.9034	20.2389	9.1802	1.4223	0.6451	2.1319	0.9670
2001	1.2139	0.5506	5.4123	2.4550	3.8207	1.7330	22.6681	10.2821	1.8811	0.8532	2.4405	1.1070
2002	0.9755	0.4425	6.3984	2.9023	3.1717	1.4387	23.8425	10.8148	1.1685	0.5300	2.8881	1.3100
2003	0.9651	0.4378	4.0961	1.8580	1.4766	0.6698	25.2613	11.4583	1.1690	0.5302	2.0062	0.9100
2004	0.8919	0.4045	4.3879	1.9903	2.3303	1.0570	32.3047	14.6532	1.4696	0.6666	2.7293	1.2380
2005	0.7476	0.3391	6.3098	2.8621	3.0509	1.3839	30.1489	13.6753	1.9113	0.8670	4.2637	1.9340
2006	0.8076	0.3663	6.1125	2.7726	3.1067	1.4092	27.8735	12.6432	1.1442	0.5190	3.9860	1.8080
2007	0.7133	0.3235	5.4078	2.4529	4.1711	1.8920	24.7451	11.2242	1.0924	0.4955	2.4229	1.0990
2008	0.5317	0.2412	5.6616	2.5680	4.0176	1.8224	29.3704	13.3222	1.2454	0.5649	2.4846	1.1270

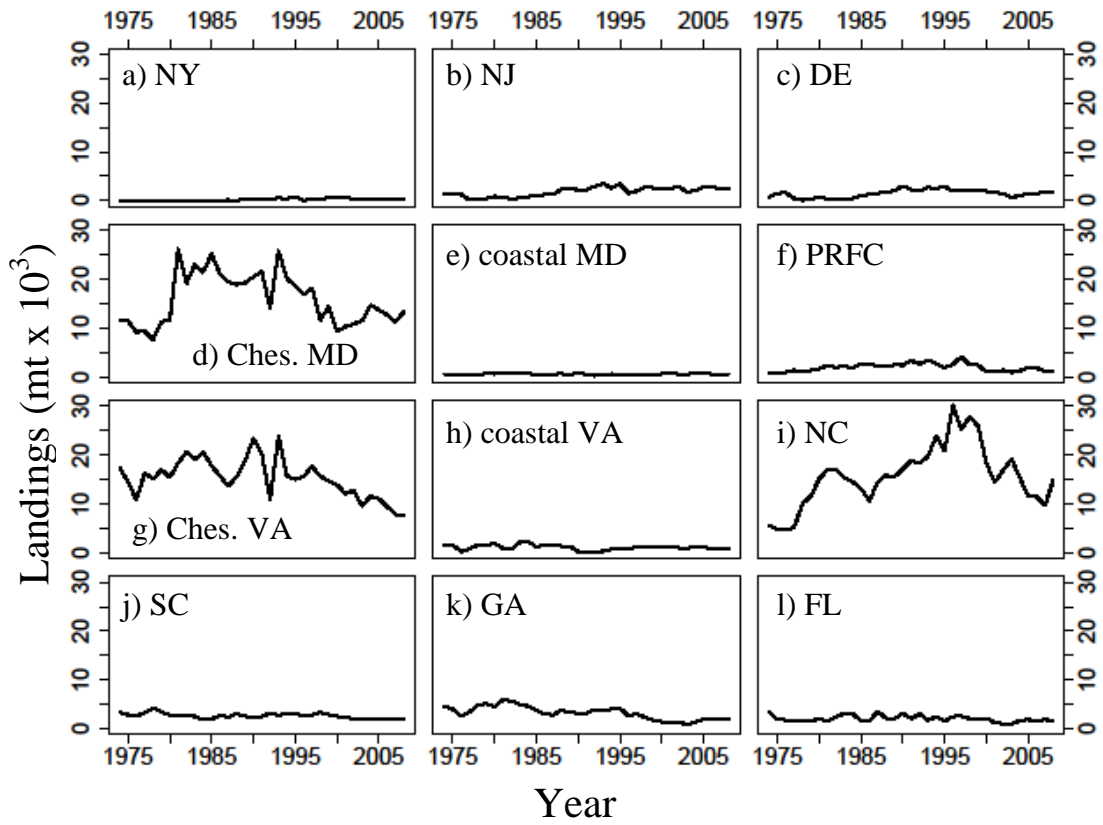


Figure 2.11. Raw time series for landings from a) New York, b) New Jersey, c) Delaware, d) Chesapeake Bay Maryland, e) coastal Maryland, f) Potomac River, g) Chesapeake Bay Virginia, h) coastal Virginia, i) North Carolina, j) South Carolina, k) Georgia, and l) Florida for 1974-2008.

Petitgas 2009). While this approach allows for identification of breakpoints, it does not allow for the estimation of their effect on the time series. Structural change models have also been used to objectively identify breakpoints in time series (Bai & Perron 2003). However, as with the CUSUM approach, this method also identifies the intervention point, but not its magnitude. In contrast, intervention analysis will not objectively identify when breaks occur, but will identify the magnitude of the change if a breakpoint is specified (Fogarty & Miller 2004). To assess the potential of reporting changes affecting individual time series, I used an ARIMA framework (Chatfield 1989). There were no missing data points for the time period used in the study with the exception of the shorter time series for the coastal bays in Maryland, described above. The data from each state/region were assessed for stationarity, an underlying assumption for time series analysis, using the autocorrelation (ACF) and partial autocorrelation (PACF) functions. Plots were generated to show the ACF versus lag to indicate the appropriate lag for differencing.

I implemented an intervention analysis within an ARIMA framework to assess the impact of known reporting changes for each state. I used the entire available time series for the intervention analyses, which for all but New York and the coastal bays of Maryland and Virginia was 1950 so that all possible data were included in estimating how the time series should be corrected. Including all of the available information in the intervention analysis was important to help determine if the proposed intervention was artificial or if it was the result of inherent variability in the population. It should be noted that since Maryland coastal bays were back-projected from the original Maryland data the intervention analysis for this time series included

back-projected data for the period of 1950-1984 and reported data for the remainder of the time series. This was important because Chesapeake Bay Maryland was used to create the back-projected values so any interventions found in the Chesapeake Bay Maryland landing may also apply to the projected Maryland coastal bays landings.

I defined a binary {0,1} intervention vector to represent each potential intervention (0's for years prior to interventions, 1's for years post intervention). The intervention vectors were used as independent variables in the fitting of the harvest time series from each state. The final model can be written as:

$$c_t = \Theta + \omega(B)I_t + ((\theta_i(B))/(\phi_i(B)))z_t \quad [\text{Eq. 2.2}]$$

where the subscript t refers to year, c is the catch, Θ is a constant, B is the backshift operator, ω is an estimated parameter based on the importance of the intervention (I_t), and θ and ϕ are polynomial parameters related to a moving average and autoregressive time series models that result from a model fitting with residuals (z) that are a pure white noise process (Forgarty & Miller 2004). The appropriate order for the moving average and autoregressive terms was determined using the auto.arima function in R(v.2.11.1), which uses Akaike's Information Criterion (AIC) to find the order of polynomial parameters that give the best model fit and has residuals that do not differ from a pure white noise process. The estimated regression parameters (ω , θ , ϕ) from the model fitting were sequentially tested to determine if the magnitude of the effect is significantly different from zero using a t-test ($\alpha = 0.05$). If the effect is significant, it was included and the ARIMA model was rerun.

If the intervention term was found to be significantly different from zero, the intervention vector was used to create an adjusted catch time series in which all landings were “expressed” in terms of the most recent reporting method, which assumes that the current reporting method in each state leads to the most accurate landings estimates. All time series analyses were conducted in R v. 2.11.1 (Appendix B).

I explored the potential for reporting changes in the time series for each region. There was no evidence for significant interventions in nine of the twelve time series. For these nine regions I used the original time series in subsequent analyses. However, significant interventions were present in the catch time series for Chesapeake Bay in Maryland ($t = 5.43, p < 0.05$) and Virginia ($t = 3.90, p < 0.05$) and the coastal bays in Maryland ($t = 4.86, p < 0.05$; Table 2.5). Maryland’s intervention for both the coastal and Chesapeake Bay landings occurred in 1981 when the state switched from a self-reporting system to one where a statistical survey was conducted based on the reports of a small group of volunteer fishermen. This change caused almost a three-fold spike in landings between 1981 and 1982. The implementation of the intervention corrected the pre-1981 landings based on the post-1981 landings, suggesting that during earlier years of the time series underestimation of blue crab landings was common (Figure 2.12a, b). In Virginia the intervention occurred in 1993 when the state switched from a dealer-based to a fisher-based reporting system. The intervention suggests that landings were being underestimated in the years before 1993 (Figure 2.12c). After the corrections were put in place for Maryland and

Table 2.5. Results of significant intervention analyses for Chesapeake and coastal Maryland and Virginia landings in the Chesapeake Bay for the period of 1950-2008.

	Ches. Bay MD (\pm SE)	coastal MD (\pm SE)	Ches. Bay VA (\pm SE)
ω_{1981}	- 12.4151 (2.2862)	-0.2051 (0.0422)	N/A
ω_{1993}	N/A	N/A	- 13.0652 (3.3509)
θ	- 0.6246 (0.1019)	-1.0000 (0.0369)	not significant
ϕ	not significant	0.3346 (0.1085)	not significant
AIC	299.72	-97.21	314.12
AIC _c	300.16	-96.67	314.34
RMSE	2.8795	0.121	3.3228

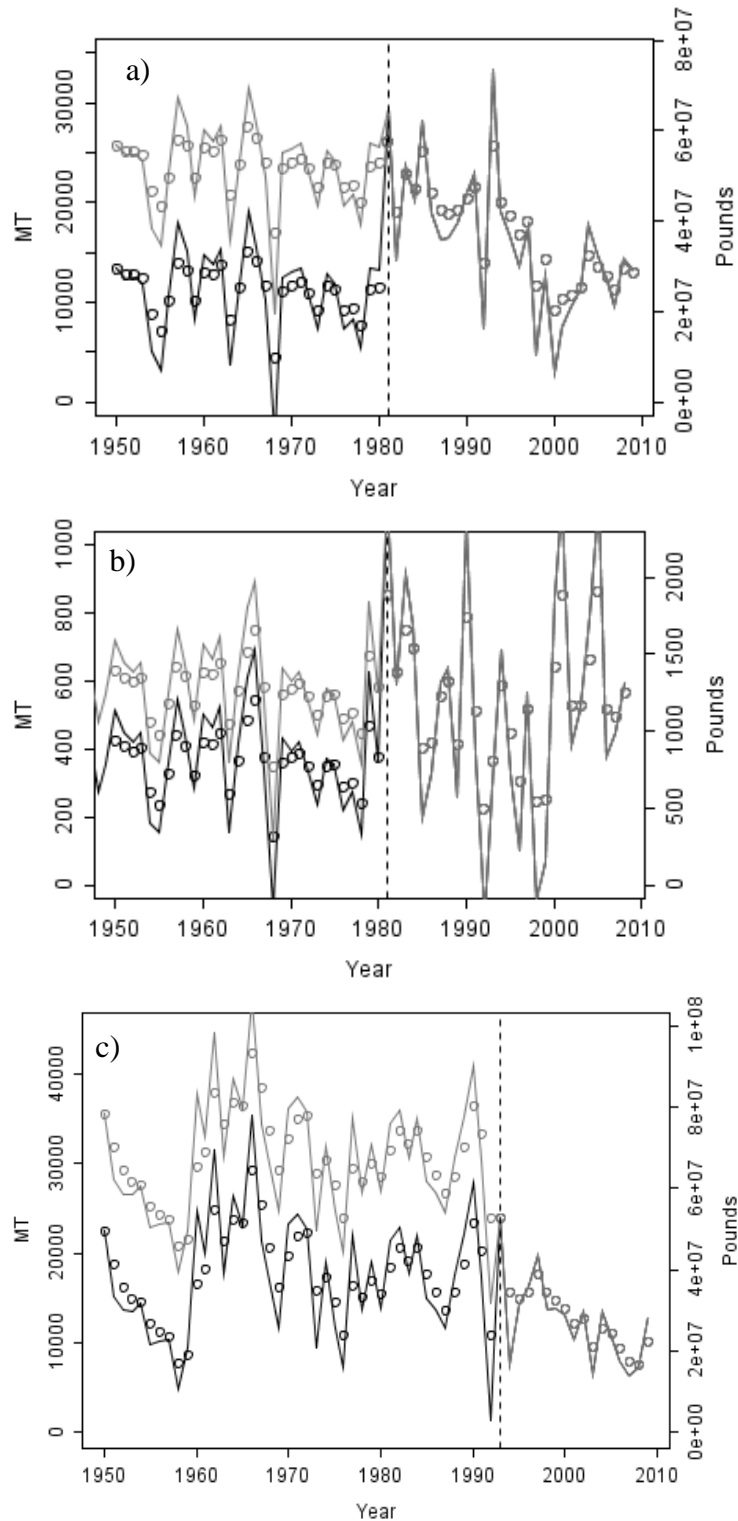


Figure 2.12. Corrected time series for a) Chesapeake Bay Maryland b) coastal Maryland and c) Chesapeake Bay Virginia. Black line represents the ARIMA model fit on the original data (black circles) and the grey line represents the ARIMA model fit on the corrected time series (grey circles). The dotted vertical lines represent the imposed interventions.

Virginia, the 12 state landing time series were assumed to be in a comparable form that could be used in my analyses.

To be able to use these time series in my subsequent analyses I had to convert all time series from biomass to abundance. I received and used pounds to numbers conversions for soft and hard crabs in each state except Georgia (Table 2.6a,b). Since both South Carolina and Florida had very similar conversions to each other, and they both border Georgia, I used Florida's conversions for Georgia. The landings time series in units of numbers of crabs were used in the Collie-Sissenwine catch-survey model (Table 2.7).

Blue crab recreational landings are difficult to quantify, but can be quite substantial in some states. To account for recreational landings, landings data were inflated by a percentage of commercial landings that were thought to best estimate the amount of recreational fishing occurring in that state. These percentages were determined by talking with state agencies and reading past stock assessments (Table 2.8). Thus aggregate landings used in analyses reflect the best estimate of the total removals from the population resulting from both commercial and recreational fisheries.

Catch-survey analysis

A catch-survey analysis (CSA) uses both aggregate landings and survey abundance indices to calculate the total abundance of a population (Collie & Sissenwine 1983). The Collie-Sissenwine equation used in my study was altered slightly to allow for a pulse fishery in the middle of the year. This modification applies half of the natural mortality on the population before the fishery occurs and

Table 2.6. Pound to number conversions for a) all regions except b) Delaware Bay. Values indicate the number of crabs pound⁻¹.

a)	State	Hard Crab Conversion	Hard Female Conversion	Hard Male Conversion	Soft/Peeler Conversion
	Delaware		see Table 2.6b		
	New Jersey		see Table 2.6b		
	Maryland		3.23	2.38	reported in numbers
	Virginia		3.56	2.60	reported in numbers
	North Carolina	3	N/A	N/A	3
	South Carolina	2	N/A	N/A	4.5
	Georgia	2*	N/A	N/A	4*
	Florida	2	N/A	N/A	4

* Values based on neighboring states' conversion factors

b)	Market Grade	Landings Unit	Common Unit Equivalent	Numbers per Landings Unit
	#1 Male Hard Crab; pot	bushel	40 lb	93.8
	#1 Male Hard Crab; dredge	bushel	40 lb	114.0
	#2 Male Hard Crab; (both gears)	bushel	40 lb	134.7
	#3 Female Hard Crab; (both gears)	bushel	40 lb	123.0
	Hard Crab (unspecified male); dredge	bushel	40 lb	114.492
	Hard Crab (unspecified male); pot	bushel	40 lb	110.477
	Hard Crab (unspecified); dredge	bushel	40 lb	122.322
	Hard Crab (unspecified); pot	bushel	40 lb	114.844
	Hard Crab (unspecified); pot; Apr	bushel	40 lb	118.277
	Hard Crab (unspecified); pot; May	bushel	40 lb	117.673
	Hard Crab (unspecified); pot; Jun	bushel	40 lb	114.479
	Hard Crab (unspecified); pot; Jul	bushel	40 lb	114.990
	Hard Crab (unspecified); pot; Aug	bushel	40 lb	113.391
	Hard Crab (unspecified); pot; Sep	bushel	40 lb	114.076
	Hard Crab (unspecified); pot; Oct	bushel	40 lb	114.504
	Hard Crab (unspecified); pot; Nov	bushel	40 lb	114.097
	Peeler	bushel	62.49 lb	300
	Peeler	pound	-	4.801*
	Peeler	numbers	0.2083 lb*	-

Table 2.7. Landings in numbers of individuals (millions) for each region of the study area.

Year	Delaware Bay	Chesapeake Bay	coastal MD & VA	North Carolina	South Carolina	Georgia	Florida
1968		353.26					
1969		359.95					
1970		389.57					
1971		409.45					
1972		406.01					
1973		346.97					
1974		372.49					
1975		350.93					
1976		310.45					
1977		354.80					
1978	0.87	332.69		67.65			
1979	1.50	370.88		77.47	15.47		
1980	5.15	362.81		101.19	12.44		
1981	2.34	402.33		113.74	12.24		
1982	2.38	373.14		113.43	12.63		
1983	2.83	387.49		102.28	11.20		
1984	2.83	385.78		97.01	8.47		
1985	6.42	393.86		87.91	8.91	16.70	
1986	6.99	353.55		71.07	12.05	13.30	
1987	8.26	325.04		96.94	10.86	12.63	
1988	8.42	337.13		105.89	13.81	17.00	
1989	11.42	363.81	1.26	103.86	11.54	14.79	
1990	15.93	403.92	0.81	114.57	10.46	14.39	14.24
1991	12.87	393.87	0.43	125.78	11.00	14.01	9.32
1992	13.54	274.80	0.19	122.09	14.50	17.61	13.71
1993	14.03	350.90	0.54	131.99	12.54	16.47	7.98
1994	13.49	259.26	0.96	159.97	14.39	17.89	11.03
1995	17.57	244.29	1.03	139.65	14.09	18.85	7.05
1996	19.12	242.59	0.80	202.04	11.88	11.91	11.31
1997	24.27	275.26	1.29	168.65	12.46	14.13	11.75
1998	30.78	207.21	1.07	186.07	15.11	10.51	9.27
1999	29.66	217.93	0.92	173.24	13.16	8.09	9.27
2000	24.85	175.09	1.27	122.16	11.52	6.71	9.79
2001	24.18	170.22	1.42	96.33	11.06	5.61	5.53
2002	26.24	171.30	1.14	113.05	9.04	6.60	4.70
2003	18.62	155.04	1.05	128.39	8.76	3.86	4.21
2004	25.83	184.70	1.40	102.73	9.36	6.31	7.68
2005	34.76	179.03	1.51	76.77	8.90	8.92	8.48
2006	33.15	158.99	0.96	76.55	8.46	8.23	6.60
2007	35.96	133.13	0.99	64.69	8.31	9.04	8.56
2008	34.62	143.14	1.05	99.43	8.99	8.58	7.05

Table 2.8. Values of natural mortality (M) and proportion of recreational landings used in the CSA models.

ADMB Model	M	Proportion Recreational Landings
Delaware Bay	0.8	12%
Chesapeake Bay	0.9	8%
coastal MD & VA	0.9	8%
North Carolina	0.87	1%
South Carolina	0.8	12%
Georgia	0.9	10%
Florida	1.0	18%

applies the remainder of the natural mortality after the fishery. The final population model was:

$$N_{t+1} = ((N_t + R_t) e^{-M/2} - C_t) e^{-M/2} \quad [\text{Eq. 2.3}]$$

where N_t is the total number of fully recruited individuals in a population in year t , C_t is the number of vulnerable individuals that were caught by the fishery in year t , R_t is the number of recruits in a population in year t , and M is the natural mortality rate. However, since we can't directly measure the population abundance of adults and recruits we must estimate abundance based on the relative abundances (i.e., indices) from the survey data.

Population abundances within the CSA model are for the beginning of the model year so it was necessary to adjust for differences in the timing of the surveys and the fisheries in the different regions. This was done by multiplying initial abundance by e^{-Mt} where t is the proportion of the year that occurred before the survey. The adjusted abundance time series were used to calculate the catchability coefficient, q , which is used to relate the survey abundance to the absolute population size such that:

$$n_{t,\text{est}} = q_n \hat{N}_t e^{\eta t} \quad \text{and} \quad r_{t,\text{est}} = q_r \hat{R}_t e^{\delta t} \quad [\text{Eqs. 2.4 \& 2.5}]$$

where $e^{\eta t}$ and $e^{\delta t}$ are lognormally distributed errors. The equation for calculating catchability of a survey is:

$$q_{n,s} = \exp\left(\frac{\sum (\log(n_{t,s,\text{obs}}) - \log(N_{t,s}))}{k_s}\right) \quad [\text{Eq. 2.6}]$$

where k_s is the number of years in the survey. Catchability for the Chesapeake Bay winter dredge survey was fixed at 1, which assumes that this survey is a measure of absolute abundance (Miller et al. 2011).

Assessments were conducted for Delaware Bay, Chesapeake Bay, the coastal bays of Maryland and Virginia, North Carolina, South Carolina, Georgia, and Florida using the same CSA assessment model. Aggregate landings time series from each region were used as the catch time series. Therefore, landings from individual states for the Delaware Bay, Chesapeake Bay, and coastal bays were combined as one catch time series for the CSA models. At least one survey was available for each of the CSAs, with two surveys for Delaware Bay and coastal Maryland and Virginia, three surveys for Florida, and four surveys for Chesapeake Bay (Table 2.1). Natural mortality estimates varied for each region (Table 2.8). A major assumption of my CSA model is that catch is known exactly in each year of the model. Initial abundance of adults and recruits and recruitment deviations from year to year are estimated parameters in the model.

Parameters were estimated by minimizing the objective function, which was the sum of negative log-likelihood functions from each survey and penalties for abundance going below zero and for exploitation not following a prior distribution. Lognormal observation errors were assumed for all surveys except the Chesapeake Bay winter dredge, which was assumed to have a normal distribution based on the extensive number of stations sampled each year (Miller et al. 2011). The negative log-likelihood equation for each survey (s), except the winter dredge survey in the Chesapeake Bay, was:

$$L_s = k_s * \log(\sigma_s) + 1/(2\sigma_s^2) * \sum (\log(n_{t,s,obs}) - \log(n_{t,s,est}))^2 \quad [\text{Eq. 2.7}]$$

where σ_s is the log-scale standard deviation for the survey s , which was obtained from the Delta-GLM analysis jackknifing. The winter dredge likelihood equation was:

$$L_s = \sum \log(n_{t,s,est} * CV_s) + 1/(2 * (n * CV_s)^2) * \sum (n_{t,s,obs} - n_{t,s,est})^2 \quad [\text{Eq. 2.8}]$$

where CV_s is the coefficient of variation.

Two penalty terms were also included in the objective function. The first was a penalty to penalize estimation of negative abundances. Only models with this penalty equal to zero were considered to be potential models for that region. The second penalty penalized extremes in exploitation rates, both large and small. This was done by using a prior on exploitation rates that constrained them to be between zero and one and created a penalty based on how much the average exploitation rate deviated from the peak of the distribution curve (Figure 2.13). The prior had a beta distribution and was calculated using the equation:

$$\text{prior} = -(\alpha - 1) * \log(\bar{u}) - (\beta - 1) * \log(1 - \bar{u}) \quad [\text{Eq. 2.9}]$$

where \bar{u} is the average exploitation rate for the model period and α and β are terms used to create the shape of the distribution. Due to this exploitation penalty the exploitation equation had to incorporate a mortality term:

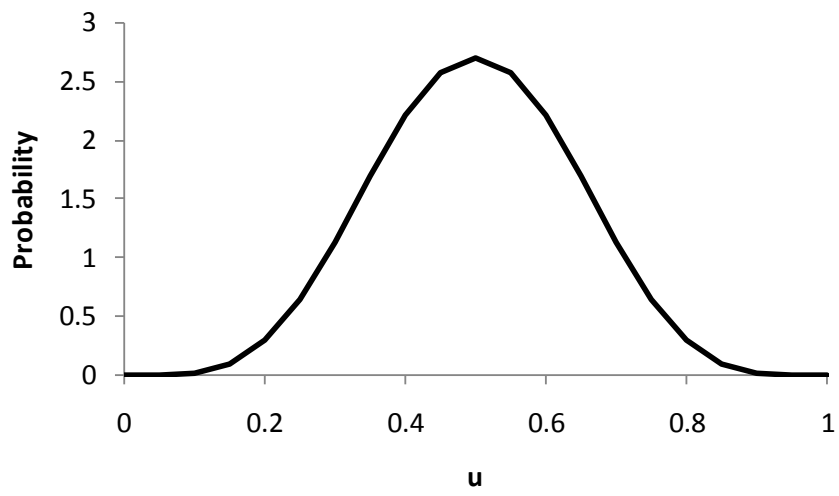


Figure 2.13. Prior distribution used for the exploitation rate penalty used in the stock assessment models.

$$u_y = C_y / ((N_y + R_y) e^{-M/2}) \quad [\text{Eq. 2.10}]$$

because without this it would use abundance at the beginning of the year and exploitation would never be able to reach one, which is the upper cutoff value for the prior distribution. The assessment models were implemented in AD Model Builder (<http://admb-project.org>). ADMB codes and data sets are presented in Appendix C.

I developed seven region-specific assessments. Each implementation required jurisdiction-specific estimates of the timing of each survey, recruitment, and exploitation within the year. Region specific estimates of the natural mortality rate parameter, M , were also provided (Table 2.5). Each CSA used these parameter estimates together with annual fishery-independent survey indices for recruits and adults and a time series of catch in each jurisdiction. The model estimated (together with associated uncertainties) the initial recruit and adult abundance, time series of recruitment deviations, exploitation rates and trajectories of annual recruit and adult abundances.

Results

Satisfactory catch survey analyses that met the convergence criterion for the ADMB maximum gradient component (1×10^{-4}) were developed for each of the seven jurisdictional models. Each model provided estimates of the initial adult and recruit abundance and deviations in recruitment each year being estimated by the model (Table 2.9; Figure 2.14). Exploitation rates seemed to be reasonable for each region based on what managers in each jurisdiction believe to be the approximate amount of

Table 2.9. Model fits and parameter estimates from the CSA stock assessment models.

System	# of parameters	Convergence Criterion	neg LL	R0 (millions)	N0 (millions)	mean recruitment deviation
Delaware Bay	33	-8.5795 e-005	94.5214	41.847	20.2882	-3.7097E-07
Chesapeake Bay	43	-3.673 e-005	248.255	585.094	201.548	-7.32E-09
coastal MD & VA	22	9.9434 e-006	31.6049	8.424	3.082	2.305E-07
North Carolina	33	-9.0615 e-005	-69.4736	138.489	11.2022	5.16129E-08
South Carolina	32	8.5057 e-005	33.7626	27.8115	6.8188	4.33333E-08
Georgia	26	-4.583 e-005	1.9378	188.813	63.4482	1.41667E-07
Florida	21	9.9527 e-005	16.0412	43.5678	1.0000	-2.1053E-08

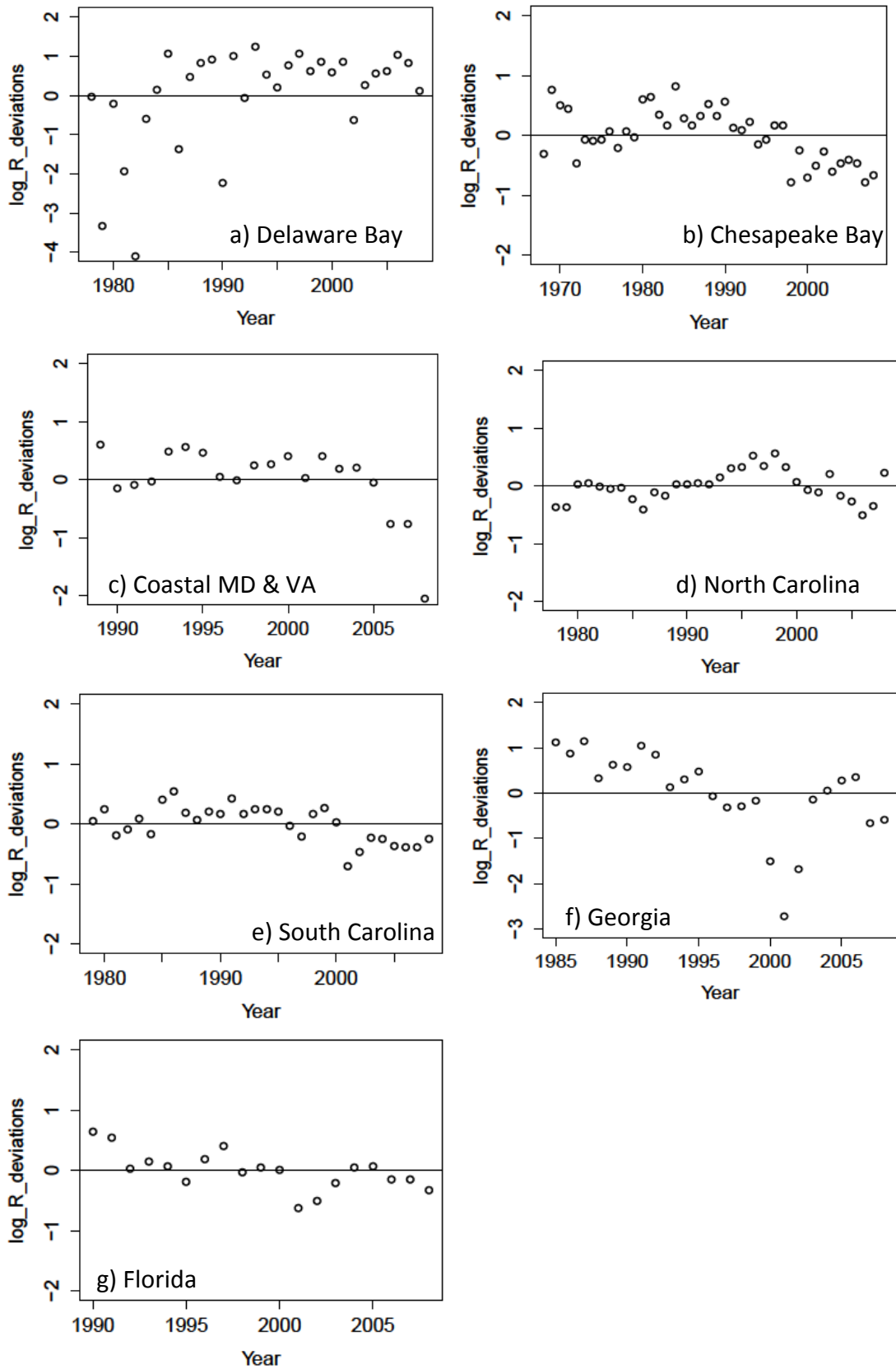


Figure 2.14. Log recruitment deviations estimated in each of the CSA models.

exploitation, further suggesting that each CSA was providing a believable estimate of abundance (Table 2.10). A brief description of the model fits and abundance estimates from each state is provided here.

Delaware Bay:

Overall, the best fitting model well described the dynamics of blue crab in the Delaware Bay (Table 2.9). The model estimates fitted the observed patterns in fishery-independent and fishery-dependent data well. Inspection of the model results suggests that there were no substantial biases in the model fits. The Delaware Bay model fit the Delaware survey much better than the New Jersey survey for both adults and recruits (Figure 2.15 a,b; 2.16a,b). There was a very large peak in Delaware observed recruitment in 1985 that the model cannot fully duplicate. The CSA suggested that the initial abundance of recruits and adults in 1978 were 41.85 and 20.29 million respectively (Table 2.9). The model estimated that, in 2008, the recruits and adults were at 133 and 166% of their 1978 abundance (Table 2.11). Estimated adult abundance for Delaware Bay was calculated to be at a time series low in 1983 followed by a two year increase in abundance. From 1985-2002 adult abundance remained fairly high and then decreased through the mid-2000s and began to recover in the last few years of the time series (Figure 2.17). Predicted recruit abundance was extremely variable throughout the entire time series (Figure 2.18).

Table 2.10. Exploitation rates calculated from the CSA models for each region. Note that exploitation in the last year may not be accurate due to how exploitation is calculated.

Year	Delaware Bay	Chesapeake Bay	coastal MD & VA	North Carolina	South Carolina	Georgia	Florida
1968		0.761					
1969		0.342					
1970		0.368					
1971		0.406					
1972		0.755					
1973		0.706					
1974		0.760					
1975		0.721					
1976		0.553					
1977		0.734					
1978	0.023	0.596		0.705			
1979	0.087	0.674		0.782	0.746		
1980	0.184	0.385		0.716	0.549		
1981	0.168	0.355		0.760	0.690		
1982	0.423	0.389		0.811	0.744		
1983	0.179	0.487		0.772	0.580		
1984	0.080	0.311		0.709	0.497		
1985	0.072	0.406		0.751	0.326	0.114	
1986	0.159	0.444		0.736	0.341	0.095	
1987	0.143	0.390		0.779	0.367	0.077	
1988	0.103	0.335		0.882	0.546	0.153	
1989	0.116	0.391	0.185	0.756	0.467	0.139	
1990	0.382	0.384	0.178	0.790	0.429	0.142	0.622
1991	0.157	0.492	0.107	0.858	0.364	0.103	0.401
1992	0.245	0.403	0.046	0.882	0.531	0.132	0.804
1993	0.131	0.464	0.089	0.849	0.486	0.187	0.539
1994	0.157	0.457	0.138	0.877	0.551	0.228	0.730
1995	0.276	0.434	0.153	0.753	0.573	0.227	0.637
1996	0.249	0.355	0.154	0.867	0.592	0.200	0.733
1997	0.239	0.372	0.286	0.868	0.760	0.311	0.617
1998	0.374	0.514	0.223	0.801	0.743	0.264	0.667
1999	0.358	0.486	0.182	0.878	0.574	0.189	0.668
2000	0.354	0.535	0.221	0.841	0.560	0.305	0.722
2001	0.299	0.494	0.307	0.744	0.938	0.654	0.730
2002	0.670	0.397	0.214	0.886	0.879	0.830	0.606
2003	0.476	0.428	0.210	0.797	0.674	0.120	0.396
2004	0.480	0.485	0.282	0.851	0.656	0.127	0.523
2005	0.577	0.453	0.372	0.729	0.676	0.136	0.563
2006	0.398	0.414	0.415	0.857	0.671	0.110	0.528
2007	0.446	0.437	0.546	0.680	0.661	0.197	0.701
2008	0.712	0.458	1.540	0.576	0.639	0.247	0.726

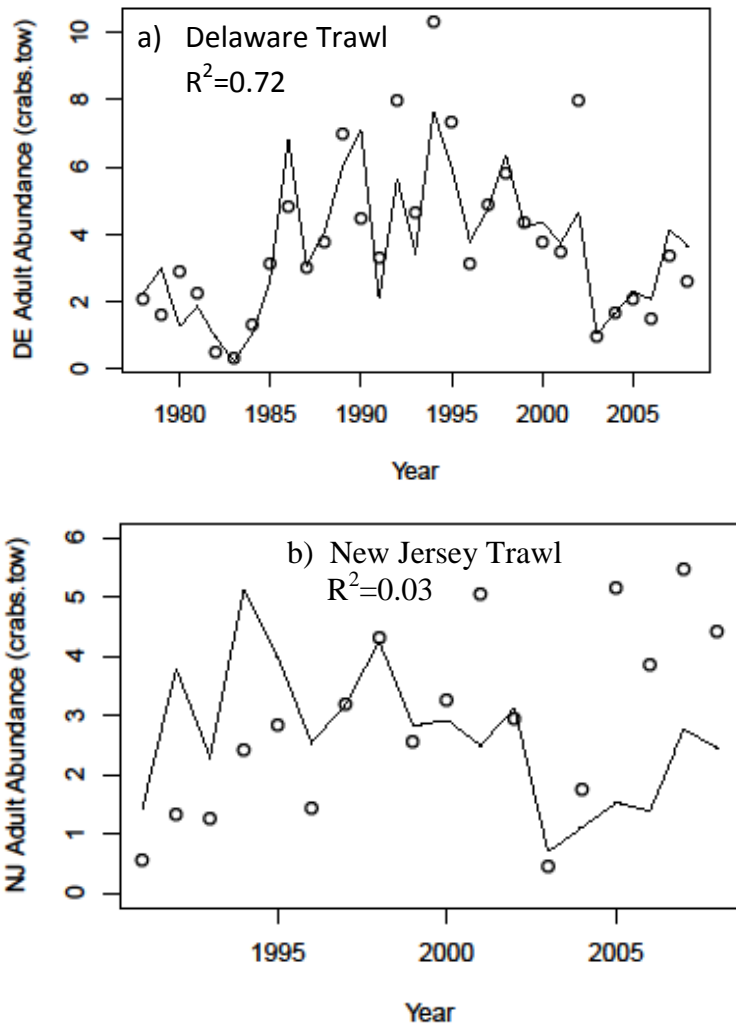


Figure 2.15. Model fits for the adults in the catch survey models for a) the Delaware trawl and b) the New Jersey trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

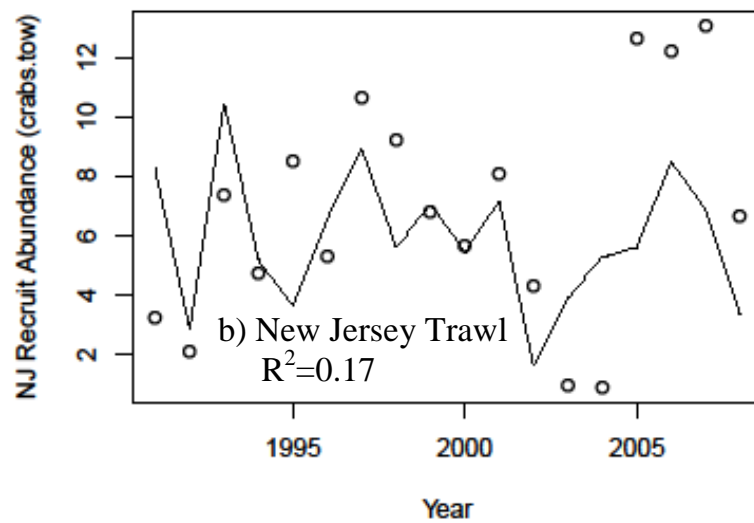
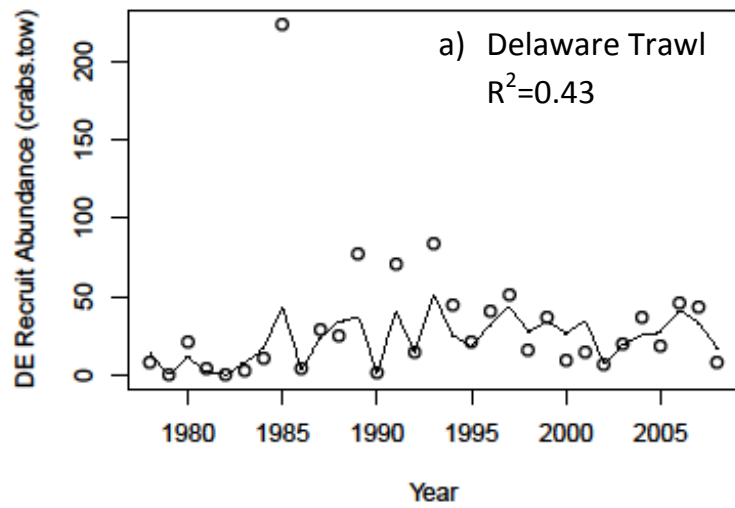


Figure 2.16. Model fits for the recruits in the catch survey models for a) the Delaware trawl and b) the New Jersey trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

Table 2.11. Comparison of abundance of recruits (R), adults (N), and total abundance (T) for the first (0) and last (2008) years for each stock assessment model.

	Del.Bay	Ches.Bay	coastal	NC	SC	GA	FL
R0	41.847	585.094	8.424	138.489	27.812	188.813	43.568
R2008	47.694	411.531	0.588	249.498	20.320	34.103	16.279
R2008/R0	1.140	0.703	0.070	1.802	0.731	0.181	0.374
N0	20.288	201.548	3.082	11.202	6.819	63.448	1.000
N2008	33.598	118.326	0.568	19.940	3.200	25.776	2.612
N2008/N0	1.656	0.587	0.184	1.780	0.469	0.406	2.612
T0	62.135	786.642	11.506	149.691	34.630	252.261	44.568
T2008	81.292	529.857	1.156	269.438	23.520	59.879	18.891
T2008/T0	1.308	0.674	0.100	1.800	0.679	0.237	0.424

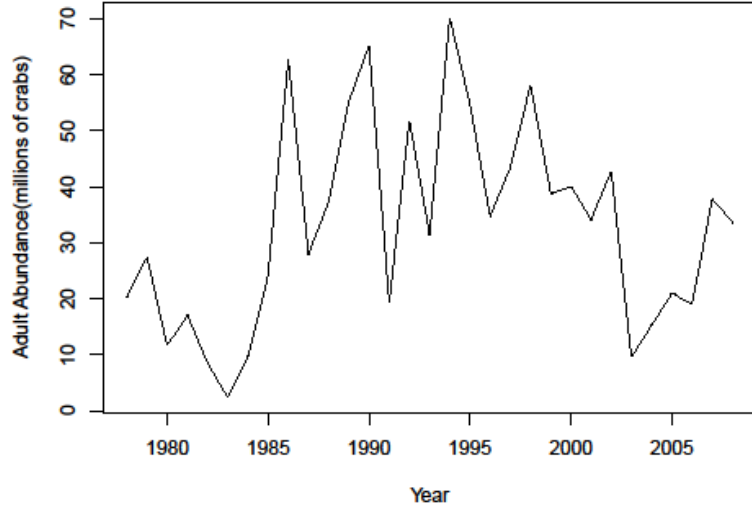


Figure 2.17. Adult absolute abundance estimated from the Delaware Bay CSA.

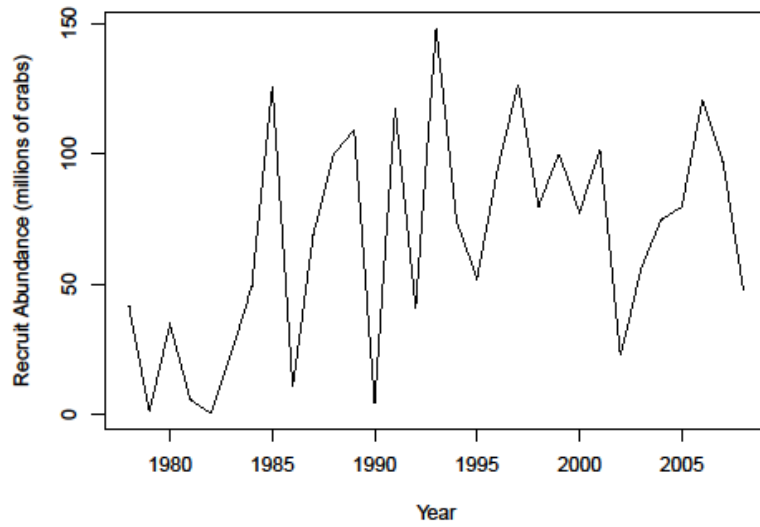


Figure 2.18. Recruit absolute abundance estimated from the Delaware Bay CSA.

Chesapeake Bay:

The CSA model produced an acceptable fit to the observed data for Chesapeake Bay (Table 2.9). The Chesapeake Bay model was best able to describe the pattern in the winter dredge adult survey. This is perhaps not surprising given that the model assumed that this survey provided an absolute estimate of abundance with a relatively low CV. The CSA also described the VIMS trawl survey data well. However, the MD trawl and ChesMMAp survey had poor fits for adults (Figure 2.19a-d). The winter dredge recruit survey was the best predictor of the three recruit surveys, but large observed peaks and decreases in the early years of the time series were not matched by the model (Figure 2.20c). The VIMS and MD trawl recruit models did not have a very good fit (Figure 2.20a,b). The CSA suggested that the initial abundance of recruits and adults in 1968 were 585.1 and 201.6 million respectively (Table 2.9). The model estimated that in 2008, the recruits and adults were at 70.3 and 58.7% of their 1968 abundance (Table 2.11). Absolute adult abundance was estimated to have been high in the early 1970s followed by a steep decrease and low abundance through 1980. An increase through the 1980s was prevalent, and through the 1990s and 2000s a steady decrease in abundance occurred (Figure 2.21). Recruit absolute abundance was estimated to be quite variable with years of high recruitment in the early 1970s and in three out of four years between 1980 and 1983. Recruitment was estimated to be fairly low throughout the 2000s (Figure 2.22).

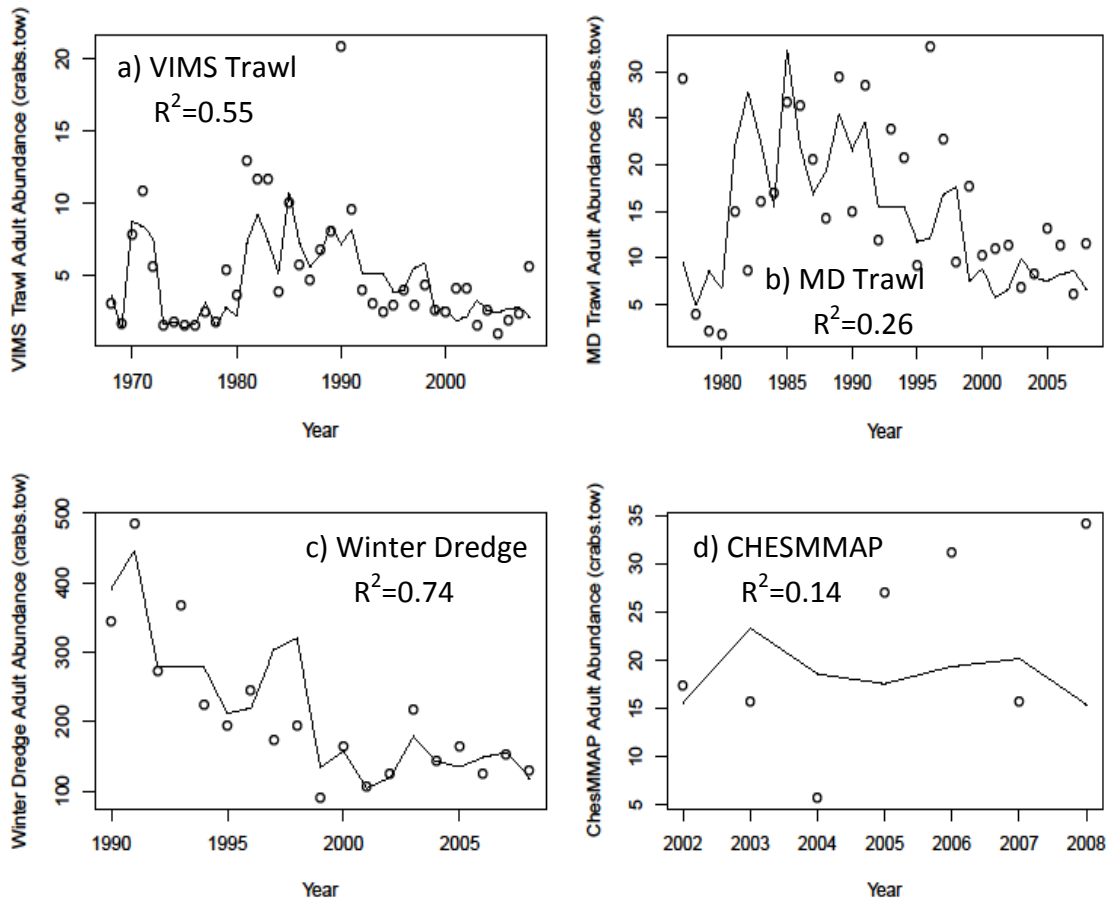


Figure 2.19. Model fits for the adults in the catch survey models for a) the VIMS trawl b) the Maryland trawl c) the winter dredge and d) ChesMAPP trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

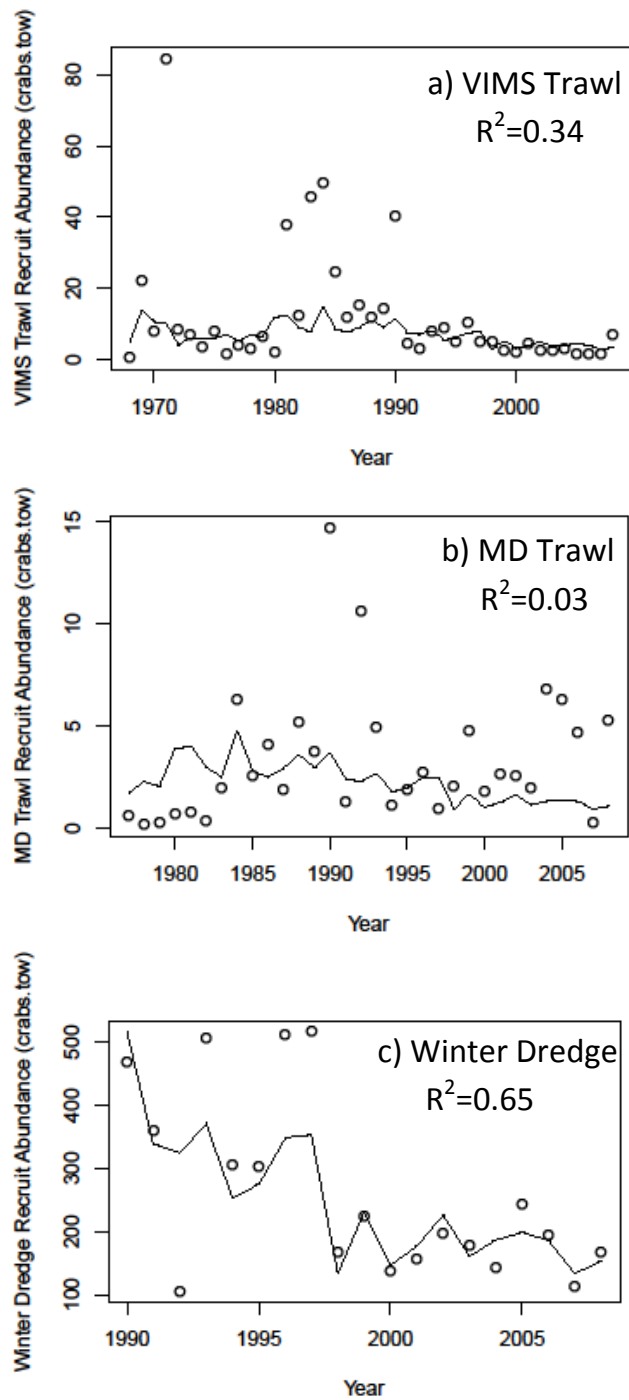


Figure 2.20. Model fits for the recruits in the catch survey models for a) the VIMS trawl b) the Maryland trawl and c) the winter dredge. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

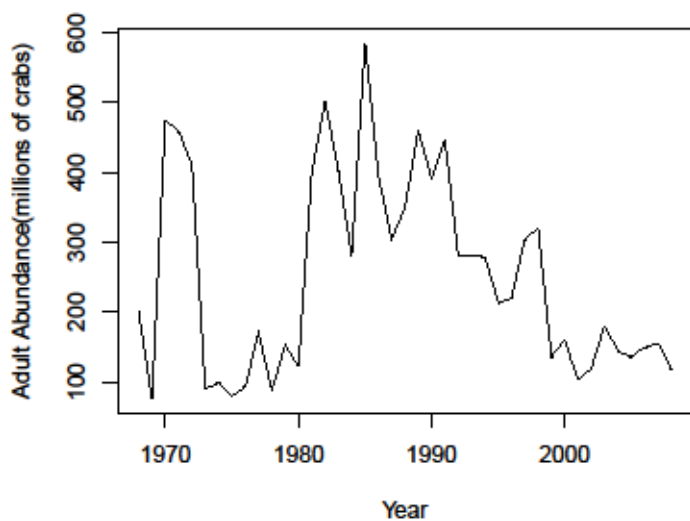


Figure 2.21. Adult absolute abundance estimated from the Chesapeake Bay CSA.

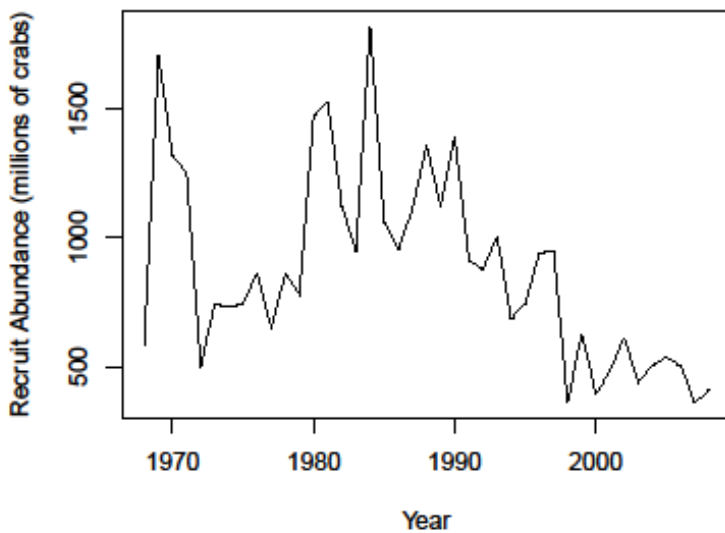


Figure 2.22. Recruit absolute abundance estimated from the Chesapeake Bay CSA.

Coastal Maryland and Virginia:

The CSA model produced an acceptable fit to the coastal Maryland and Virginia observed data (Table 2.9). The trawl survey did a much better job at predicting abundance in the coastal bays of Maryland and Virginia than the seine survey. The model fit tended to follow the general trend of the time series, but the magnitudes varied between the observed and predicted values. In most cases there was no particular bias in this difference in magnitude with the exception of the adult trawl survey, where the estimated values tended to be an underestimate of observed values for the period of 1989-2005 (Figure 2.23a,b; 2.24a,b). The CSA suggested that the initial abundance of recruits and adults in 1989 were 8.42 and 3.08 million respectively (Table 2.9). Absolute adult abundance was estimated to be relatively high through 2005 followed by a steep decrease in the last three years of the time series (Figure 2.25). Estimated absolute recruit abundance followed a very similar pattern except the decrease in abundance began a year earlier (Figure 2.26). The model estimated that in 2008, the recruits and adults were at 6.98 and 18.4% of their 1989 abundance (Table 2.11).

North Carolina:

The CSA model produced an acceptable fit to the observed data from North Carolina (Table 2.9). The model fit for North Carolina suggested that the adult North Carolina survey was a very good index of abundance, as the model fit followed the observed values almost exactly (Figure 2.27). The recruit abundance did not have a good fit, but the general pattern was followed in both time series with no obvious bias

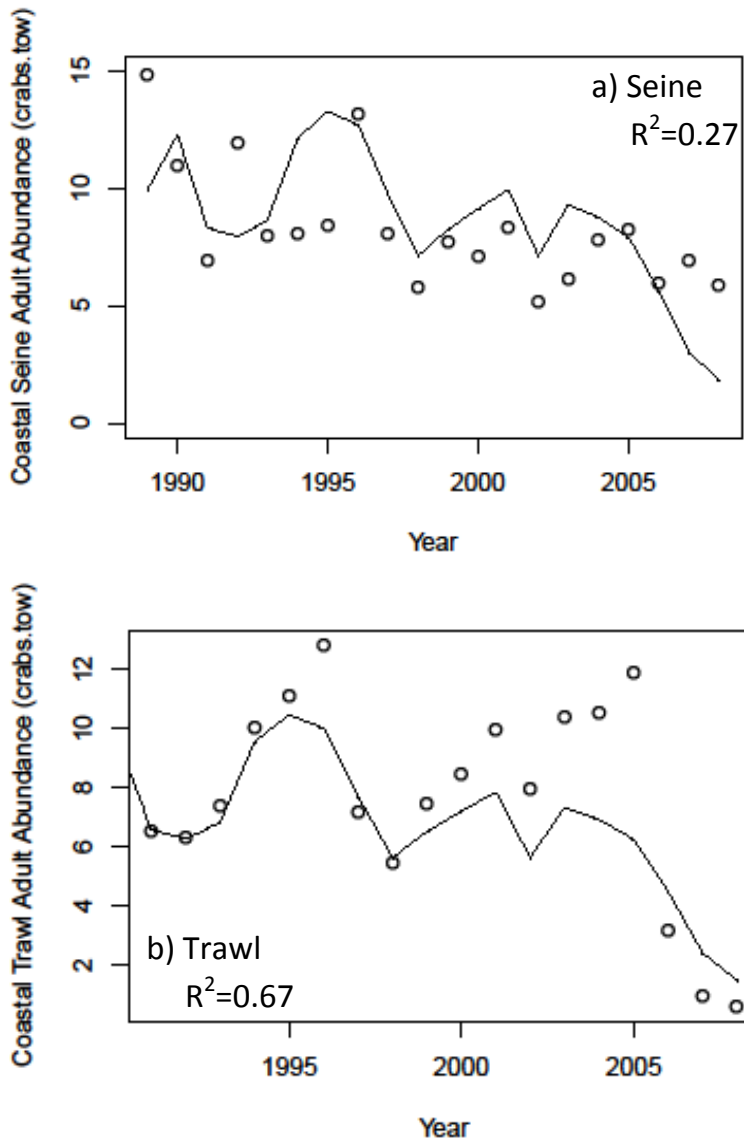


Figure 2.23. Model fits for the adults in the catch survey models for a) the coastal Maryland seine and b) the coastal Maryland trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

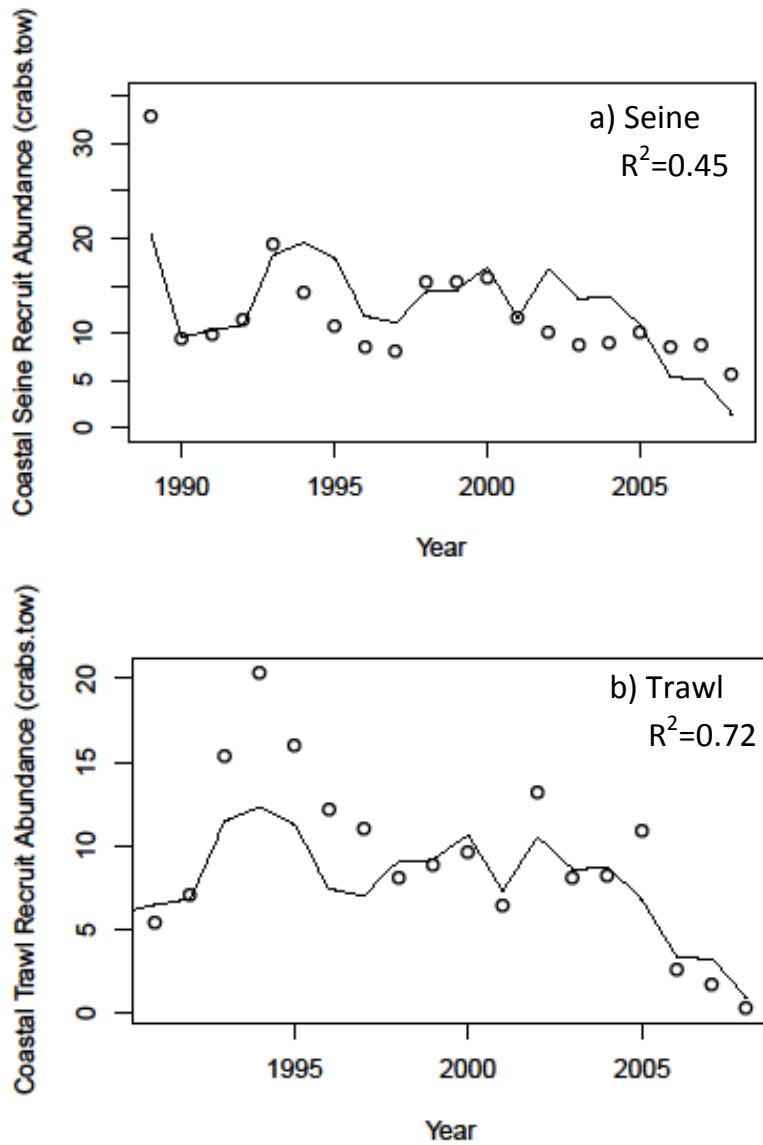


Figure 2.24. Model fits for the recruits in the catch survey models for a) the coastal Maryland seine and b) the coastal Maryland trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

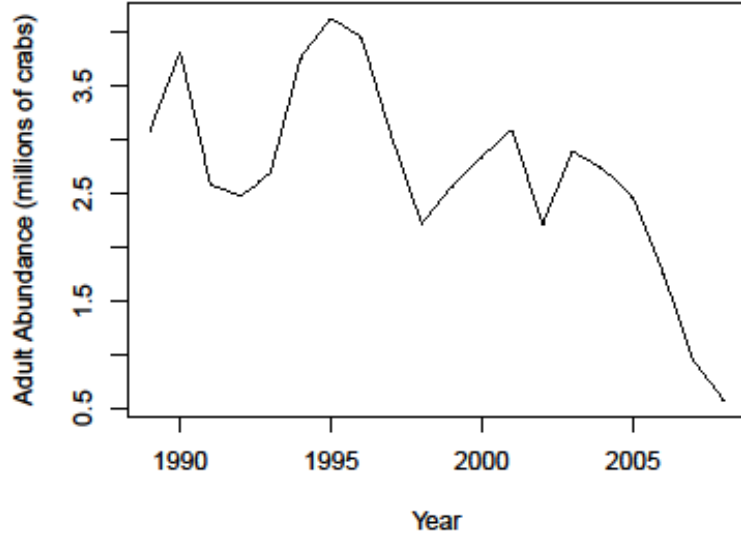


Figure 2.25. Adult absolute abundance estimated from the coastal Maryland and Virginia CSA.



Figure 2.26. Recruit absolute abundance estimated from the coastal Maryland and Virginia CSA.

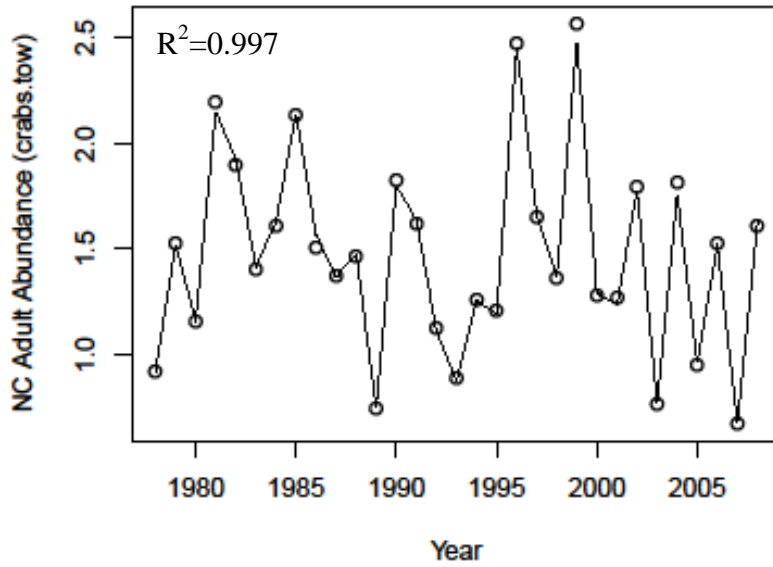


Figure 2.27. Model fits for the adults in the catch survey models for the North Carolina trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

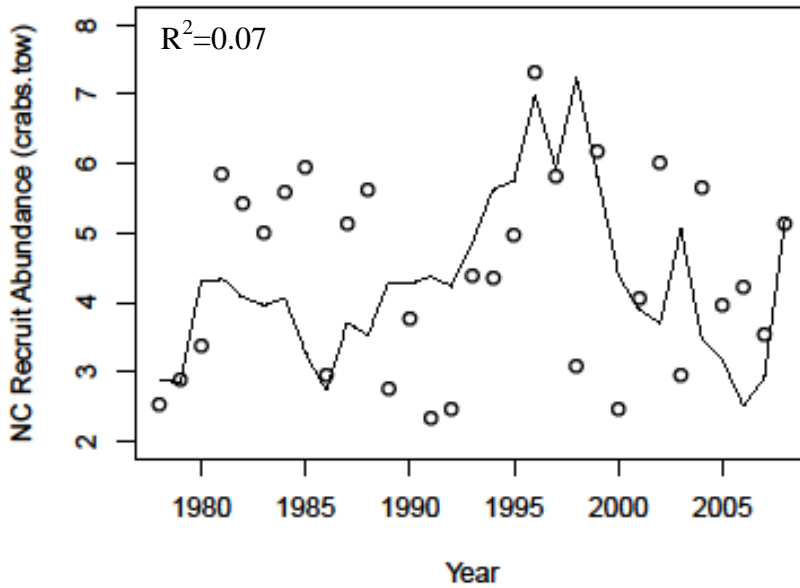


Figure 2.28. Model fits for the recruits in the catch survey models for the North Carolina trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

(Figure 2.28). The CSA suggested that the initial abundances of recruits and adults in 1978 were 138.5 and 11.2 million respectively (Table 2.9). The estimated absolute adult abundance was extremely variable over time, with the highest peaks in 1996 and 1999 (Figure 2.29). Recruit absolute abundance was steady, but low, for the first portion of the time series up until about 1994. Through the late 1990s recruitment was very high; in some cases being almost double the recruitment of some of the earlier years in the time series. After 1999 recruitment fell back to the pre-1994 levels where it leveled off except for a year of very low recruitment in 2006 (Figure 2.30). The model estimated that in 2008, the recruits and adults were at 180 and 178% of their 1978 abundance (Table 2.11).

South Carolina:

Like North Carolina, the South Carolina model had a very good fit for the adult South Carolina survey with only minor deviations between the observed and predicted values in most years (Figure 2.31). The CSA model produced an acceptable fit to the observed data (Table 2.9). The recruit indices were not as good of a fit for the survey (Figure 2.32). The CSA suggested that the initial abundance of recruits and adults in 1979 were 27.8 and 6.8 million respectively (Table 2.9). Adult absolute abundance was estimated to increase rapidly in the mid-1980s and remained high until the mid-1990s when it began decreasing. Very low adult abundance was reached in 2002 and although it recovered a little bit it has remained low for the remainder of the time series (Figure 2.33). Absolute recruit abundance was variable, but high until about 1995 when it remained variable but began decreasing, reaching a

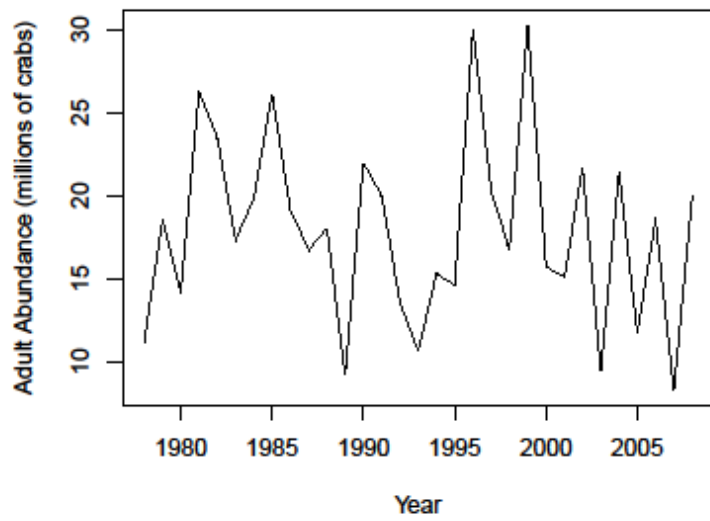


Figure 2.29. Adult absolute abundance estimated from the North Carolina CSA.

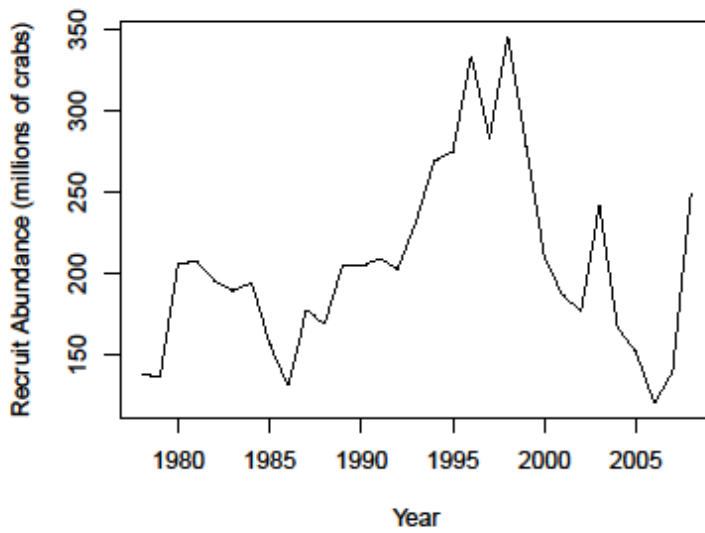


Figure 2.30. Recruit absolute abundance estimated from the North Carolina CSA.

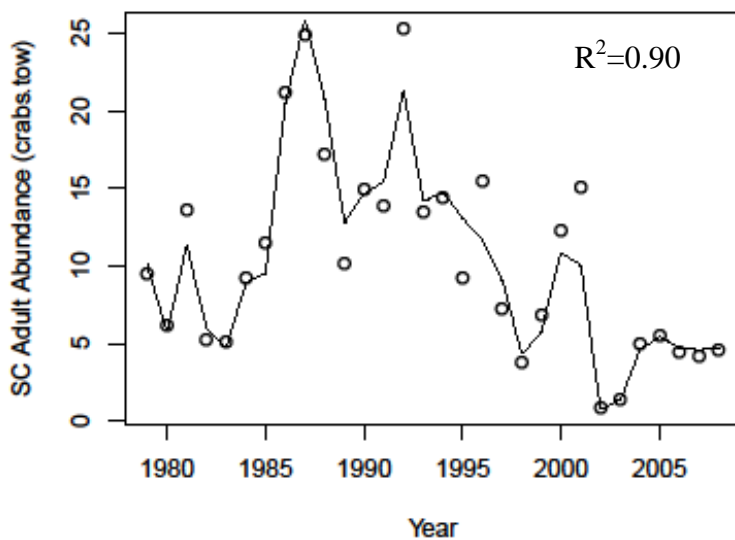


Figure 2.31. Model fits for the adults in the catch survey models for the South Carolina trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

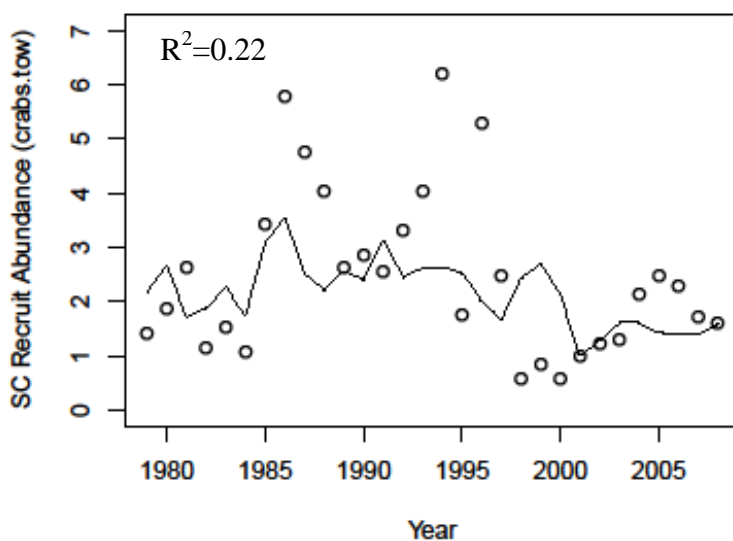


Figure 2.32. Model fits for the recruits in the catch survey models for the South Carolina trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

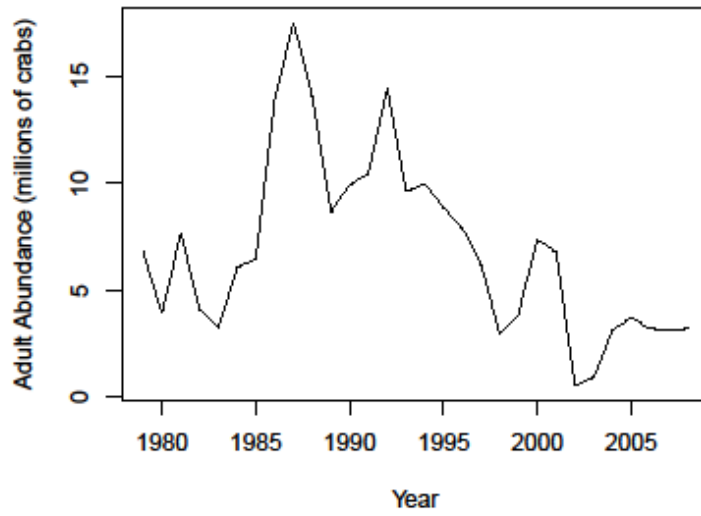


Figure 2.33. Adult absolute abundance estimated from the South Carolina CSA.

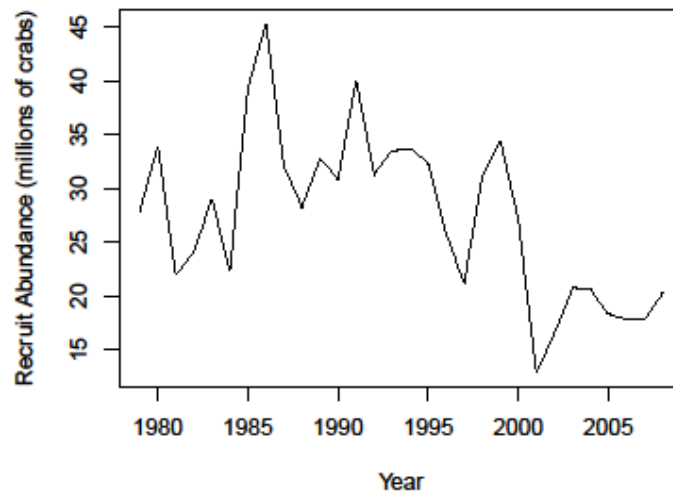


Figure 2.34. Recruit absolute abundance estimated from the South Carolina CSA.

very low level in 2001 (Figure 2.34). The model estimated that in 2008, the recruits and adults were at 73.1 and 46.9% of their 1979 abundance (Table 2.11).

Georgia:

The CSA model produced an acceptable fit to the Georgia observed data (Table 2.9). The Georgia adult survey had a very good model fit (Figure 2.35). The recruit model had an R^2 value that indicated a good fit, but there was an apparent bias of underestimation by the model during the first ten years of the survey (Figure 2.36). The CSA suggested that the initial abundance of recruits and adults in 1985 were 188.8 and 63.4 million respectively (Table 2.9). Predicted absolute adult abundance was predicted to have been on a fairly steady decline through the early 2000s followed by a slight recovery for the remainder of the time series, with abundance recovering to a little bit less than half its peak abundance (Figure 2.37). Recruitment absolute abundance followed the same pattern with slightly more variability (Figure 2.38). The model estimated that in 2008, the recruits and adults were at 18.1 and 40.6% of their 1985 abundance (Table 2.11).

Florida:

The CSA model produced an acceptable fit to the observed data from Florida (Table 2.9). Of the three Florida surveys the IRM survey was the best predictor of adult abundance, although the TQM survey also was moderately good at predicting except in 2006 where there was a peak in the observed indices that wasn't represented in the model estimate (Figure 2.39a-c). The JXM survey had a moderately good fit

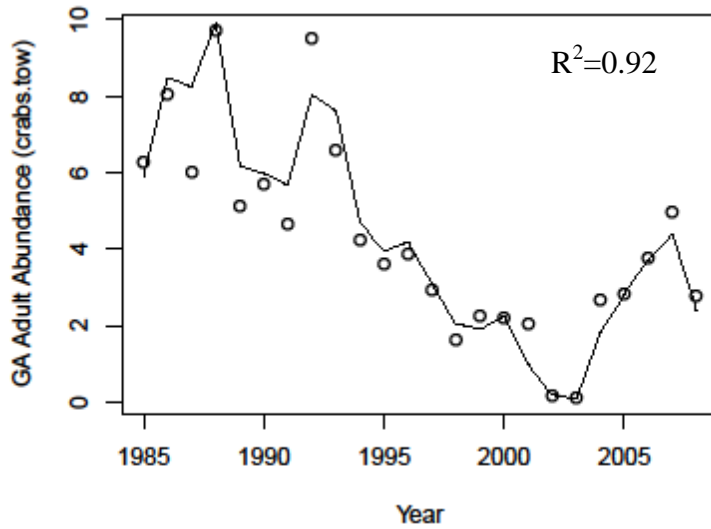


Figure 2.35. Model fits for the adults in the catch survey models for the Georgia trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

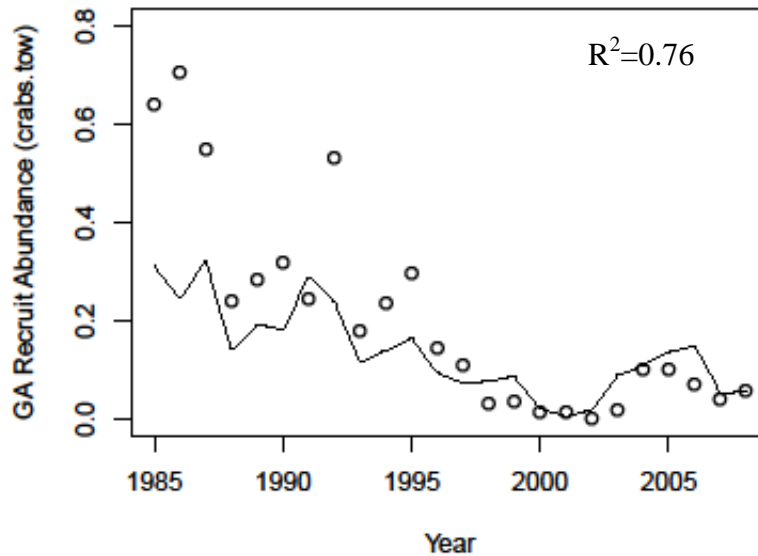


Figure 2.36. Model fits for the recruits in the catch survey models for the Georgia trawl. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

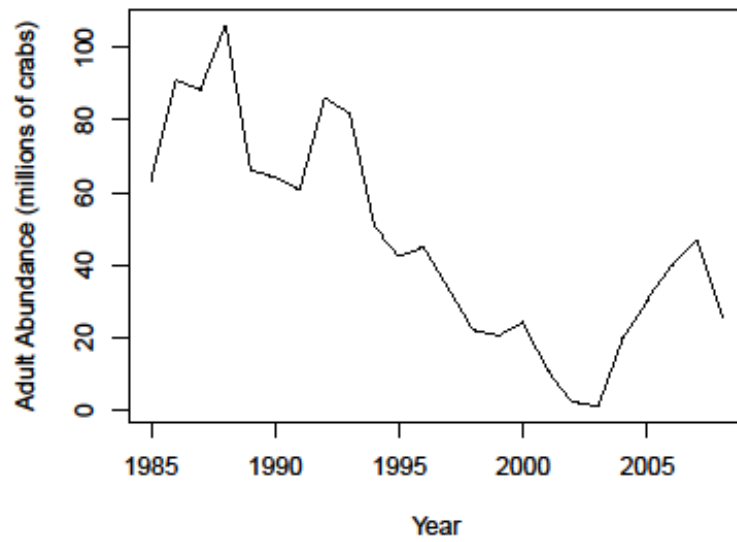


Figure 2.37. Adult absolute abundance estimated from the Georgia CSA.

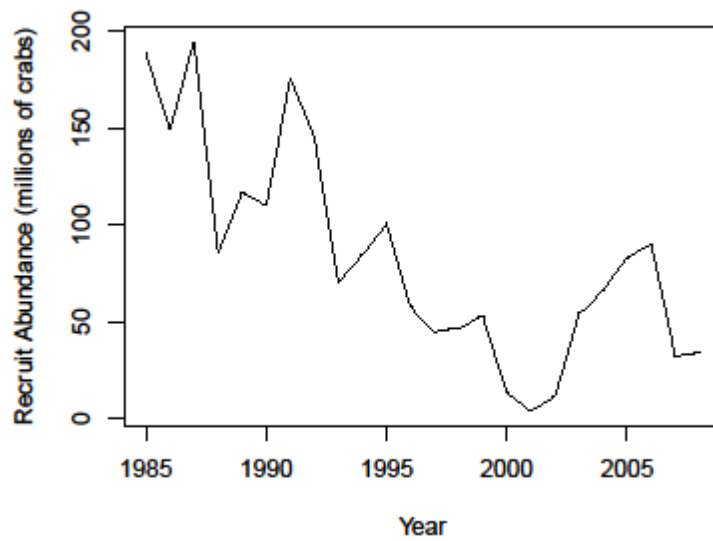


Figure 2.38. Recruit absolute abundance estimated from the Georgia CSA.

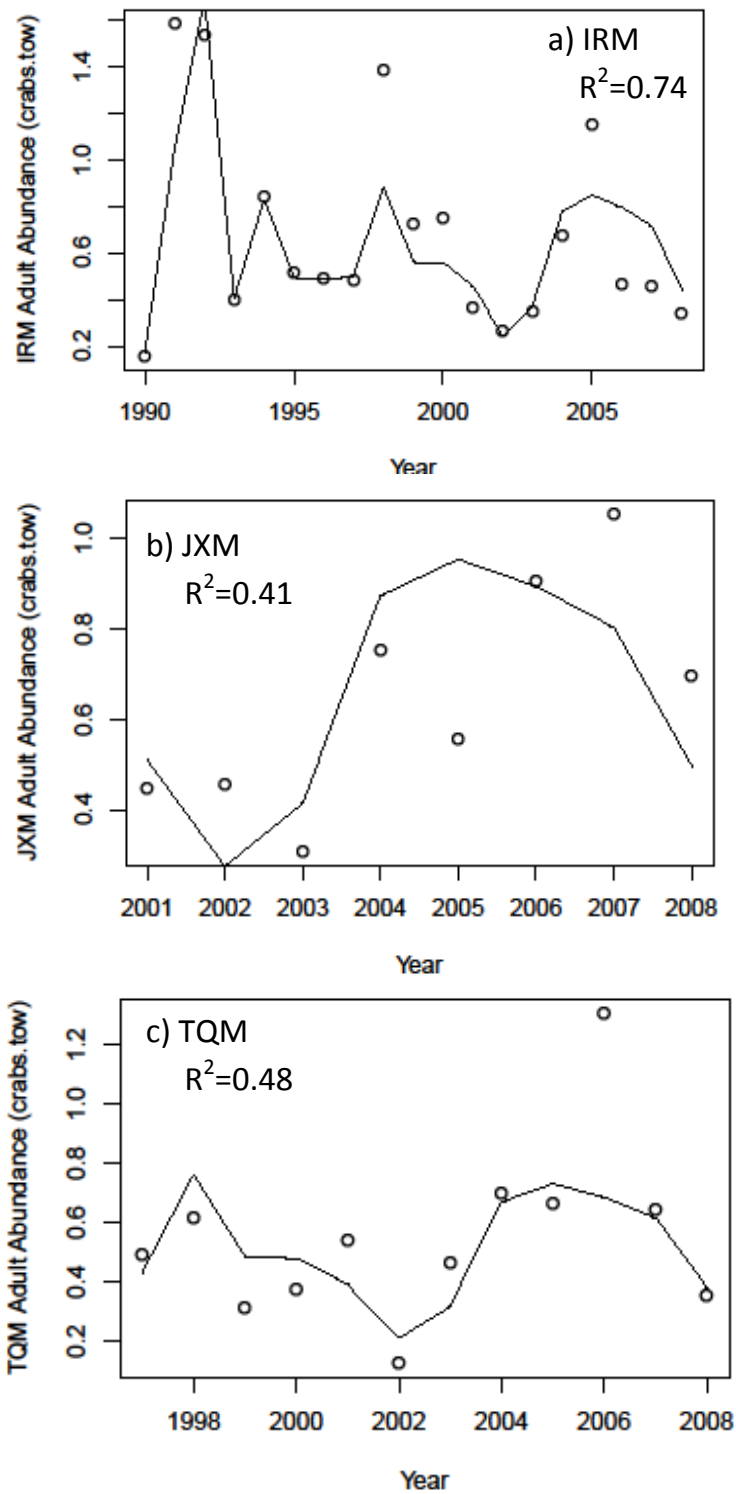


Figure 2.39. Model fits for the adults in the catch survey models for a) the FL IRM b) the FL JXM and c) the FL TQM. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

for adults and does a much better job than the IRM survey at predicting recruit abundance (Figure 2.40a,b). The CSA suggested that the initial abundance of recruits and adults in 1990 were 43.6 and 1.0 million respectively (Table 2.9). Estimated adult abundance had fluctuated since 1990 with a large peak in 1992 followed by a steep decrease in 1993 and then fairly steady abundance for the remainder of the time series (Figure 2.41). Recruitment started out very high in the first two years and decreased in 1992, where it held fairly steady until another dip in 2001. The recruit abundance recovered back to pre-2001 levels by 2002 and remained stable for the remainder of the time series (Figure 2.42). The model estimated that in 2008, the recruits and adults were at 37.4 and 261% of their 1990 abundance (Table 2.11).

Comparison with previous assessments

Since the previous stock assessments did not necessarily separate age-0 and age 1+ at the same size as I did in my study I was only able to compare total abundance estimates, except in Florida where the assessment abundance results were only reported for adult crabs and therefore adult abundances were compared. My abundance estimates for Chesapeake Bay were highly correlated with those estimated by Miller et al. 2011 ($r = 0.98$, $p < 0.0001$; Figure 2.43b). My Delaware Bay model results for total abundance was also significantly correlated with the findings of Wong (2009; $r = 0.696$, $p < 0.0001$), but the Wong (2009) results tended to be higher than of the estimates derived from my model (Figure 2.43a). My model and the Murphy et al. (2007) adult abundance estimates for Florida were significantly correlated ($r = 0.573$, $p = 0.0203$), but the Murphy et al. estimates were lower than

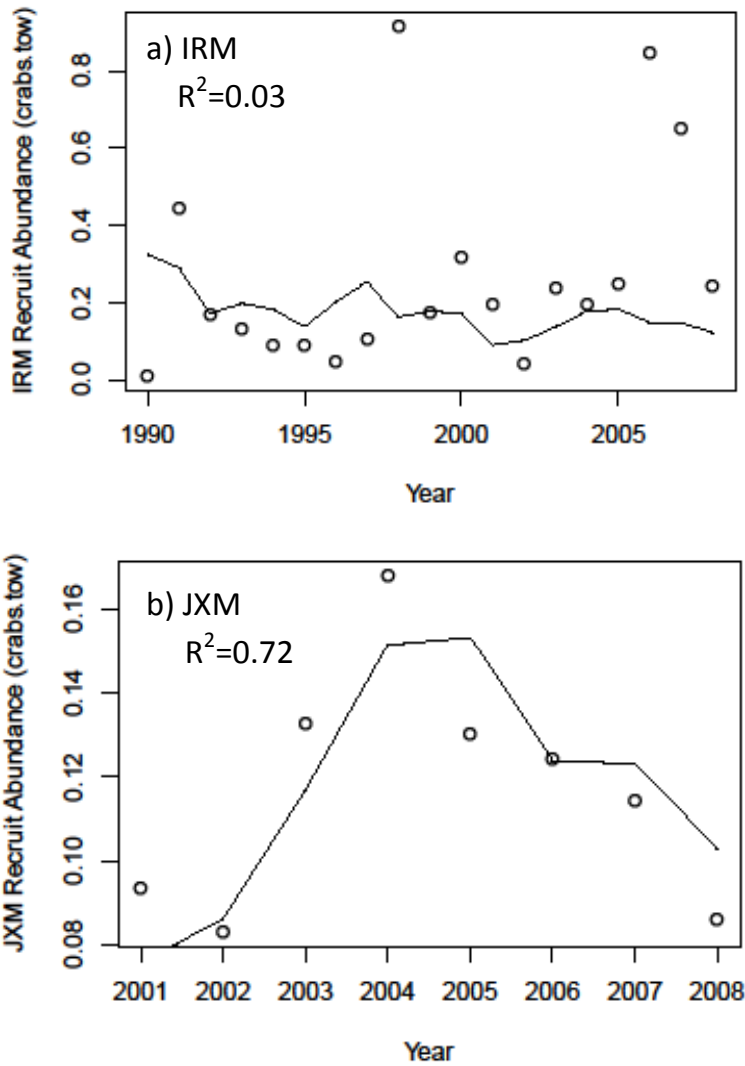


Figure 2.40. Model fits for the recruits in the catch survey models for a) the FL IRM b) the FL JXM and c) the FL TQM. The observed time series is represented by the open points and the fitted time series from the model is depicted by the line. R^2 values represent the correlation between observed and predicted values.

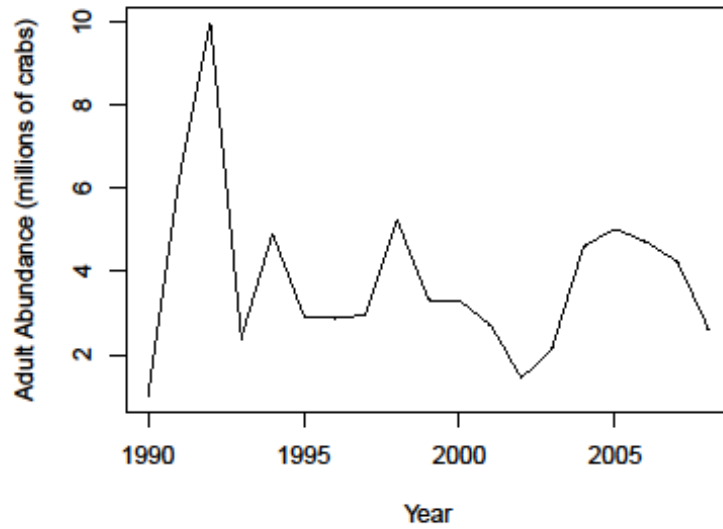


Figure 2.41. Adult absolute abundance estimated from the Florida CSA.

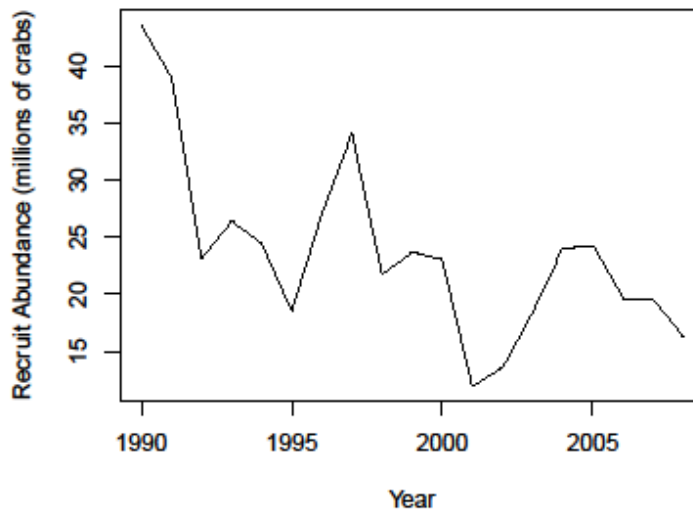


Figure 2.42. Recruit absolute abundance estimated from the Florida CSA.

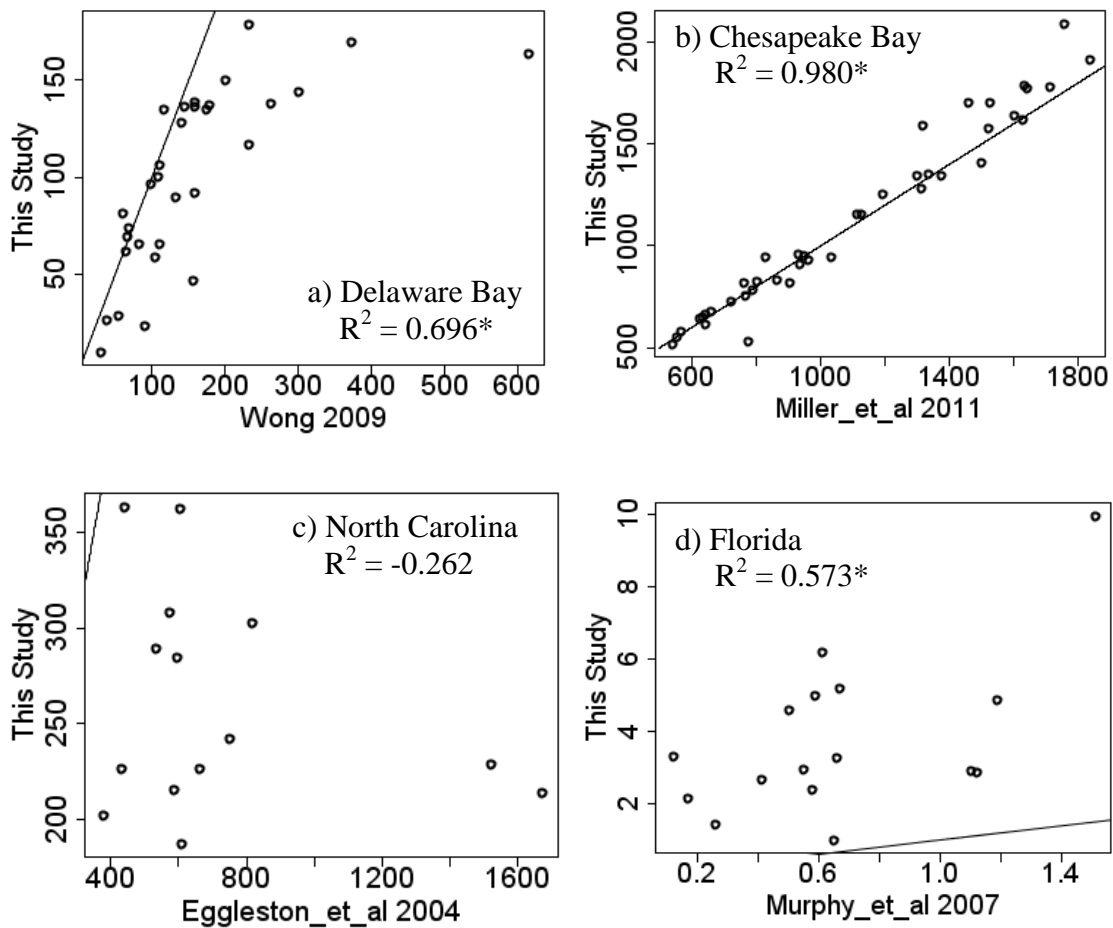


Figure 2.43: Scatterplots comparing previous stock assessment abundance estimates to the abundance estimates from this study's CSA model for a) Delaware Bay b) Chesapeake Bay c) North Carolina and d) Florida. R^2 values are displayed on each graph and significant correlations are indicated by *.

mine (Figure 2.43d). This may be because the 2007 Florida stock assessment only reported exploitable crab abundance while mine looked at age-1+ crabs and therefore my minimum size was lower so more crabs would be included in my abundance estimate. Estimates for my and Eggleston et al.'s assessment of North Carolina stocks were not correlated ($r = -0.262$, $p = 0.3653$) and the Eggleston et al. (2004) estimates were higher than the estimates obtained in my model (Figure 2.43c). One potential explanation for this is that the North Carolina stock assessment used two surveys in their model while mine used only one. I chose to only use one survey based on advice from state employees that the second survey (P195) was not sufficiently spatially explicit to represent the entire North Carolina blue crab population.

Discussion

A CSA model was successfully developed for each of the seven regions along the U.S. east coast. The results for individual regions were significantly correlated with three out of four previous stock assessment abundance estimates, suggesting that these results are robust.

The CSA results for each jurisdiction provides estimates of recruit and adult abundance at the beginning and end of the modeled period that can be used to assess the status of blue crab in each region (Table 2.11). CSA results suggest that five of seven regions have seen population declines over the last two decades. Only two regions, Delaware Bay and North Carolina, have seen an increase in total abundance and recruit abundance over the course of the modeled period. Delaware Bay, North

Carolina, and Florida have witnessed increases in adult abundance since the first year of their respective surveys, but for Florida total population size was only 42% of what it was in 1990 despite the increase in adult population. Of all the other states the largest decrease in population was in the coastal bays of Maryland and Virginia, where populations in 2008 were estimated to be at only 10% of their 1989 abundance. Georgia's blue crab abundance was also estimated to be much lower than it was in 1985 with the 2008 population size being only 24% of what it was at the beginning of the survey.

One would not expect by chance alone five of seven regions to show substantial declines. I hypothesize that blue crab populations along the east coast are declining because of a similar response to a common driver. Several potential mechanisms could be put forward as the common driver. Most directly, because all seven populations are exploited commercially, one could hypothesize that unsustainable levels of exploitation are affecting blue crab populations. However, North Carolina had the highest average exploitation rate of the seven regions, yet witnessed an increase in population over the duration of its survey while Georgia and the coastal bays of Maryland and Virginia had some of the lowest exploitation rates and yet experienced population declines. Blue crab populations in each jurisdiction are managed under different frameworks and regulations. One could hypothesize that reference points have been miss-specified, or management has been ineffective in attaining the reference points in five of the seven jurisdictions. Alternatively one could hypothesize that reference points are appropriate and two of the seven populations are simply more resilient.

An alternative explanation would invoke a common response to an environmental driver, a Moran effect (Moran 1953). If this mechanism were responsible, one would expect to observe that neighboring states were more similar in their dynamics than more distant states. However, the two states that experienced increases are not neighboring suggesting that a Moran effect may not be responsible for the observed pattern.

The CSA models also estimated the recruitment deviations from the mean recruitment for each year of the model. The mean deviations for each system were approximately zero. However, some of the models show a trend in the deviations that in some cases could potentially explain the population changes seen in the ratio of abundance in the beginning and end of the survey (Figure 2.14). Delaware Bay recruitment started out below the mean for most of the first half of the time series and then became largely positive during the latter portion of the survey, which may explain the increase in abundance between the beginning and end of the survey. The Chesapeake Bay has had low recruitment over the past decade, which could have led to the decrease in population size between the beginning and end of the model. The adult population in the coastal Maryland and Virginia bays was at very low abundance at the end of the model run and this could be representative of the highly negative recruitment deviations in the last three years of the model. Georgia experienced a similarly large decrease for three years although this decrease occurred in the early 2000s so it may be possible that this population is still recovering from those low recruitment years. Florida's recruitment deviations have all been fairly

close to the mean, but there has been a pattern of a slight decrease since the initiation of the survey. North Carolina's deviations show no pattern or trends.

The results of these models give some indication of which surveys are most valuable for evaluating the status of blue crab populations as the analyses led to better fits for some surveys in comparison with others. The Delaware trawl survey, the Chesapeake Bay winter dredge survey, the coastal Maryland trawl survey, the North Carolina trawl survey, the South Carolina trawl survey, the Georgia trawl survey, and the Florida IRM survey all performed very well when it came to predicting adult abundance ($0.67 \leq R^2 \leq 0.997$). The North Carolina survey in particular is almost perfectly correlated with predicted adult abundances ($R^2=0.997$). In general, the recruit abundance was not predicted as well as adult abundance by the surveys with the exceptions of the coastal Maryland trawl and the Florida JXM which both were better at predicting recruit abundance. The best models for predicting recruit abundance were the Delaware trawl, the Chesapeake Bay winter dredge, the coastal Maryland trawl, the Georgia trawl, and the Florida JXM survey ($0.43 \leq R^2 \leq 0.76$) while the Maryland trawl, the North Carolina trawl, and the Florida IRM survey were very poor at predicting recruit abundance ($R^2 < 0.1$).

Stock-assessment models are only able to perform well if the data used as input is reliable. Based on the fits from the models and the results it seems that at least one survey from each state created a reliable index for at least one of the two age-classes. The Delaware trawl, the Chesapeake Bay winter dredge, the coastal Maryland trawl, and the Georgia trawl seem to be the most reliable in terms of indexing both adult and recruit abundance. North and South Carolina both have very

good surveys for predicting adult abundance, but recruit abundance was not well predicted. This is particularly interesting for North Carolina where the survey was developed with one of the main objectives being catching juveniles. However, even though the CSA indicates a poor fit, the graph does show that the model picks up the general trends in recruit abundance observed in the survey so it may be possible to pick up on general trends for recruits. Florida seems to have two surveys that are each reliable for a different age-class, with the IRM survey being useful for picking up patterns in adult abundance and the JXM survey being a good predictor of recruit abundance. The New Jersey trawl, the Maryland trawl, and the ChesMMA trawl did not perform well in their respective models in predicting the abundance of either age-class ($R^2 < 0.27$). This suggests that these three surveys are not very useful at predicting patterns in blue crab abundance. The remaining surveys all contain some information about their respective blue crab population, but they do not seem to be as reliable as some of the other surveys since the fit was only moderate.

Overall the CSA models were an effective way to look at how abundance has changed over time. However, some additional parameters could be added to the model in order to obtain more information about how blue crab populations should be managed. One suggestion would be to incorporate a stock-recruitment relationship into the model in order to be able to estimate reference points directly from the model as was done in a recent stock assessment for the Chesapeake Bay (Miller et al. 2011). Estimating reference points directly from the model would be extremely useful for managers because it would eliminate having to arbitrarily choose a target and threshold exploitation level as the model would indicate what levels are sustainable for

harvesting blue crab in that region. Incorporating this relationship into the models I have presented in this chapter may prove challenging, particularly in states where only one survey is conducted. Another potential addition to the model would be adding some deviation around catch as this model assumes catch is known exactly while in reality there are likely errors in the reported catch due to misreporting. Again, this would add more parameters to the model so getting the model to stabilize may be a challenge. Both of these additions to the model would increase the amount of information about how blue crab populations have changed through time and what policies management agencies should put in place to ensure the sustainability of blue crab populations along the east coast of the United States into the future.

Chapter 3: Synchrony among blue crab populations along the U.S. Atlantic coast

Abstract

Inter-annual variability in the abundance of populations is known to exist, but the mechanisms behind these fluctuations are often not well understood. Blue crab, *Callinectes sapidus*, occurs in coastal waters all along the eastern U.S. and its populations exhibit high degrees of inter-annual variation in abundance. This study aimed to quantify the amount of synchrony in the variability among blue crab populations along the east coast and to gain insight into the mechanisms behind any synchrony found using principal component analysis and dynamic factor analysis. These analyses were conducted on both landings data and absolute abundance estimates obtained in Chapter 2. I determined that a latitudinal pattern in abundance among the states existed in both the landings and abundance data and that a combination of the Gulf Stream Index and larval mixing in the coastal ocean may be important drivers for the fluctuations of blue crab. The Chesapeake Bay appears to be an anomaly in that the abundance of its blue crab population does not match the latitudinal trend seen in the other states.

Introduction

Understanding the mechanisms responsible for the observed inter-annual variations in abundance of populations remains a central challenge in ecology. In some cases, populations appear to be regulated through density-dependent processes that act to maintain a population at a stable equilibrium (Murdoch 1994; Turchin 1995; Berryman 2002). The level of variability in abundance is believed to vary inversely with the degree of density-dependent feedback. Two generally accepted density-dependent mechanisms, either competition or predation, invoke intra-specific interactions and determine the degree of regulation in a particular population (Hixon et al. 2002). Both of these processes can regulate population size by limiting population growth at high densities, either through increased competition for resources or increased incidence of predation. Density-dependent processes can introduce correlations in abundances among interacting populations.

Density-independent control of populations has also been suggested (Andrewartha & Birch, 1954). Under this modality, two populations may fluctuate in a similar manner due to a common external driver affecting both populations. This is termed synchronization. Two density-independent processes may induce synchronization. Dispersal of individuals may cause exchanges of individuals between different populations, thereby inducing synchronization in the dynamics of both populations (Cowen et al. 2006). A common response to environmental factors can also induce synchronization. This was first demonstrated by Moran (1953) who analyzed the dynamics of lynx and snowshoe hare populations in Canada. Moran showed that the regional winter temperature variability acted to couple the dynamics

of both species. Synchronization resulting from a similar response to an external, abiotic factor is termed a Moran effect. The Moran effect has been exhibited in a number of studies for a variety of environmental factors including the El Niño Southern Oscillation (ENSO; Cheal et al. 2007; Lima et al. 2001; Lima et al. 2002) and the North Atlantic Oscillation (NAO; Fromentin & Planque 1996; Post & Stenseth 1999; Forchhammer et al. 1998). Regardless of whether dispersal or a Moran effect is the primary mechanism for synchronization it is believed that the degree of synchrony will decrease as the geographic distance between two populations increases (Liebhold et al. 2004). This inverse relationship between geographical separation and synchrony has been termed spatial synchrony.

The Atlantic seaboard of North America is characterized by a wide, shallow shelf that can be divided into a few large, connected marine ecosystems (LMEs- Sherman 1994). Many marine and estuarine species are broadly distributed across this shelf (Longhurst 2001). Because of these large-scale distributions, individual populations within these LMEs likely experience forcing from common environmental factors. The NAO is one such broad index of climate variability. The NAO index quantifies this phenomenon by subtracting the average pressure difference between Iceland and the Azores from the pressure difference in an individual year. When the index is positive, the NAO is termed to be in a strong phase and leads to stronger westerlies and warmer, wetter conditions from North Africa through Siberia and to a lesser extent the United States. During negative or weak phases, westerlies are weaker and conditions become much colder and dryer in northern Europe and the United States (Hurrell et al. 2003). Importantly, because of

the highly connected nature of marine populations on the U.S. Atlantic seaboard, the NAO may have differential effects on populations with centers of their distributions that differ latitudinally.

Other large-scale climate indices may also act as the primary influence of the dynamics of marine populations along the Atlantic seaboard. The Gulf Stream Index (GSI) is an index that has been measured since 1966 to categorize the north wall of the Gulf Stream offshore of Cape Hatteras. The GSI was created by using sea surface temperature observations to determine the position of the north wall of the Gulf Stream. A principal component analysis (PCA) was then conducted for each year to reveal the pattern in the variation in position of the north wall between 79-65°W. The GSI is defined as the eigenvalue of the first principal component for that year (Taylor 1996). The meandering of the north wall is thought to be influenced by the NAO due to stronger water flows during a positive phase leading to the north wall of the Gulf Stream moving further north. However, this response is known to be lagged between one and two years (NEFSC 2009; Taylor & Stephens 1998).

Sunspot cycles have also been suggested as a large scale phenomenon that could influence fluctuations in individual populations (Hurt et al. 1979). Sunspots are dark spots on the sun that are the result of areas of high magnetic activity that inhibit convection and reduce surface temperature on the sun. The number of sunspots on the sun varies through time and has been found to fluctuate on approximately an 11 year cycle (Fröhlich & Lean 1998). Even though the sunspots themselves represent cooler areas of the sun, solar irradiance increases when the sunspot number is high because the areas directly surrounding the sunspot are very bright (Rind 2002). There

is debate as to whether the sunspot cycles will help counteract climate change in the coming decades (Hansen & Lasis 1990; Fröhlich & Lean 1998).

Analyzing the degree of synchronization among populations and with environmental variables is an inherently multivariate problem. There are several multivariate techniques that could be employed in such analyses. Principal component analysis (PCA) is a type of multivariate ordination technique that can be used to group variables into categories and is applicable to a variety of fields (McGarigal et al. 2000). PCA takes a number of measured correlated variables and combines them to create completely independent principal components such that the first principal component explains most of the variability (McGarigal et al. 2000). Within fisheries, PCA has been applied to look at factors that affect fish assemblages, such as habitat type (Stein et al. 1992) and environmental characteristics (Kodric-Brown & Brown 1993). A combination of biological and physical time series data has been examined in the Northwest Pacific region with PCA to determine the timing and duration of regime shifts (Hare & Mantua 2000). PCA was also incorporated into the South Carolina stock assessment to obtain principal components of environmental variables in order to determine which environmental factors were to be incorporated into the stock-recruitment model of the assessment (Harris 2000).

One disadvantage of PCA for the analyses of multiple time series is that the technique does not explicitly account for the temporal autocorrelation in each dataset. Dynamic factor analysis (DFA) is a multivariate dimension reduction technique that reduces many time series into a fewer number of common trends and explicitly accounts for the temporal autocorrelation (Zuur 2003a). DFA identifies common

trends using Akaike's Information Criterion (AIC). The degree of association between the common trends and environmental drivers can then be assessed. Although a fairly new technique to ecologists, DFA has been applied to other disciplines for some time. One example is from the field of psychology where one study sought to determine whether a number of physiological responses to stimuli were due to one common process (i.e. 1 trend) or if each response was independent (Molenaar 1985). Ecologists began utilizing DFA over the last decade through studies such as analyzing environmental influences on zooplankton in the Balgzand tidal flat area of the Wadden Sea, Netherlands (Zuur et al. 2003a) and examining the fluctuations in groundwater quality in Everglades National Park, U.S. through time (Muñoz-Carpena et al. 2005). The technique was first applied to fishery issues to explore patterns among 13 time series from the Norwegian lobster (*Nephrops norvegicus*) landings in northern Europe (Zuur et al. 2003b). Zuur et al. (2003b) found that there were three common trends among 12 of the 13 time series. Importantly, none of these common trends were significantly related to either of the two explanatory variables, North Atlantic Oscillation (NAO) and sea surface temperature. Zuur & Pierce (2004) used DFA to determine the influence of the NAO and sea surface temperatures on squid landings in the Atlantic. DFA was also applied to 12 cephalopod catch-per-unit-effort (CPUE) time series where it was found that a model with two common trends and sea surface temperature and upwelling as explanatory variables was the best model. This model indicated that a decrease in CPUE had occurred throughout the course of the time series (Erzini et al. 2005). Megrey et al. (2009) used DFA to examine the synchrony of functionally analogous

species in two Atlantic and two Pacific systems in order to detect regime shifts.

Other examples of DFA using fisheries are still fairly rare although interest in the technique seems to be growing.

The blue crab, *Callinectes sapidus*, is one species that occurs on the Atlantic seaboard that could potentially be synchronized as a result of dispersal, environmental forces, or a combination of both due to their complex life history. Blue crabs are found in estuarine and coastal ecosystems in the western Atlantic, commonly ranging from Cape Cod to northern Argentina, although they can be found as far north as Nova Scotia during warm conditions (Williams 1974). Genetic and tagging data suggest spatially separated populations along the Atlantic coast (McMillen-Jackson et al. 1994; McMillen-Jackson & Bert 2004). The life cycle of each population follows a general pattern, although the timing of key events may vary latitudinally (Hines 2007). In particular, winter temperature appears to be an important control in regulating abundances and the timing of events (Bauer & Miller 2010). Adults mate in estuarine waters in autumn. Impregnated females subsequently migrate to the mouth of the estuary where they release larvae into the coastal ocean. Larvae undergo several molts in the coastal ocean during which time they are potentially susceptible to mixing with neighboring populations via currents (Hines 2007). At the end of the larval period, larvae are transported into estuaries where they settle as juveniles and remain for the duration of their lives with negligible migration to other estuaries. The geographic separation of populations suggests that the Moran effect could play a potentially large role in synchronization of adult blue crabs.

Here, I propose to quantify the degree of synchrony among blue crab populations along the Atlantic seaboard and four key environmental variables: the North Atlantic Oscillation (NAO), the Gulf Stream Index (GSI), sunspot number, and regional winter temperature. I used both absolute abundance time series estimated from a common catch-survey assessment model applied to seven principal regions and aggregate catch data (fishery-dependent) from eight regions as a proxy for abundance in each population (Chapter 2). The regions analyzed were New York (aggregate catch data only), Delaware Bay, Chesapeake Bay, MD & VA coastal bays, North Carolina, South Carolina, Georgia and Atlantic Florida. I present analyses for the landings and absolute abundance estimates separately. The same approaches were used to analyze both data sources. Data were analyzed first using PCA to determine whether there is any latitudinal pattern in the degree of synchrony among blue crab populations along the east coast of the United States. Subsequently, I used DFA to determine the extent to which environmental variables, if any, explain any of the synchronization evident in crab populations. Finally, based on all of these results I speculated on the mechanisms behind population fluctuations to determine if mixing of larvae, the Moran effect, or a combination of both are playing a role in driving trends in blue crab abundance. More specifically, I tested one aspect of Moran's hypothesis that the degree of synchrony among population pairs would be negatively correlated with the distance separating pairs of populations.

Methods

To evaluate the spatial structure in the catch time series from each of the eight regions I conducted PCAs (McGarigal et al. 2000; R v. 2.11.1; Appendix D). PCA eliminates multicollinearity of the variables (in this case the states) and creates the same number of new variables, known as principal components, which are orthogonal to one another and are each made up of a linear combination of the original variables. I ran two PCAs using landings data to look at each state's landings individually (state PCA) and to look at each blue crab population (region PCA) by combining Maryland and Virginia into Chesapeake Bay and Delaware and New Jersey into Delaware Bay. I also conducted three PCAs using the absolute abundance time series derived from individual assessments applied to each region (Chapter 2). Separate analyses were conducted for total abundance, juvenile abundance, and adult abundance. It should be noted that all abundance time series were on the region level because the catch-survey models that yielded these time series were conducted for each population rather than for each state separately. Each landings/abundance time series served as the variable and years served as the records in the analysis.

The loadings on the first two PCA axes were plotted for each analysis and a matrix of distances between each point was calculated using the `dist` function in R (Appendix D). This matrix of PCA separation distances was compared to geographical distance between populations. Geographical distances were determined by estimating the center of each state or region on a map of the east coast (Figure 3.1) and then latitudes and longitudes were obtained using ArcGIS (Table 3.1). These values were converted to Northing and Easting measurements and Matlab was used to

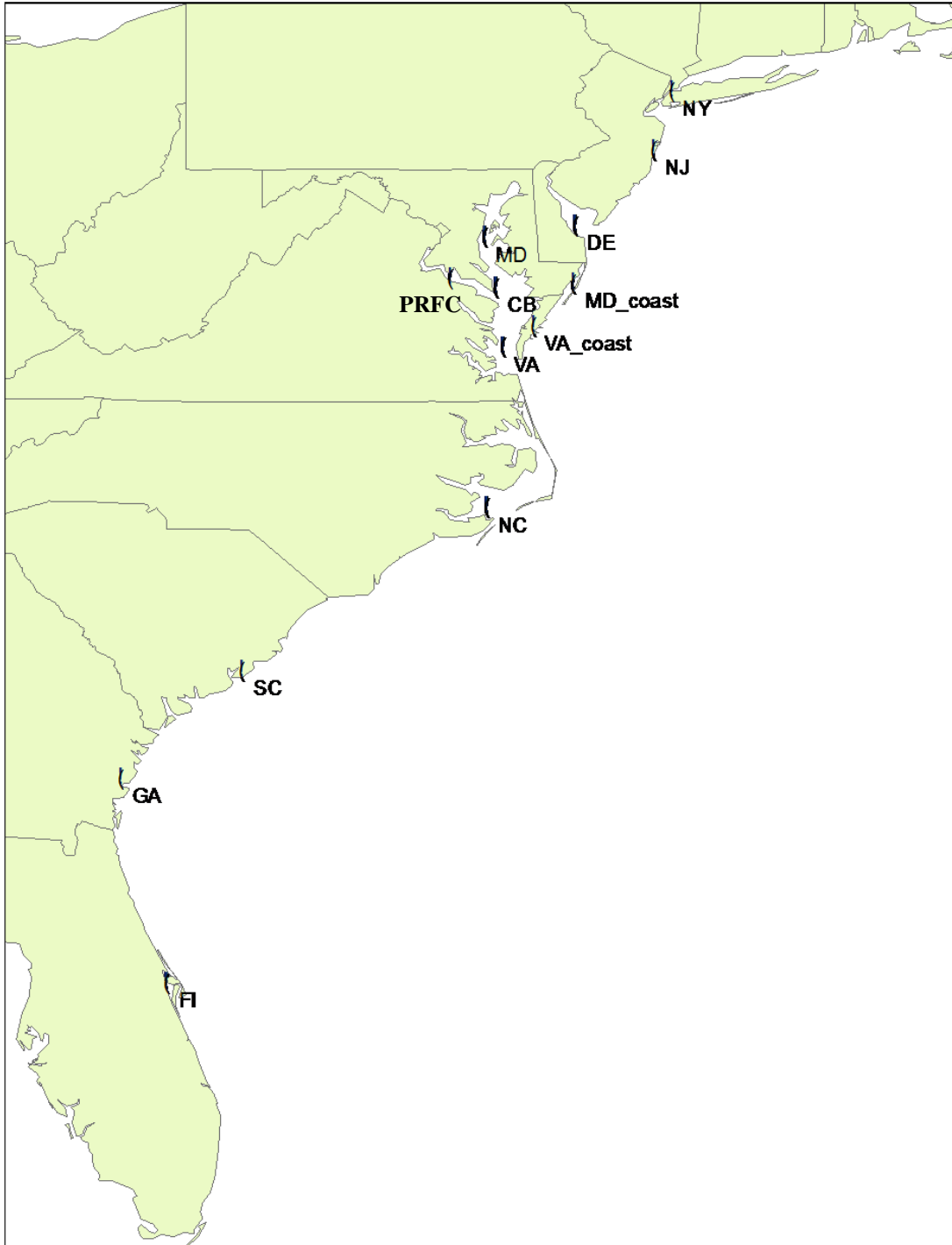


Figure 3.1. Map of the east coast of the United States showing where the geographic centers for each state/region were chosen to obtain latitude/longitude estimates for calculating geographic distance between jurisdictions.

Table 3.1. Latitude, longitude, northing, and easting used to calculate geographical distances between states and regions.

State/Region	Latitude	Longitude	Northing (m)	Easting (m)
NY	40.8130	-73.8331	4518655	598416
NJ	40.0119	-74.0822	4429482	578329
DE/Del. Bay	38.9856	-75.1401	4315184	487863
MD	38.8277	-76.3875	4298568	379559
PRFC	38.2620	-76.8581	4236519	337439
MD_coast	38.1961	-75.1717	4227584	484964
Ches. Bay	38.1328	-76.2296	4221269	392235
VA_coast	37.6119	-75.7244	4162997	436069
VA	37.3276	-76.1349	4131823	399455
NC	35.1328	-76.3560	3888617	376464
SC	32.9065	-79.7034	3641665	621256
GA	31.4380	-81.3613	3478205	465664
FL	28.6488	-80.7297	3169105	526412

calculate the Euclidean distances between each of the points (Table 3.2; Appendix E). A linear regression was conducted for each state or region in order to look at the correlation between the PCA and geographical distances. I ran these regressions for all of the landings and abundance PCAs.

The second type of multivariate analysis conducted on these data was dynamic factor analysis (DFA). Zuur et al. (2003a) provides details of the model structure so it is only summarized here. The underlying DFA model may be written as:

$$\mathbf{y}_t = c + \mathbf{Z}\alpha_t + \mathbf{D}\mathbf{x}_t + \mathbf{e}_t \quad [\text{Eq. 3.1}]$$

where c is a constant level parameter that allows the trends to move up or down to better fit the time series, \mathbf{y}_t is a vector of landings at time t , α_t is a vector of common trends at time t which is multiplied by a matrix \mathbf{Z} of factor loadings for each state onto those common trends, \mathbf{x}_t is a vector of explanatory variables at time t which is multiplied by matrix \mathbf{D} of regression parameters for each state in relation to those explanatory variables, and \mathbf{e}_t represents random error with the assumption that $\mathbf{e}_t \sim \mathbf{N}(0, \mathbf{H})$ where \mathbf{H} is a symmetric, non-diagonal covariance matrix. Using this covariance matrix increases the amount of parameters in the model compared to using a simple diagonal matrix, but AIC values were always lower for the non-diagonal matrix.

Four DFA analyses were run utilizing the normalized, regional environmental data to examine trends among the different blue crab populations. I used winter

Table 3.2. Euclidean geographical distances between states/regions. Distances are in kilometers.

	NY	NJ	DE/Del. Bay	Ches. Bay MD	coastal MD	PRFC	Ches. Bay VA	coastal VA	NC	SC	GA	FL
NY	0	91.4070	231.5645	310.3817	312.3992	384.3300	361.8686	390.9586	667.9899	877.2871	1048.8850	1351.4696
NJ		0	145.7670	238.0087	222.4402	308.6465	279.2556	302.0794	577.3082	788.9857	957.9262	1261.4463
DE/Del. Bay			0	109.5717	87.6479	169.7517	134.0331	160.7592	440.8737	686.6016	837.2742	1146.7279
Ches. Bay MD				0	127.0785	74.9941	78.3309	146.8766	409.9624	699.9559	824.8695	1138.9700
coastal MD					0	147.7954	92.9444	81.0075	355.9091	601.5619	749.6283	1059.2909
PRFC						0	56.8780	123.0175	350.0838	659.0924	769.0788	1084.0129
coastal MD & VA							82.9313	73.4383	318.3446	577.4040	717.5302	1028.6406
Ches. Bay							0	72.9182	333.0258	623.2106	746.6839	1060.6855
Ches. Bay VA								0	244.2902	538.0058	656.9631	971.0534
coastal VA									280.7800	553.2461	685.4320	997.9903
NC									0	347.7187	419.9941	734.9712
SC										0	225.6727	481.9840
GA											0	315.0129
FL												0

North Atlantic Oscillation (NAO) averaged from December-March each year (data obtained from the National Weather Service Climate Prediction Center) and the Gulf Stream Index (GSI) averaged annually (data obtained from Marine Biological Association of the United Kingdom, Plymouth, United Kingdom) as possible explanatory variables (Figure 3.2). I looked at NAO and GSI separately even though they are significantly correlated ($r=0.43$, $p=0.01$) because the NAO is a more complex phenomenon than the Gulf Stream Index and therefore blue crab populations may be influenced more by one than the other. However, I did not use both explanatory variables in the same DFA model because of the likelihood of an interaction. I also used sunspot number (SSN) averaged annually (data obtained from NASA Marshall Flight Space Center- Solar Influences Data Analysis Center) as a possible large-scale explanatory variable.

For a more localized parameter I chose to examine the possibility of winter temperature as an explanatory variable. Blue crabs north of Cape Hatteras overwinter while those in the south are active year-round so temperature during the winter may be very important in predicting patterns of blue crab abundance. Since my study area was so large and I wanted to limit the number of explanatory time series I used in the DFA, I created one time series of temperature for the northern region of my study area and one for the southern region. I used data from Reynolds et al. (2002), who used an optimum interpolation of NOAA *in situ* and satellite data to create a time series of average monthly temperatures for two spatial regions that broadly covers the northern and southern portion of my study area (Figure 3.3). Sea surface temperatures were determined from a data assimilation model (Carton & Giese 2008)

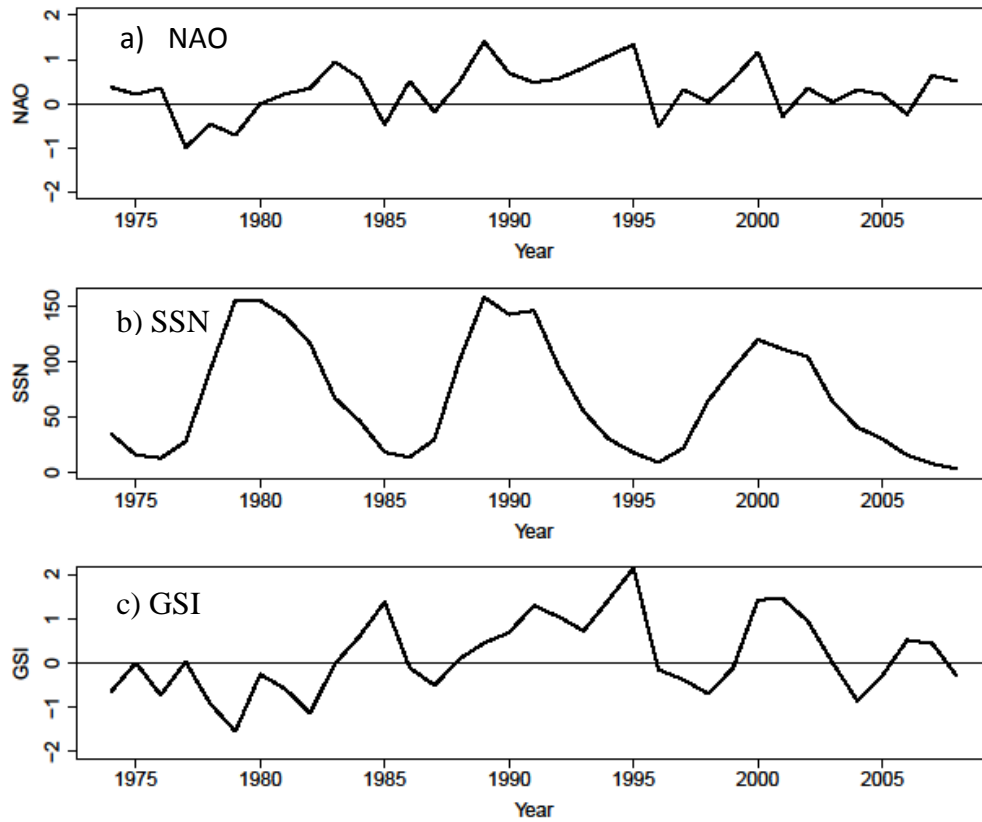


Figure 3.2. Time series for a) North Atlantic Oscillation (NAO), b) sunspot number (SSN), and c) Gulf Stream Index (GSI) that were used as explanatory variables in the DFA from 1974-2008.

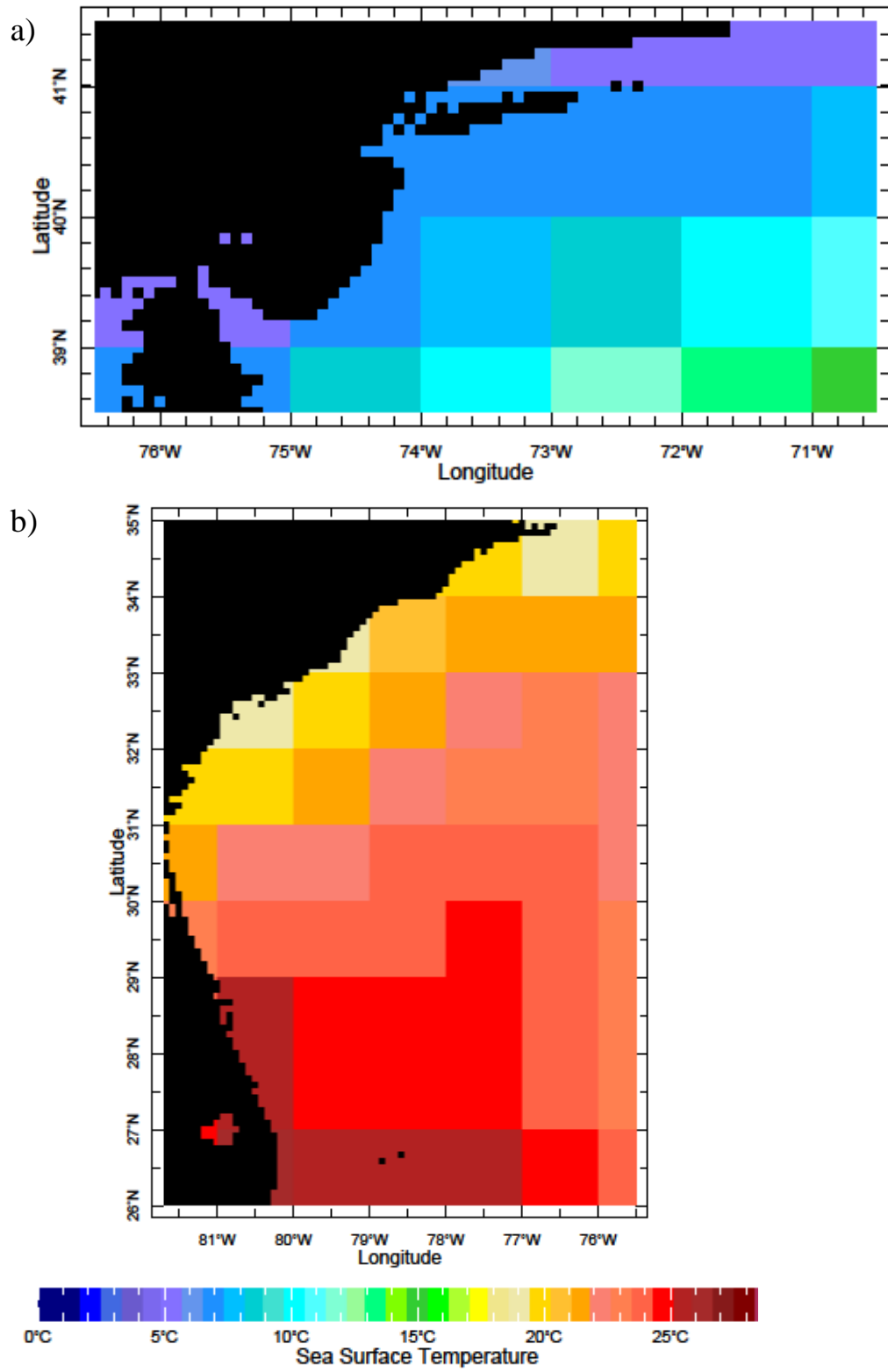


Figure 3.3. Maps of the a) northern and b) southern regions used to calculate winter temperature.

that allowed for reconstruction back to the 1950s so I was able to obtain temperature estimates for the longest time series of 1974-2008 for the landings DFA. For the years where both observed and modeled data were available I used the observed data in the time series, although the two sets of data were highly correlated (for the north $r=0.994$, $p<0.0001$; for the south $r=0.986$, $p<0.0001$). Since I was interested in looking at winter temperature I averaged monthly temperature from December through March and used these averages as the time series in the DFAs (Figure 3.4). Each set of DFA analyses examined between 1-5 common trends for each of the explanatory variables (the two temperature time series were used in the same model), combinations of explanatory variables when deemed appropriate, and without any explanatory variables included. Akaike's Information Criterion (AIC) was used to determine which of the model runs was best for describing the landings or abundance data. All states and years of the time series were included in the analysis (1974-2008 for landings; 1990-2008 for abundance). All DFA analyses were conducted in R v. 2.11.1 (R Core Development Team 2007) using a commercial interface designed specifically to implement DFA algorithms (Brodgar v. 2.6.6 – Highland Statistics Ltd, Newburgh, Scotland).

Results

The state-level landings PCA yielded an acceptable ordination of the landings data. The first two principal components in the state-level landings PCA explained 60.6% of the variance. The 1st principal component (PC1) separated the northern from the southern states, as the northern states loaded positively on PC1 while the

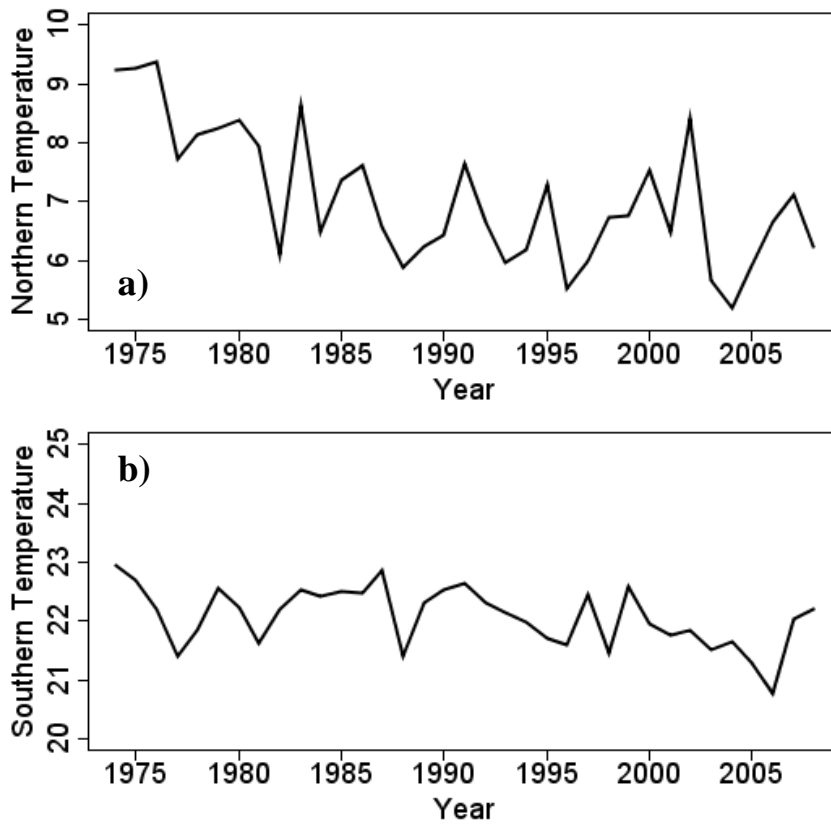


Figure 3.4. Time series for a) northern and b) southern winter temperature that was used as explanatory variables in the DFA for the period of 1974-2008.

southern states loaded negatively (Figure 3.5). Additional spatial information was retained in PC2. A general anti-clockwise ordination of states by latitude on PC1 and PC2 is evident in Figure 3.5. There was also evidence of a decadal trend as the years (scores) grouped together around the plot with the earlier years of the time series associating with the southern states and the more recent years with the northern states. However, landings from both Maryland and Virginia portions of the Chesapeake Bay and from their coastal bays appear anomalous.

The first two axes of the region-level landings PCA explained 59.5% of the variance in the data. The same general pattern as the state landings PCA was evident in the regional landings PCA except PRFC was outweighed by Maryland and Virginia so Chesapeake Bay was in the same area as Virginia and Maryland were in the state-level landings PCA (Figure 3.6).

The PCA for the assessment-derived total abundance of blue crabs in each region explained 69.4% of the variance on the first two principal components and was deemed to have acceptable ordination. All of the regions loaded negatively on the 1st principal component (PC1). Spatial separation between northern and southern states is evident on the 2nd principal component (PC2). Delaware Bay, the MD and VA coastal bays, and North Carolina load negatively on PC2, South Carolina has a slightly negative loading very close to zero and Georgia and Florida load positively. Chesapeake Bay has a slightly positive loading, which does not follow the general latitudinal pattern (Figure 3.7). The scores (years) form a pattern on the plot as well with the early 1990s being negatively loaded on PC1 and positively loaded onto PC2, the mid-late 1990s negatively loading on both PC1 and PC2, the early 2000s

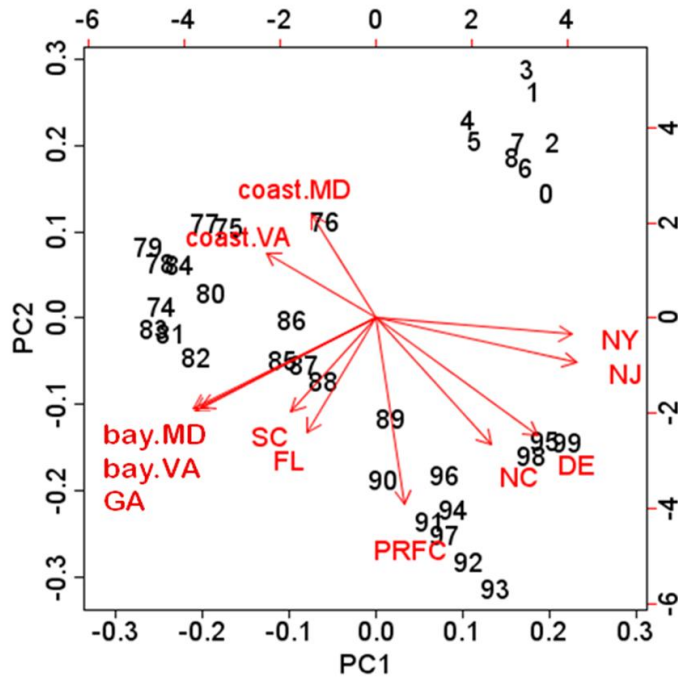


Figure 3.5. PCA results for the 1st two principal components (60.6% of the overall variance explained) for looking at landings data at the state-level. The scores represent the individual years of the time series.

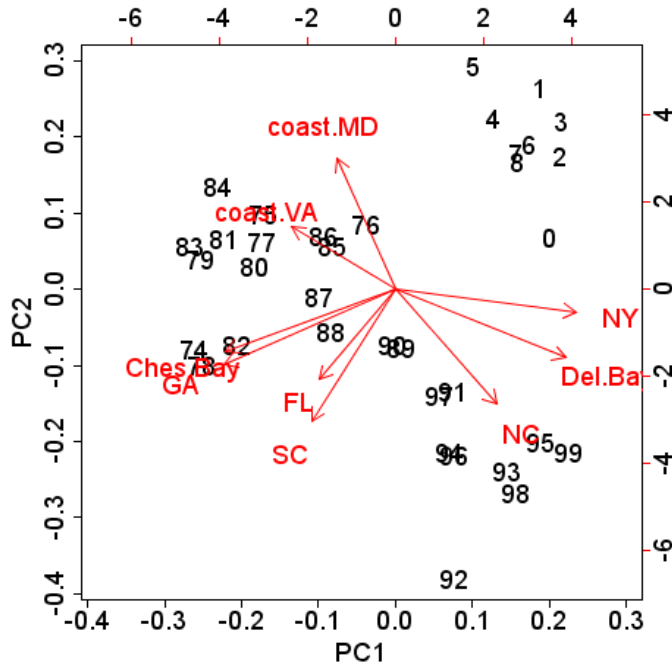


Figure 3.6. PCA results for the 1st two principal components (59.5% of the overall variance explained) for looking at blue crab landings at the region-level. The scores represent the individual years of the time series.

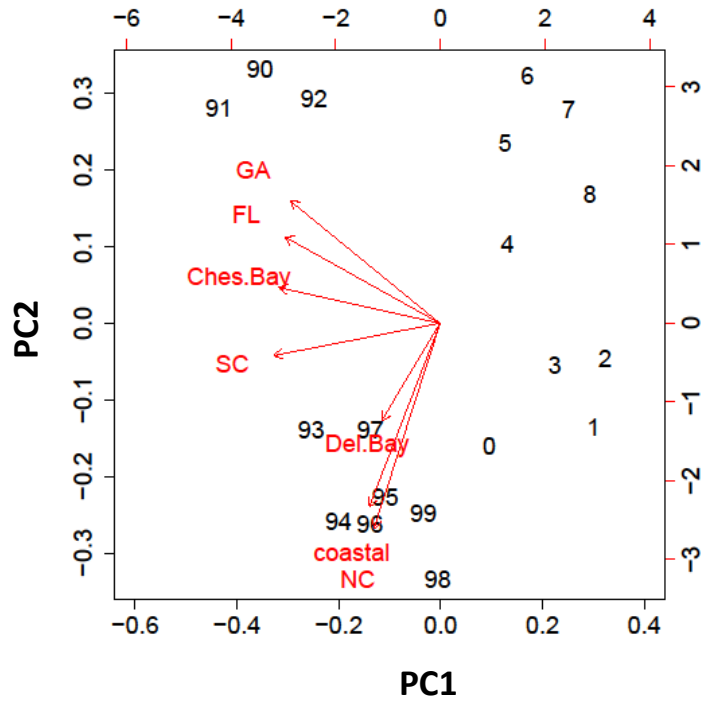


Figure 3.7. PCA results for the 1st two principal components (69.4% of the overall variance explained) for total abundance. The scores represent the individual years of the time series.

positively loading on PC1 and negatively loading on PC2, and the mid-late 2000s loading positively on both principal components. Therefore, the early 1990s associate with the southern states and the mid-late 1990s associate very closely with the northern states.

The assessment-derived recruit abundance PCA shows a very similar pattern to the total abundance PCA with 63.2% of the variance explained by the 1st two principal components (Figure 3.8). The main differences between this and the total abundance PCA was Delaware Bay has a fairly neutral loading on both PC1 and PC2 in the recruit PCA, with loadings very close to zero and the loadings on PC2 for South Carolina and Chesapeake Bay are stronger than they were in the total abundance PCA, but are associated in the same general direction. This orients Chesapeake Bay closer to Florida and Georgia making the anomaly of Chesapeake Bay more pronounced than it was for the total abundance. The scores on the plot are associated in the same pattern as the total abundance PCA.

The patterns in the assessment-derived adult abundance PCA differed slightly from those in the total abundance and recruit PCAs and explained 65.0% of the variance on the 1st two principal components. All states loaded negatively on PC1, with the exception of North Carolina, which has a PC1 loading just above zero. PC2 suggests a latitudinal pattern, but it is not as clear as in the other two PCAs (Figure 3.9). North Carolina and the coastal bays load the most negatively followed by Delaware Bay and Chesapeake Bay. South Carolina loads slightly positively and Georgia and Florida have high positive loadings. The scores also form a slightly

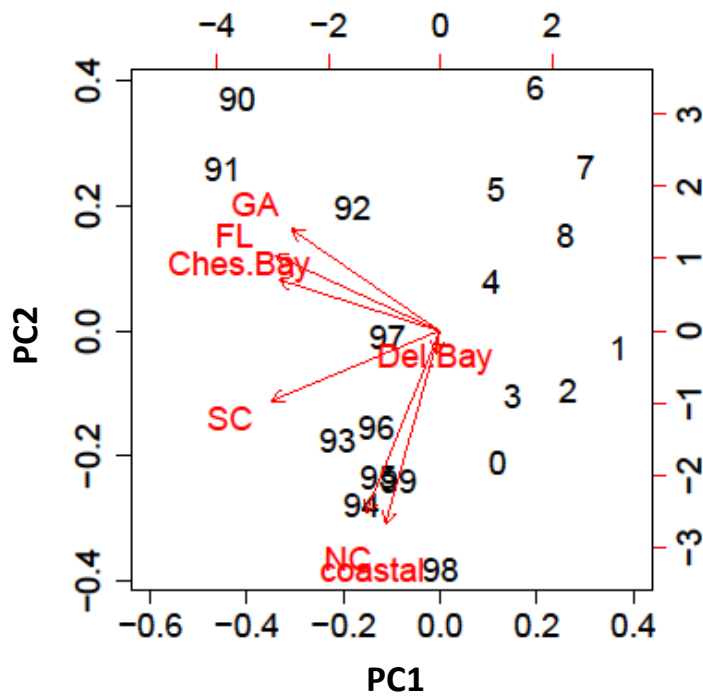


Figure 3.8. PCA results for the 1st two principal components (63.2% of the overall variance explained) for recruit abundance. The scores represent the individual years of the time series.

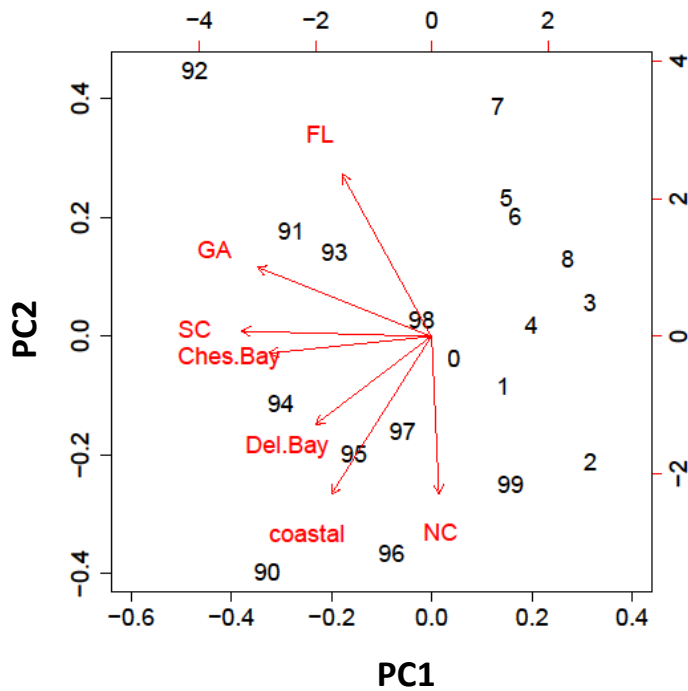


Figure 3.9. PCA results for the 1st two principal components (65.0% of the overall variance explained) for adult abundance. The scores represent the individual years of the time series.

different pattern than the other PCAs with the 1990s loading negatively on PC1 and the 2000s loading positively and no discernible patterns on PC2.

Further support for the presence of spatial synchrony comes from the comparison of landings geographic distances (Table 3.2) and PCA distances (Table 3.3). The states towards the edge of the study range (New York, New Jersey, Georgia, and Florida) have a positive relationship between the two distance measurements and the states in the middle of the study range have a slope close to zero and do not have very good fit (Figure 3.10). These results lead to the same conclusion as the landings PCA that the northern states exhibit broadly similar patterns in landings and abundance and that these patterns are different than those demonstrated by the southern states, which are also internally coherent. The mid-Atlantic states have no distinguishable relationship because they are between the two groups of populations and therefore potentially have characteristics of each. If Chesapeake Bay is dropped from the regression analysis due to the fact that it didn't fit the pattern the rest of the states displayed in the PCA this pattern becomes stronger (Figure 3.11). The abundance PCA distance regression comparisons also loosely suggests that the PCA distance is positively correlated to the geographic distance although the landings data has a slightly clearer pattern (Figure 3.12a-c). The adult abundance analysis shows the best correlation between the two since there is a much smaller Chesapeake Bay anomaly so the PCA distance follows a similar pattern to the geographic distance. In all abundance distance analyses the southern states had the least discernible relationship between PCA and geographic distance.

Table 3.3. PCA distance matrix for a) state landings b) region landings c) total abundance d) recruit abundance and e) adult abundance.

a) State

			Ches. Bay	coastal		Ches. Bay	coastal					
	NY	NJ	DE	MD	MD	PRFC	VA	VA	NC	SC	GA	FL
NY	0	0.0799	0.2911	0.7786	0.6254	0.5830	0.7946	0.6604	0.3489	0.6087	0.7940	0.6020
NJ		0	0.2179	0.7703	0.6781	0.5263	0.7865	0.6997	0.2865	0.5936	0.7849	0.5787
DE			0	0.6853	0.7682	0.3304	0.7010	0.7496	0.0967	0.5023	0.6971	0.4661
Ches. Bay MD				0	0.5830	0.4920	0.0162	0.4514	0.5967	0.1833	0.0168	0.2255
coastal MD					0	0.8299	0.5912	0.1406	0.7388	0.5531	0.5979	0.6074
PRFC						0	0.5044	0.7553	0.2417	0.3437	0.4972	0.2811
Ches. Bay VA							0	0.4583	0.6122	0.1991	0.0092	0.2403
coastal VA								0	0.7036	0.4478	0.4656	0.5075
NC									0	0.4149	0.6077	0.3744
SC										0	0.1958	0.0643
GA											0	0.2350
FL												0

b) Region

			coastal	coastal					
	NY	Del. Bay	MD	VA	Ches. Bay	NC	SC	GA	FL
NY	0	0.1700	0.8243	0.7816	0.8960	0.3920	0.7771	0.9095	0.6935
Del. Bay		0	0.9304	0.8406	0.8588	0.2425	0.6811	0.8625	0.6265
coastal MD			0	0.2766	0.7597	0.9858	0.9632	0.8104	0.8120
coastal VA				0	0.4836	0.8292	0.7111	0.5347	0.5634
Ches. Bay					0	0.7118	0.3356	0.0531	0.2595
NC						0	0.4713	0.7027	0.4564
SC							0	0.3000	0.1515
GA								0	0.2464
FL									0

c) Total Abundance

		coastal					
	Del. Bay	MD & VA	Ches. Bay	NC	SC	GA	FL
Del. Bay	0	0.5055	0.2608	0.3233	0.3765	0.7181	0.6260
coastal MD & VA		0	0.7137	0.7786	0.2065	0.2642	0.1541
Ches. Bay			0	0.0658	0.5367	0.9525	0.8521
NC				0	0.5990	1.0182	0.9176
SC					0	0.4705	0.3605
GA						0	0.1102
FL							0

d) Recruit Abundance

		coastal					
	Del. Bay	MD & VA	Ches. Bay	NC	SC	GA	FL
Del. Bay	0	0.5268	0.5712	0.5599	0.5137	0.5920	0.5763
coastal MD & VA		0	0.8544	0.8042	0.3961	0.1688	0.0798
Ches. Bay			0	0.0670	0.5232	0.9977	0.9319
NC				0	0.4614	0.9519	0.8826
SC					0	0.5632	0.4747
GA						0	0.0981
FL							0

e) Adult Abundance

	coastal						
	Del. Bay	MD & VA	Ches. Bay	NC	SC	GA	FL
Del. Bay	0	0.2734	0.2376	0.4191	0.3776	0.5539	0.8439
coastal MD & VA		0	0.5048	0.6733	0.1079	0.2912	0.6357
Ches. Bay			0	0.3044	0.6037	0.7905	1.0742
NC				0	0.7812	0.9176	1.1064
SC					0	0.2197	0.5989
GA						0	0.3932
FL							0

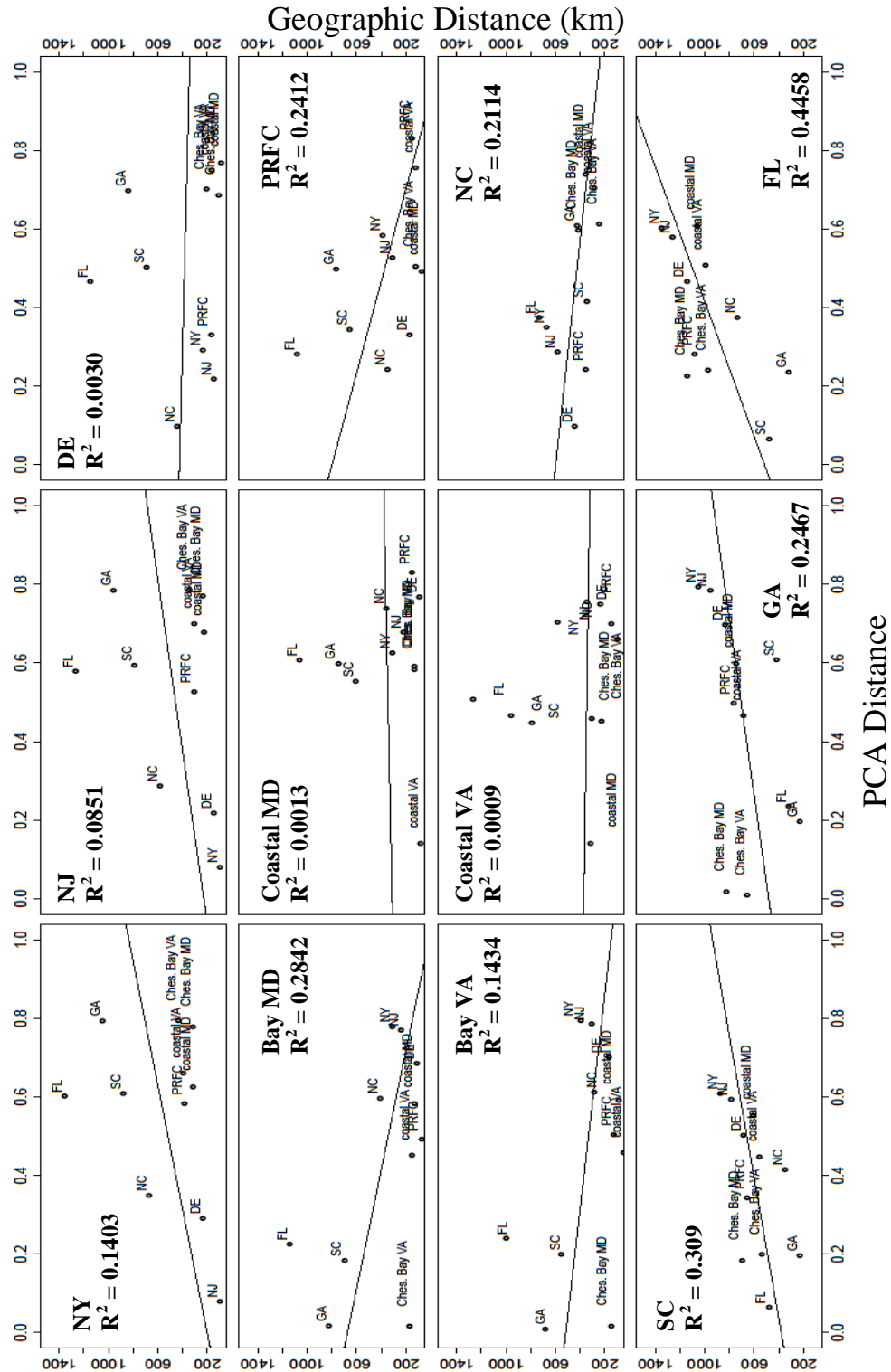


Figure 3.10. Plots showing comparison of PCA correlation distances and geographical distances between the different states. Points represent the data and the line is the linear regression. R^2 values are displayed on each plot.

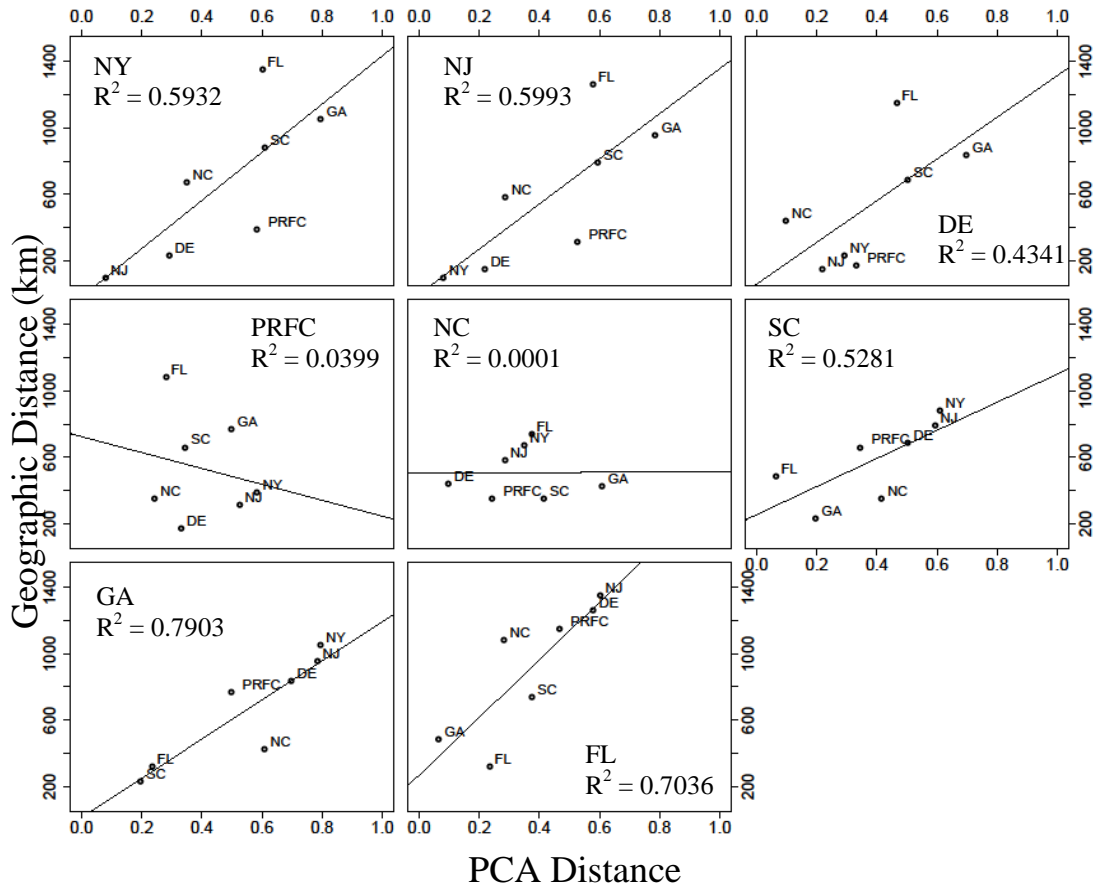
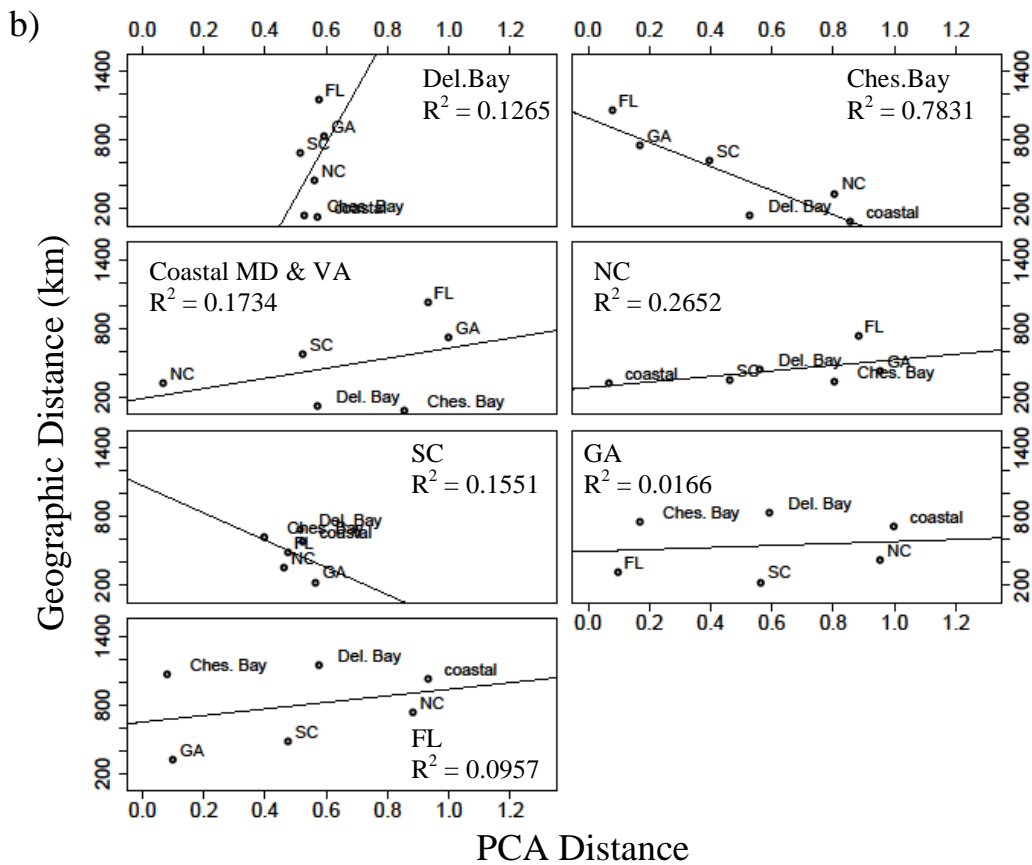
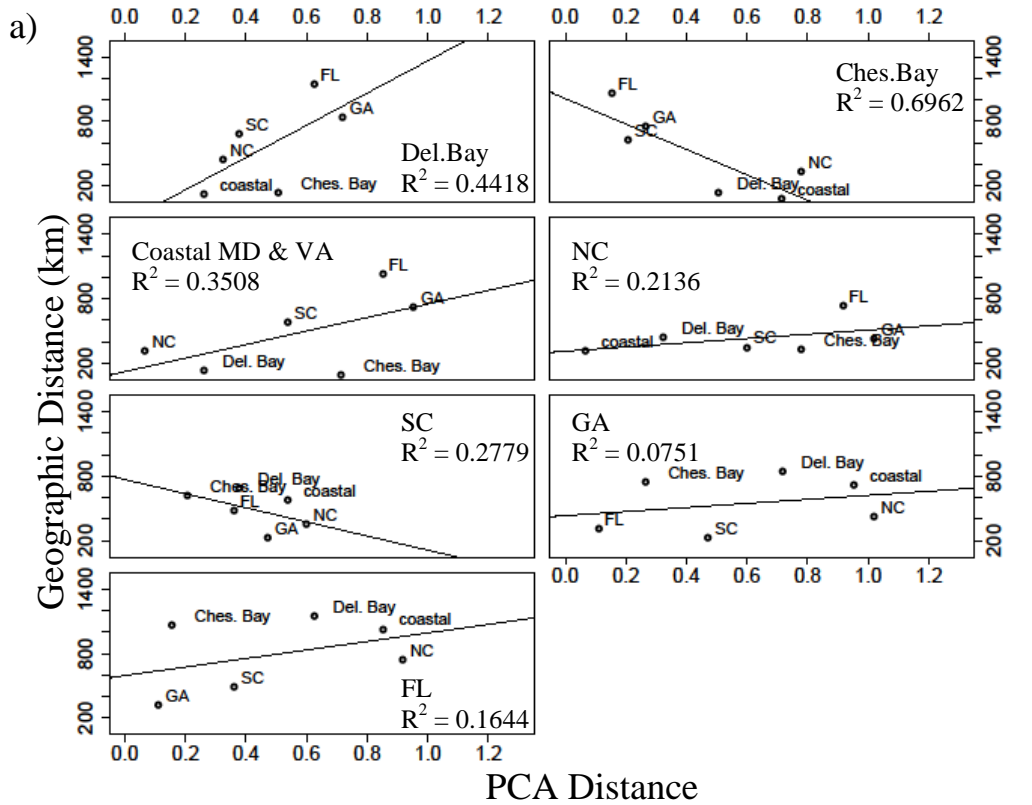


Figure 3.11. Plots showing comparison of PCA correlation distances and geographical distances between all states except both coastal and Chesapeake Bay Maryland and Virginia since they didn't fit the pattern seen in the rest of the states. Points represent the data and the line is the linear regression. R^2 values are displayed on each plot.



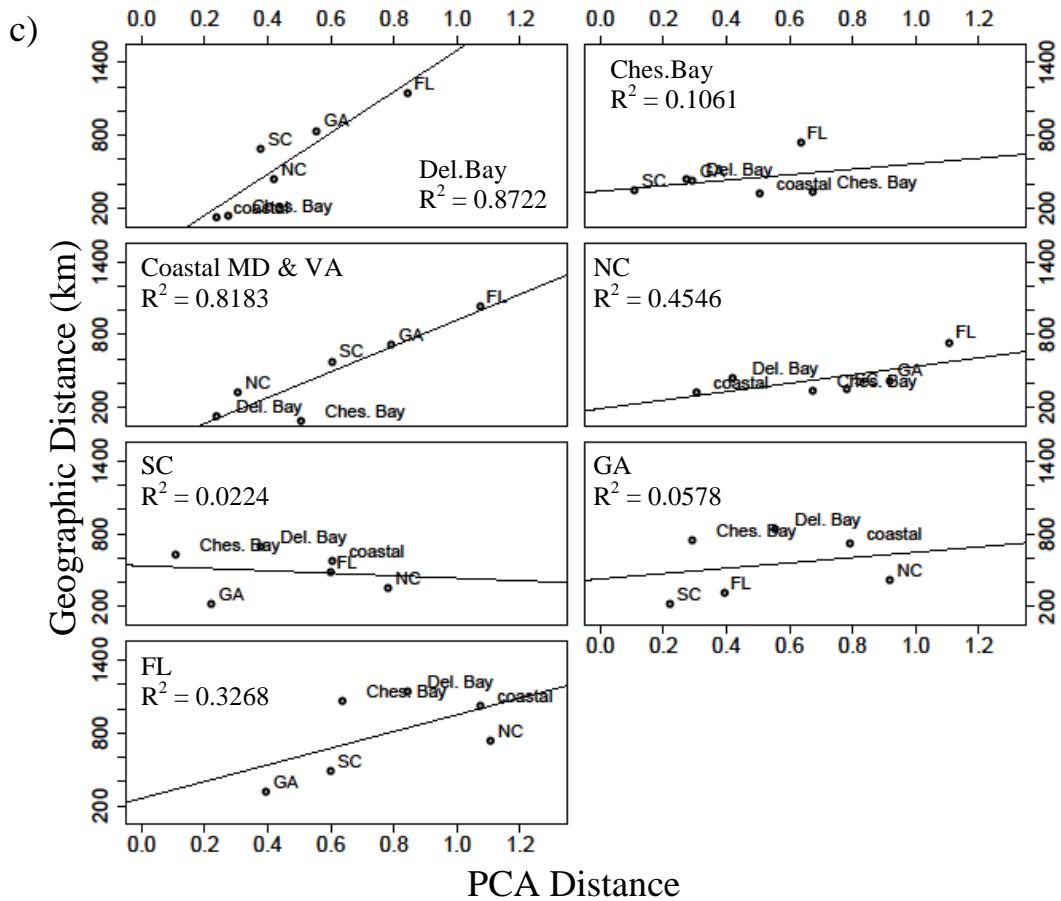


Figure 3.12. Plots showing comparison of PCA correlation distances and geographical distances between the different states for a) total abundance b) recruit abundance and c) adult abundance. Points represent the data and the line is the linear regression. R^2 values are displayed on each plot.

The best fitting DFA model (lowest AIC value) for the landings data set included three common trends with the GSI as an explanatory variable (Table 3.4). A similar latitudinal pattern to the one observed in the PCA can be seen in the results of the DFA. The factor loadings on Trend 1 have a clear latitudinal pattern with New York and Delaware Bay loading strongly and positively and Georgia and Florida loading strongly and negatively (Fig. 3.13). Trend 2 has strong positive loadings for Delaware Bay, South Carolina, and Florida and strong, negative loadings for coastal Maryland and Virginia and the pattern of the trend seems to be almost the inverse of Trend 1. North Carolina has a very strong, positive loading on Trend 3 while New York, Georgia, and Florida also loaded positively, but with loadings much closer to the 0.1 cutoff that indicates significance. The GSI was strongly correlated with South Carolina, North Carolina, Delaware, and New Jersey (Table 3.5). The model fit the observed time series for most states well ($R^2 > 0.8$). The exceptions were coastal Maryland ($R^2 = 0.26$), coastal Virginia ($R^2 = 0.35$), South Carolina ($R^2 = 0.5$), and Florida ($R^2 = 0.31$; Figure 3.14).

The best fitting DFA model for the total abundance had two common trends and the GSI as an explanatory variable (Table 3.6). The results from this analysis led to similar conclusions as the PCA with the factor loadings on the first trend primarily explaining the northern states minus the Chesapeake Bay and the second trend almost exclusively explaining the southern states plus the Chesapeake Bay (Figure 3.15). A biplot of the factor loadings for the two trends shows groupings of the states that are similar to those found in the PCA (Figure 3.16). The GSI is significantly and positively correlated with coastal Maryland and Virginia and strongly and negatively

Table 3.4. AIC values for DFA models run for the complete landings time series (1974-2008). The best model (indicated by the lowest AIC value) is indicated in **bold**.

	No Env.	GSI	NAO	SSN	Winter Temp.	Winter Temp & GSI
1 trend	760.6	754.6	755.7	766.6	771.7	762.0
2 trends	714.0	706.2	711.2	775.5	725.7	710.4
3 trends	703.8	688.7	694.4	851.9	796.1	771.4
4 trends	693.1	698.2	700.0	905.2	847.2	766.1
5 trends	703.9	696.6	704.9	-	785.6	798.2

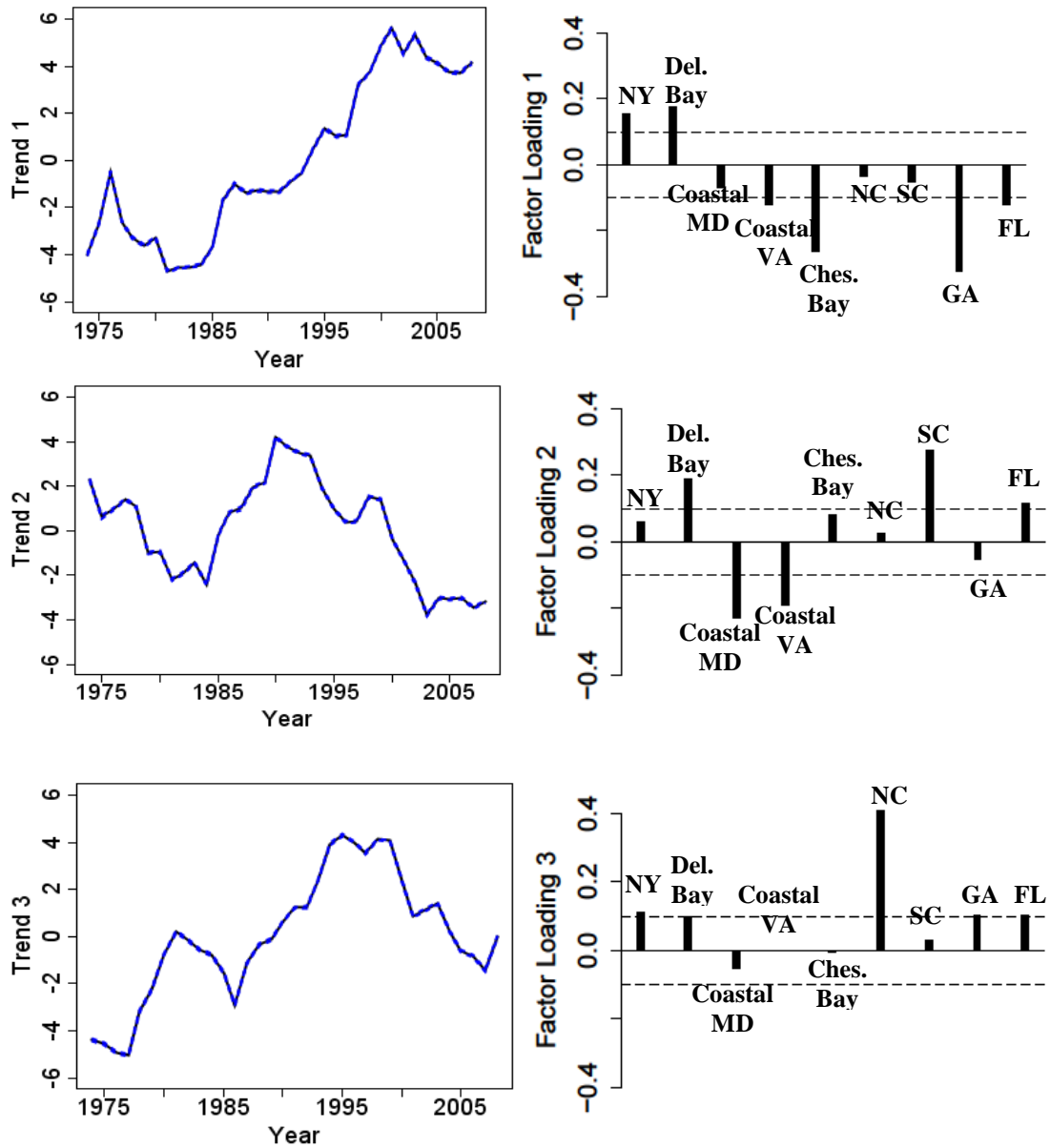


Figure 3.13. DFA trends (\pm 95% C.I.) for the best fit model for the landings data. The Gulf Stream Index was used as an explanatory variable in the analysis. Trends are in no particular order as DFA estimates all trends simultaneously. Factor loadings for each trend are also shown with correlations falling outside the dotted lines being significantly correlated with the corresponding trend based on an arbitrarily chosen cutoff level of 0.1, which was suggested by Zuur et al. 2003b.

Table 3.5. Parameter estimates for the GSI for each region that were calculated by the DFA analysis on the full time series with corresponding t-values. **Bold** values indicate a significant relationship ($\alpha = 0.05$).

State	GSI parameter	t-value
NY	0.378	4.117
DE Bay	0.264	2.511
coast MD	0.188	1.065
coast VA	-0.111	-0.648
Ches. Bay	0.028	0.369
NC	-0.250	-2.648
SC	-0.447	-2.967
GA	-0.013	-0.014
FL	-0.167	-0.997

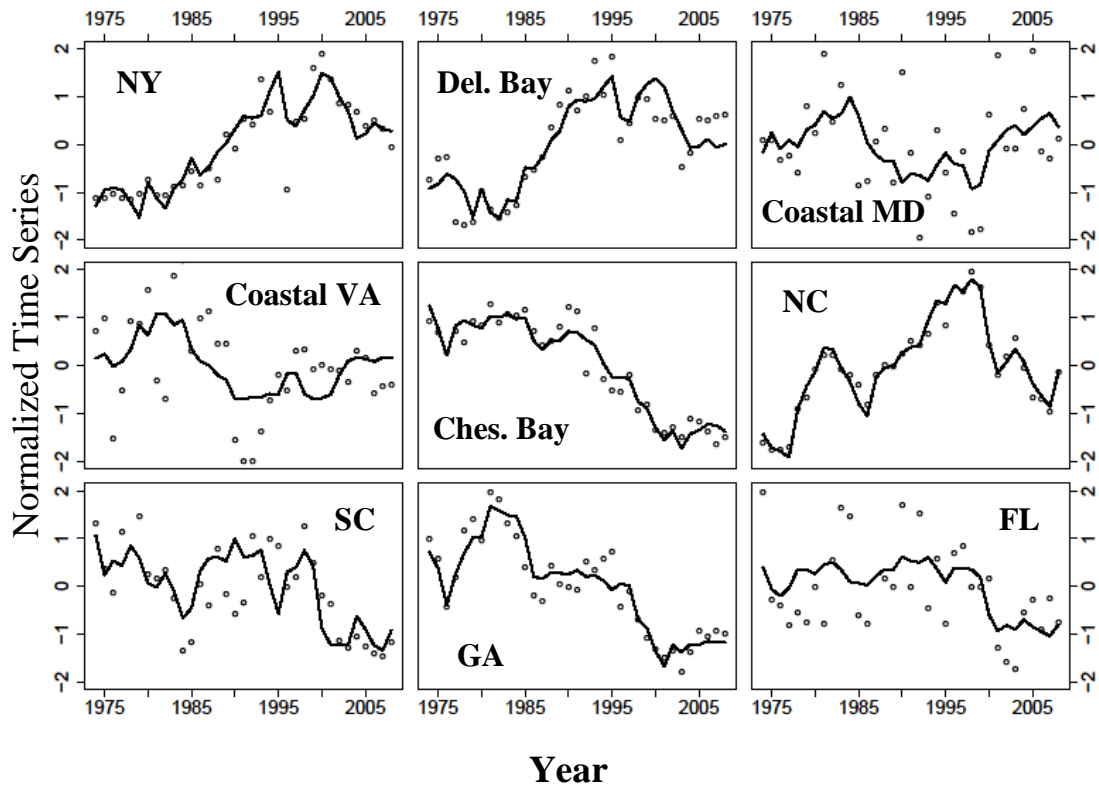


Figure 3.14. DFA model fit for the landings of each state. Points represent the normalized original time series and the solid black line depicts the model fit.

Table 3.6. AIC values for DFA models run for the total abundance time series (1990-2008). The best model (indicated by the lowest AIC value) is indicated in **bold**.

	No Env.	GSI	NAO	SSN	Winter Temp.
1 trend	328.1	320.9	329.6	325.5	332.0
2 trends	319.8	311.7	320.7	316.0	321.6
3 trends	321.2	312.7	319.8	388.7	358.0
4 trends	330.3	322.4	325.2	386.8	372.0
5 trends	336.7	326.4	333.9	357.9	365.8

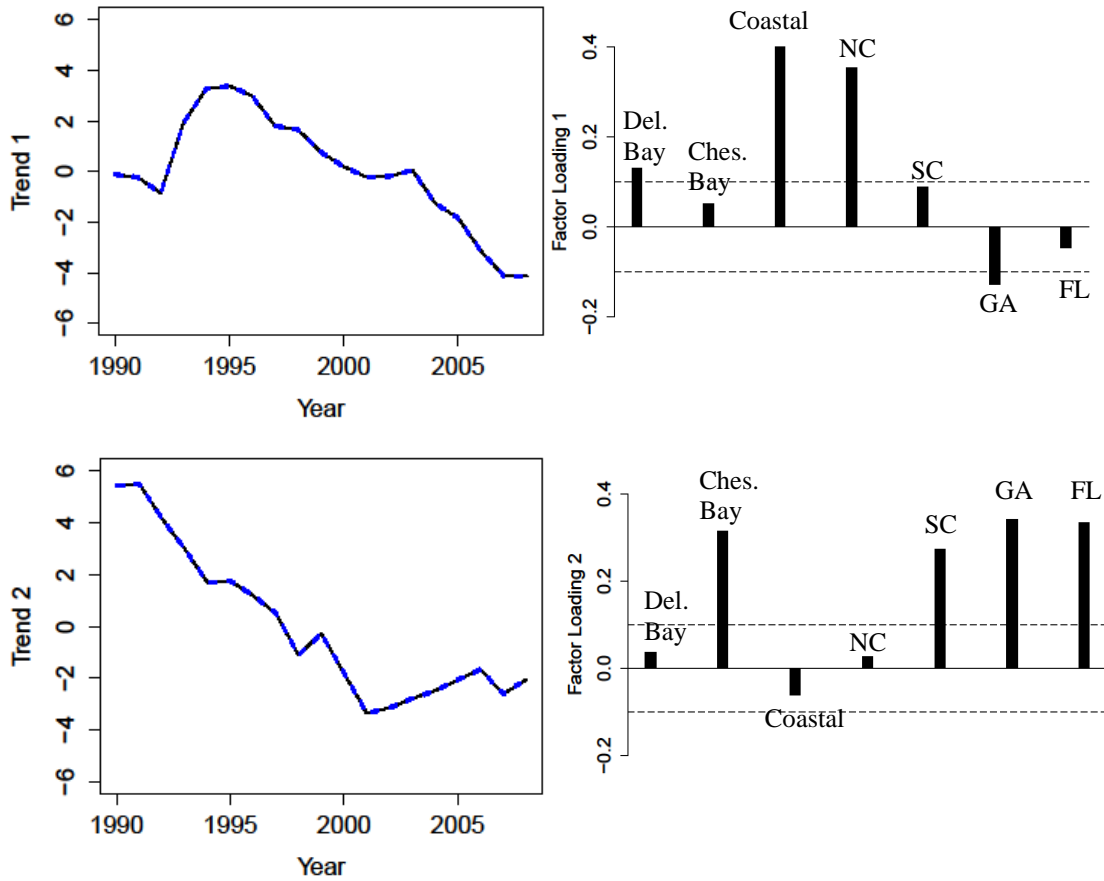


Figure 3.15. DFA trends (\pm 95% C.I.) for the best fit model for the total abundance data. The Gulf Stream Index was used as an explanatory variable in the analysis. Trends are in no particular order as DFA estimates all trends simultaneously. Factor loadings for each trend are also shown with correlations falling outside the dotted lines being significantly correlated with the corresponding trend based on an arbitrarily chosen cutoff level of 0.1, which was suggested by Zuur et al. 2003b.

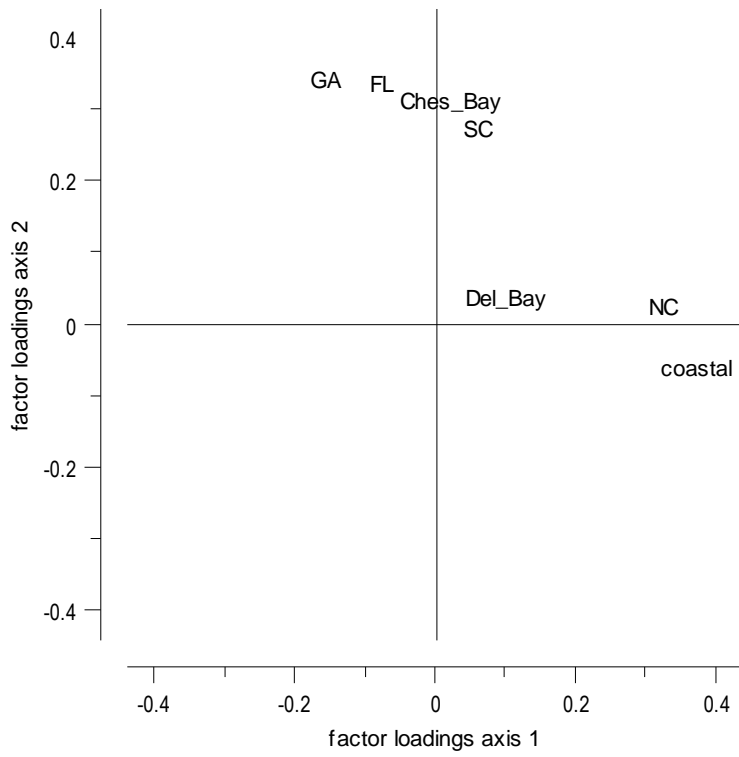


Figure 3.16. Biplot of the factor loadings for each region for the two trends from the total abundance DFA.

correlated with North Carolina and Florida (Table 3.7). It is also moderately and negatively correlated with Chesapeake Bay. The model fit the observed time series for most states well ($R^2 > 0.65$). The only exception was Delaware Bay ($R^2 = 0.11$; Figure 3.17).

As with the PCA, the juvenile abundance DFA led to very similar results as the one for total abundance. Again, the best model had two common trends with the GSI as an explanatory variable (Table 3.8). Factor loadings on each of the two trends were very similar with the exception that Delaware Bay was not significantly loaded on Trend 1 as it was in the total abundance analysis (Figure 3.18). The biplot of factor loadings shows groupings of states similar to how states were grouped in both the PCA and the total abundance DFA (Figure 3.19). The GSI was strongly and negatively correlated with North Carolina and Florida (Table 3.9). The model fit the observed time series for most states well ($R^2 > 0.6$). The exception was Delaware Bay ($R^2 = 0.03$; Figure 3.20).

As with the PCA, the adult abundance best fitting DFA model was different from the other two analyses with the best model having only one common trend with no environmental variables (Table 3.10). This trend has significant, positive factor loadings for all except North Carolina and Florida, which do not load significantly (Figure 3.21). The model fits for the observed time series are not as good as in the total abundance and juvenile DFAs. Delaware Bay ($R^2 = 0.27$), coastal Maryland and Virginia ($R^2 = 0.29$) had moderate model fits and North Carolina and Florida had poor model fits ($R^2 < 0.1$; Figure 3.22).

Table 3.7. Parameter estimates for GSI for each region that were calculated by the total abundance DFA analysis on the full time series with corresponding t-values. **Bold** values indicate a significant relationship ($\alpha = 0.05$).

State	GSI parameter	t-value
Del Bay	-0.0874	-0.34297
Ches Bay	-0.18189	-1.33209
coastal MD & VA	0.22819	1.43547
NC	-0.50971	-2.77327
SC	0.08368	0.62766
GA	0.01117	0.07585
FL	-0.43833	-2.78292

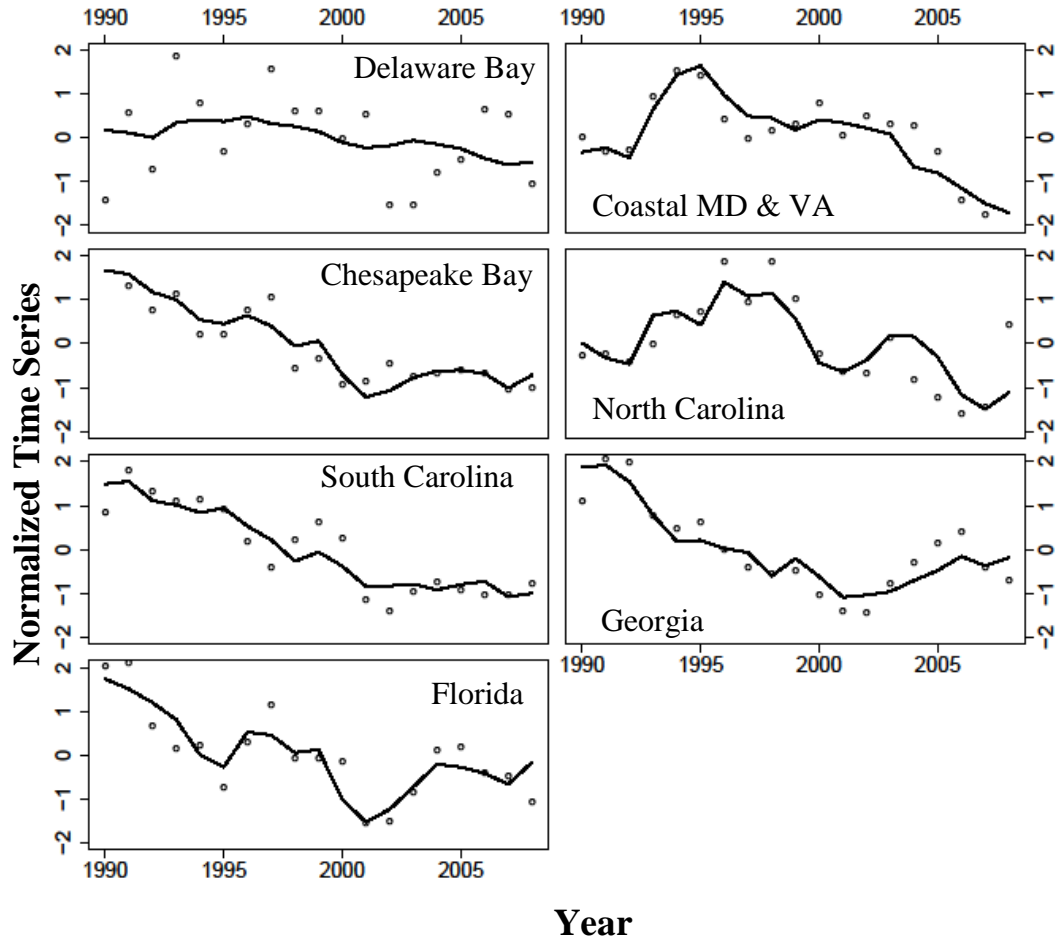


Figure 3.17. DFA model fit for the total abundance data. Points represent the normalized original time series and the solid black line depicts the model fit.

Table 3.8. AIC values for DFA models run for the recruit abundance time series (1990-2008). The best model (indicated by the lowest AIC value) is indicated in **bold**.

	No Env.	GSI	NAO	SSN	Winter Temp.
1 trend	360.8	360.0	359.9	364.5	367.2
2 trends	352.7	351.9	352.3	419.2	359.7
3 trends	358.6	353.9	353.7	371.6	373.3
4 trends	366.3	362.1	361.7	374.8	401.0
5 trends	372.7	367.9	367.8	395.0	397.1

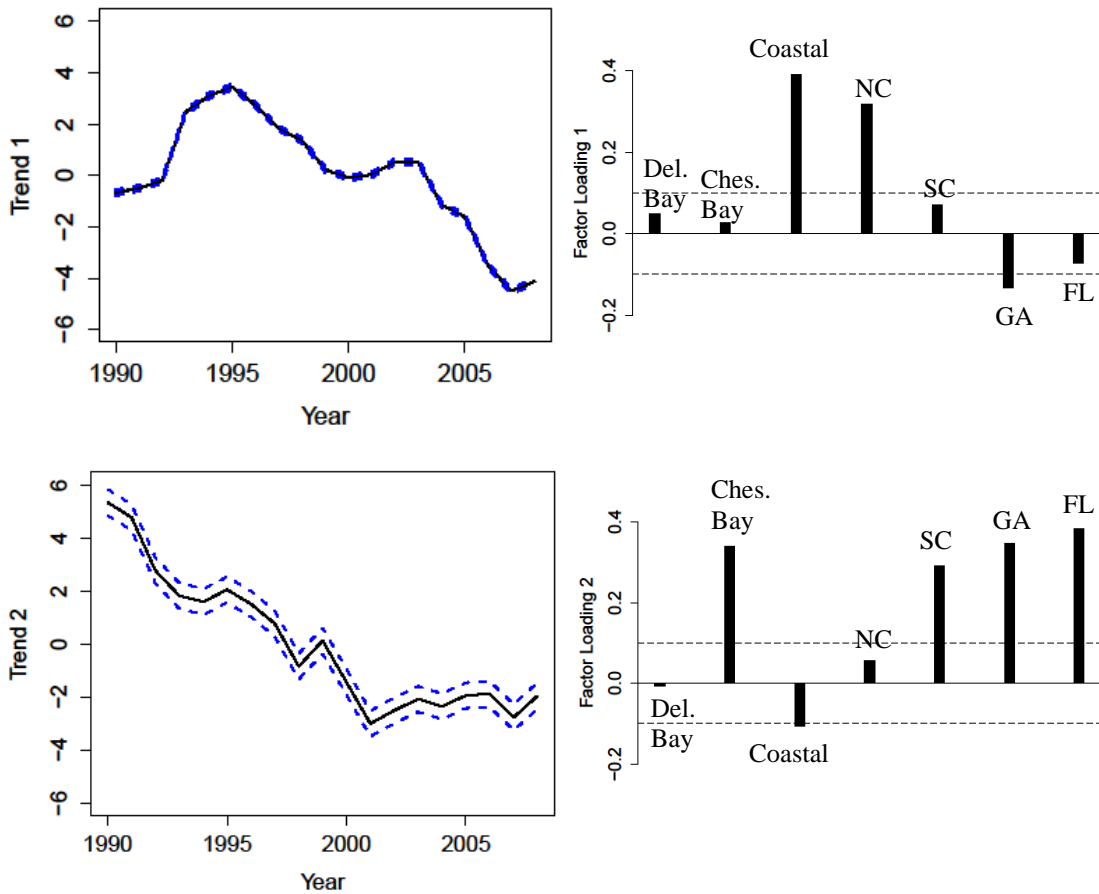


Figure 3.18. DFA trends (\pm 95% C.I.) for the best fit model for the recruit abundance data. The Gulf Stream Index was used as an explanatory variable in the analysis. Trends are in no particular order as DFA estimates all trends simultaneously. Factor loadings for each trend are also shown with correlations falling outside the dotted lines being significantly correlated with the corresponding trend based on an arbitrarily chosen cutoff level of 0.1, which was suggested by Zuur et al. 2003b.

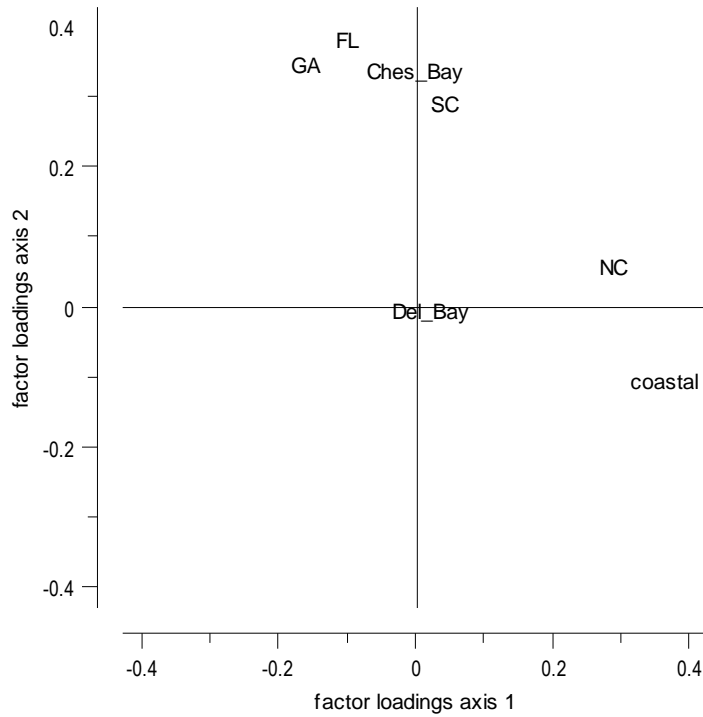


Figure 3.19. Biplot of the factor loadings for each region for the two trends from the recruit abundance DFA.

Table 3.9. Parameter estimates for GSI for each region that were calculated by the recruit abundance DFA analysis on the full time series with corresponding t-values. **Bold** values indicate a significant relationship ($\alpha = 0.05$).

State	GSI parameter	t-value
Del Bay	-0.17244	-0.64882
Ches Bay	-0.12927	-0.79029
coastal MD & VA	0.21744	1.25937
NC	-0.49631	-2.61185
SC	-0.01918	-0.109
GA	0.02782	0.14755
FL	-0.41591	-2.45989

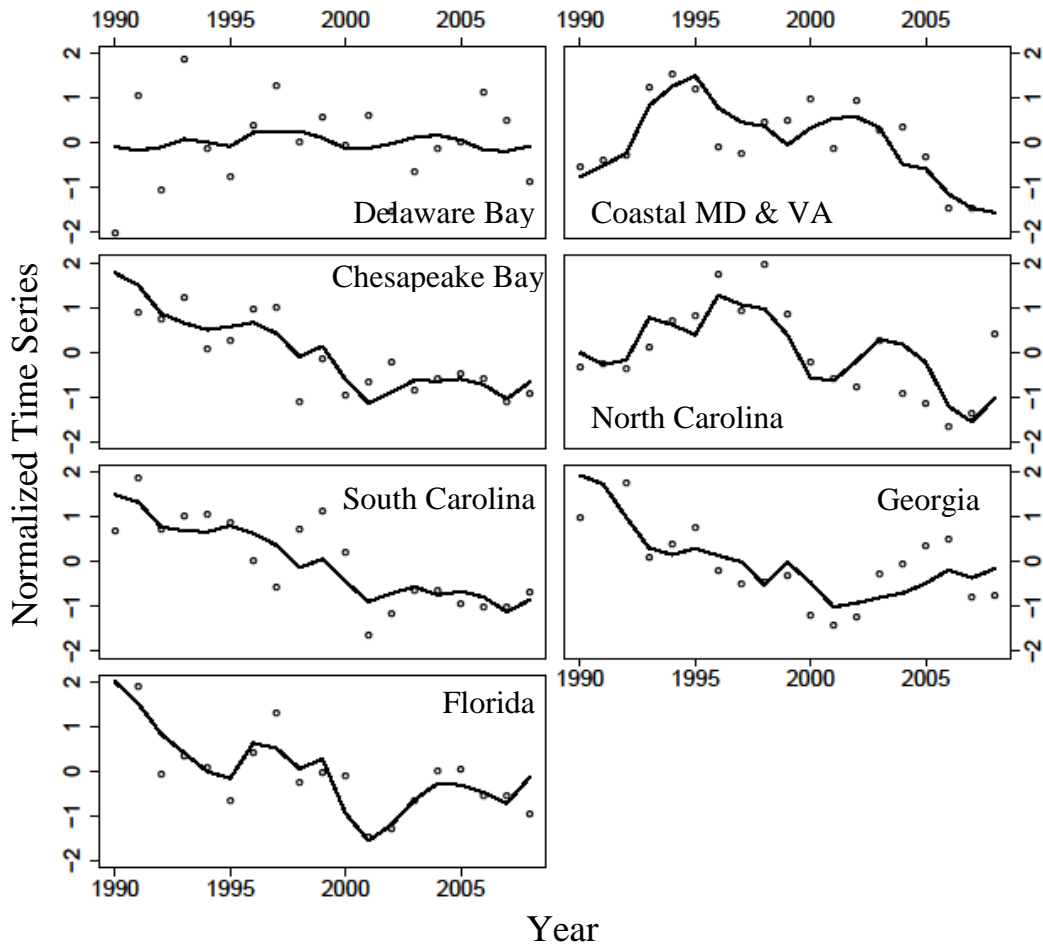


Figure 3.20. DFA model fit for the recruit abundance data. Points represent the normalized original time series and the solid black line depicts the model fit.

Table 3.10. AIC values for DFA models run for the adult abundance time series (1990-2008). The best model (indicated by the lowest AIC value) is indicated in **bold**.

	No Env.	GSI	NAO	SSN	Winter Temp.
1 trend	349.9	350.3	356.6	356.0	361.1
2 trends	351.4	351.9	358.0	504.3	362.2
3 trends	361.7	363.9	366.4	603.1	405.9
4 trends	369.4	370.0	377.8	449.6	389.6
5 trends	375.4	375.9	384.0	458.9	426.7

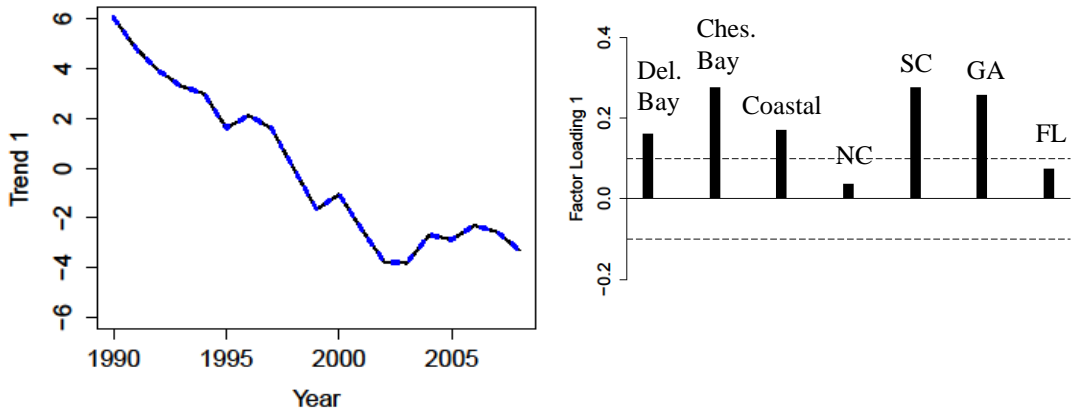


Figure 3.21. DFA trend (\pm 95% C.I.) for the best fit model for the adult abundance data. No explanatory variables were used in the analysis. Factor loadings are shown with correlations falling outside the dotted lines being significantly correlated with the corresponding trend based on an arbitrarily chosen cutoff level of 0.1, which was suggested by Zuur et al. 2003b.

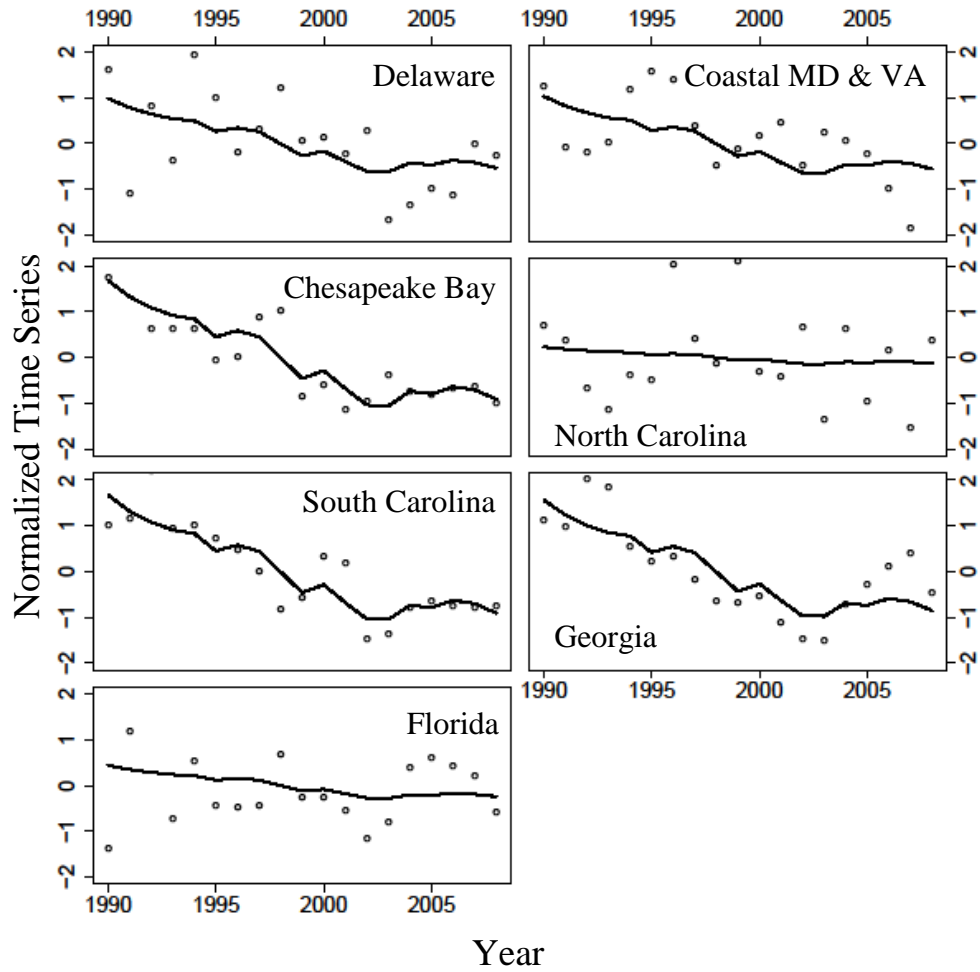


Figure 3.22. DFA model fit for the adult abundance data. Points represent the normalized original time series and the solid black line depicts the model fit.

Discussion

There is evidence of synchrony in blue crab populations along the east coast of the U.S. The synchrony was revealed as a latitudinal gradient in which northern regions, broadly defined, were internally coherent and different from populations in southern states that themselves were internally coherent. Based on the results of both the PCA and DFA, landings in New York, Delaware, New Jersey, and North Carolina have similar trends and Georgia and Florida have patterns in landings that are similar to each other and dissimilar to those in the northern states. This pattern is reinforced in the abundance PCAs but the trend is on the 2nd PC suggesting it may not be the primary driver of synchrony. The Gulf Stream Index was important for three out of the four DFAs.

Although the mechanism cannot be fully identified based on the results of this study, there is evidence that synchronization of blue crab populations along the east coast of the United States exists. The latitudinal and temporal pattern among the abundance time series in blue crab from different populations clearly indicates that there is a geographic pattern. This geographic pattern in abundance creates a parallel pattern in how many blue crabs are caught in a particular year. The latitudinal pattern could be due to either a Moran effect creating a northern and southern pattern in abundance or it could be a reflection of how crabs are caught by the fishery since it was the primary pattern in the landings PCA. However, for the three abundance PCAs the latitudinal pattern was present on PC2, which suggests the latitudinal pattern may be secondary to another pattern in abundance that drives all blue crab populations along the coast similarly. It is possible that the common driver behind

this pattern could be mixing of larval individuals. Very few studies have been done on mixing of blue crab populations and the few that have were largely focused in Delaware Bay. This work has centered on blue crab larval retention with the general conclusion that larvae released from Delaware Bay are either retained or transported southward and there is unlikely any transfer of larvae that originated in the southern estuaries into Delaware Bay (Epifanio et al. 1989; Garvine et al. 1997; Tilburg et al. 2009). Delaware Bay had the worst model fit in all abundance DFAs which could potentially be a result of not receiving larvae from other estuaries and therefore not following the trends of other estuaries as closely.

The DFA indicates that the Gulf Stream Index (GSI) improves the model fit in the landings, total abundance, and juvenile abundance models, which suggests that this climatic index plays a role in driving the observed latitudinal pattern. However, for the landings DFA the regression coefficients were only significant in North Carolina, South Carolina, Delaware Bay, and New York, meaning that it does not explain any of the similarity in landings in Georgia and Florida. The effects of the GSI tend to be stronger north of the Gulf Stream during the summer when the fishing effort tends to peak in most states and therefore Florida and Georgia may be located too far south for the GSI to have a detectable effect on blue crab landing trends (Taylor 1996). For total abundance coastal Maryland and Virginia were positively associated and North Carolina and Florida were negatively correlated with the GSI. This creates some disconnect with what the landings DFA suggested so further exploration into this matter would be useful, but could potentially be explained by the seasonal variation in the range of the GSI's influence on coastal conditions. This was

also the case for the recruit abundance DFA, which suggested that North Carolina and Florida were significantly and negatively correlated with the GSI. There are potentially other environmental factors that were not examined in this study that would improve the model fit further and aid in explaining the latitudinal pattern in blue crab landings.

Landings data provide the longest time series for indexing blue crab abundance in each state, which makes them the best option for looking at long term climatic effects. However, using landings data as an index of abundance has been criticized, as many factors beyond the abundance of the species, can affect how many blue crabs are caught in a given year, such as the economy and management regulations (Harley et al. 2001; Walters & Martell 2004). From the results presented here, it appears that landings may serve as a reliable index of abundance as similar patterns were observed in analyses for both landings and abundance. Although landings appear to be a reliable index of abundance, there are regions for which the two are discordant. Landings for the coastal and Chesapeake regions of Maryland and Virginia didn't seem to be closely associated with any of the other landings time series, but in the abundance analyses the coastal Maryland and Virginia abundances were associated with other abundance time series. There are two potential explanations for why the landings from Maryland and Virginia did not fit the latitudinal pattern. Management practices in these states may have affected the landings differently than in the other states. If this is the case, then the Maryland and/or Virginia coastal landings are decoupled from the true population dynamics of blue crab in the region and therefore landings do not represent the patterns of

fluctuation in the population. Blue crab fisheries in the Chesapeake Bay states have been fairly intense for a longer time than in the other states and therefore it is also possible that this longer period of stress on the population has caused landings to decrease in more recent years. This could help explain Maryland and Virginia's trend in coastal landings fluctuations not associating with the populations of other states.

The Chesapeake Bay landings and abundance (for all but the adults) tended to associate most closely with Florida and Georgia. Since this anomaly was seen in both data sets the idea of landings being decoupled from the true pattern of abundance does not hold for the Chesapeake Bay. Instead, it is possible that the uniqueness of Chesapeake Bay, being one of the most productive estuarine systems on Earth, may impact the population dynamics of blue crab differently compared with estuaries of other states included in the analysis (W. Boynton, Chesapeake Biological Laboratory, pers. comm.).

Overall, it is evident that there are similarities in blue crab population fluctuations along the east coast and therefore some synchrony is present. The Chesapeake Bay is an anomaly to the relationships suggested by the multivariate analyses used in this study, which may be due to the extremely productive nature of the estuary. A combination of both mixing and a Moran effect due to the GSI are valid explanations for the patterns seen here, but do not explain all of the variability seen in the populations. Although, this creates a foundation for better understanding the fluctuations in blue crab populations more studies into the mechanisms driving blue crab fluctuations are needed in order to better inform management agencies along the east coast of the United States. For example, one potential future study

would be to look further into the connectivity of blue crab populations to determine if one estuary dominates the dynamics of all blue crabs along the east coast or if all estuaries contribute equally. Better understanding the spatial component of populations could provide more insight into what drives fluctuations in abundance. It would also be useful to put more effort into examining environmental mechanisms that drive synchrony in blue crab populations. The Gulf Stream Index seems to explain a portion of the variability, but it is possible it works in conjunction with other environmental factors that were not examined in this study. If we are able to better understand the environmental factors behind blue crab fluctuations it may be possible to make predictions of what populations will do in the future and inform manager's decisions in how to maintain sustainable populations. Finally, this study presented preliminary evidence for a northern trend in blue crab abundance and a separate, southern trend. Further investigation into this latitudinal split in synchrony may be important for managers and may lead to the regional management of blue crab.

Chapter 4: Summary

Blue crab is a species of high biological and economic value and therefore the mechanisms for what drives patterns in their abundances is of interest. Multiple populations of blue crab exist along the east coast of the United States and the extent to which these populations are similar in their dynamics is not well known due to the complex life history. Understanding the mechanisms behind inter-annual variability for each of these populations can help determine if there is any synchrony in population fluctuations present among the different blue crab stocks. Two potential mechanisms that may induce synchrony for blue crab are mixing of individuals from neighboring populations during the larval stage in the coastal ocean and/or a Moran effect where an environmental variable influences the dynamics of multiple populations in a similar manner. The goal of my thesis was to use the fishery-dependent and fishery-independent data that have been collected by state agencies for a number of years to first estimate time series of absolute abundance with catch-survey models, then use multivariate techniques to determine if synchrony among blue crab populations is present, and, if so, look at possible environmental mechanisms to explain the coherence. For the second objective I ran PCA and DFA analyses for both the absolute abundance time series from the catch-survey models and for landings data alone in order to determine if the landings data did a sufficient job at illustrating patterns in abundance fluctuations.

In Chapter 2, I used a combination of landings data that were adjusted for major reporting changes that skewed landings and survey data from state-run surveys to create time series of absolute adult, recruit, and total abundance using catch-survey (CSA) models. I was able to create successful models for all seven regions in my

study area. The study provided insight into which surveys were the most reliable for predicting blue crab abundance for age-0 and age 1+ crabs. The Delaware Bay trawl, the Chesapeake Bay winter dredge, the coastal Maryland trawl, and the Georgia trawl were the most reliable surveys for providing insight into both age-classes of blue crabs. From this analysis I was also able to determine which populations have grown since the start of the survey and which have declined. All populations except Delaware Bay and North Carolina have experienced a decline in population size when comparing the last year of the model to the first year. Some of these declines seem to be attributable in part to low recruitment in the later years of the model.

Although these models performed well in my study, some additions could be made to the analysis to obtain more information about the status of blue crab populations. The first potential avenue of investigation would be to look at the interactions between explanatory variables used to create the survey indices. The Delta-GLM function that I used in this study was not able to account for any interactions, which are likely to exist due to factors such as seasonal patterns. Another important addition that could be made to the analysis would be including a stock-recruitment analysis in the models that would allow for the estimation of reference points such as a target and threshold exploitation rate and abundance. This was able to be achieved for the most recent blue crab stock assessment model for Chesapeake Bay (Miller et al. 2011), but may be more difficult for some of the other populations due to the fact that Chesapeake Bay has four fishery-independent surveys and the winter dredge is considered to be a measure of absolute abundance rather than a relative index of abundance. For states with less information available it may not be

possible to incorporate the stock-recruitment relationship directly into the CSA models. An alternative suggestion would be to perform a Ricker analysis using the time series of recruit and adult abundances that were computed by the CSA and then using the curves from this stock-recruitment relationship to determine what reference points should be used. Obtaining reference points would be very useful for the management agencies because it would aid in setting limits for how many blue crabs can be taken from a given population each year.

In Chapter 3, my goal was to determine if patterns of synchrony were present in landings and/or the absolute abundance time series estimated in Chapter 2. I used both principal component analysis (PCA) and dynamic factor analysis (DFA) to look for these patterns. Interestingly, there does appear to be synchrony present in blue crab populations along the east coast of the United States as both the landings and absolute abundance data suggest a latitudinal pattern in population structure. Populations from North Carolina northwards had similar trends in abundance and populations from South Carolina southward had similar patterns that were different from the trends in the north. Surprisingly, Chesapeake Bay did not fit into this pattern as both the landings and abundance analyses suggest this estuary's blue crab population has similar patterns in abundance to Georgia and Florida. This might be due to the highly productive nature of the Chesapeake Bay leading to different dynamics in the blue crab populations (W.Boynton, Chesapeake Biological Laboratory, pers. comm.).

The Gulf Stream Index seems to play a role in driving the dynamics of blue crab populations as it was an important environmental variable in the landings, total

abundance, and recruit abundance DFAs. Since it was an important variable in all but the adult abundance, it suggests that recruitment variability is the primary driver of how blue crab populations fluctuate and that the Gulf Stream Index plays a role in how much recruitment variability there is from year to year. This is perhaps further supported by the PCA results for the abundance data where PC1 showed all of the states loading negatively or neutrally, which could be an indication that mixing of larvae in the coastal oceans drives populations.

The synchronization analyses demonstrated that there is evidence of coherence in the abundance of blue crab populations along the western Atlantic. Some interesting future research would be to look further into the connectivity of blue crab populations in order to determine if there is one blue crab population that drives the dynamics of the entire coast or if all populations contribute equally. This is a hypothesis that has been posed for striped bass along the east coast (Murphy et al. 2008) and could potentially apply to blue crab as well if mixing is in fact an important mechanism behind synchronization. Adding a spatial component to the analyses may also provide more information about blue crab population fluctuations. One example of how spatial information could be better incorporated would be to obtain blue crab landings by NOAA code and then find of center of landings for each population and use these as the points from which geographic centers are calculated to be compared to PCA distances. Another area of future research is to look more into the mechanisms behind synchronization. The Gulf Stream Index and larval mixing are two proposed mechanisms that came out of this study, but it is likely that other environmental factors may also play a role in driving population fluctuations.

Tracking larvae in the coastal ocean would prove to be challenging, but would be interesting for understanding how much mixing between populations actually does occur. The studies from Delaware Bay indicate that there are not many foreign blue crabs migrating into Delaware Bay, but the possibility of larvae from Delaware Bay being transported into other estuaries is viable (Garvine et al. 1997; Tilburg et al. 2009). Beginning to look at the mixing potential of blue crab larvae from other estuaries would be interesting and may help us to better understand their population dynamics.

Some important future steps should be taken in order to provide further information to both inform and improve analyses regarding the synchrony of blue crab populations. Quantifying recreational landings could significantly change the results of stock assessment models since values in my model were estimated in a fairly arbitrary manner. It also may be useful to work to obtain sex-specific landings as some jurisdictions are moving towards conserving female biomass so sex-specific information may be needed for future assessments and analyses of stocks. Surveys should be reevaluated by each state in order to determine if changes need to be made to obtain better indices of abundance for blue crab. For some surveys, such as the ChesMMAP trawl, the main objective is not to catch blue crabs so altering the survey may not be reasonable. Other surveys, such as the Chesapeake winter dredge, the coastal Maryland trawl, and the Georgia trawl, should be continued as they provide a reliable index for both adult and recruit crabs.

Expanding this study to other systems may also provide insightful information about the synchrony of blue crab populations. One potential way to do this would be

to repeat these analyses for the Gulf of Mexico stocks to see if there are any patterns among those stocks and determine how these populations compare with their Atlantic counterparts. Previous work has found that there is high genetic diversity in all stocks and therefore no detectable difference has been determined between the Gulf of Mexico and Atlantic stocks so it is possible that their dynamics are similarly influenced (McMillen-Jackson et al. 1994). It also may be useful to implement sex-specific data in the synchrony analysis, at least for adults, which may provide more insight into determining if adults are indeed important for driving population dynamics or if the recruits are the more important life stage since this was inconclusive in my study.

In conclusion, my thesis has demonstrated that there is evidence that the blue crab populations along the east coast are connected in their dynamics, possibly through mixing of larvae, influence of the Gulf Stream Index, or a combination of both. Landings data seem to serve as a reasonable proxy for abundance data as many of the patterns found in my analyses were picked up by both landings and abundance data. The results from this study and those to follow could prove to be very useful to managers along the U.S. east coast in determining the best way to manage blue crab from this point forward.

Appendix A: R Code for Delta-GLM

R code for the Delta GLM function using the Delaware trawl survey as an example.

```
rm(list=ls())
library(grDevices)
library(MASS)

#BASIC SET UP

setwd("p:/Colton/deltaGLM/Delaware")

indirectory=paste(getwd(),"/Data/",sep="")
outdirectoryPlot=paste(getwd(),"/Plots/",sep="")
outdirectoryResults=paste(getwd(),"/Results/",sep="")

#CREATE AIC MATRIX
AIC<-rep(NA,3)
dim(AIC)<-c(3,1)
rownames(AIC)=c('AIC.binomial','AIC.gamma','shape.mle')
colnames(AIC)=c('GLM')

dglm<-dget('p:/Colton/deltaGLM/deltaGLM-1-7-2-PBC.r')

# now input data
infile<-"DE_Rdata, envgood.csv"

surveydata<-read.csv(paste(indirectory,infile,sep="))

##### T1 #####
# create data set for just the age 1+
selectedstage<-"T1"
surveydata<-surveydata[surveydata$Stage==selectedstage,]

# Check you have the right data
head(surveydata)

Indices<-tapply(surveydata$Count,surveydata$Year,mean)
Year<-as.numeric(rownames(Indices))
Indices<-cbind(Year,Indices)
colnames(Indices)<-c('Year','SimpleMean')

head(Indices)
#Clean up survey data to subset
glmsdat <- surveydata[,-9]
head(glmsdat)
```

```

# C stands for continuous
# F stands for factor
#Column 1: response variable (must be a continuous variable)
#Column 2: [factor that will get jackknifed error estimates, e.g. year]
#Column 3: [2nd explanatory variable] (variables 2-p can be factors or continuous)
#: :
#: :
#Column p: [pth explanatory variable]
#
# cols.bin selects the numbers of the columns to be used in the presence/absence
# cols.pos selects the numbers of the columns to be used in the abundance estimation - need
not be the same
#1= count
#2 = year
#3 = month
#4 = station
#5 = tow duration
#6 = depth
#7 = temp
#8 = salinity
DEindex<-
dglm(glmsdat,dist="gamma",types=c('C','F','F','F','C','C','C'),cols.bin=c(2,3,4,5,7,8),cols.p
os=c(2,3,4,5,6),minpos=5,write=F,J=FALSE)
GLM<-
as.data.frame(cbind(rownames(DEindex$deltaGLM.index),DEindex$deltaGLM.index))

#use if you are not jack knifing
colnames(GLM)<-c('Year','GLMIndex')
#use if you are jack knifing
#colnames(GLM)<-c('Year','GLMIndex','Jack.Mean','SE1','Jack.cv')
AIC[,1]<-deltagamma.summary$aic
Indices<-merge(Indices,GLM,by="Year",all.x=TRUE)

#write output
write.csv(Indices,file=paste(outdirectoryResults,selectedstage,"Indices.csv",sep=""),append=
FALSE)
write.csv(AIC,file=paste(outdirectoryResults,selectedstage,"AIC.csv",sep=""),append=FALS
E)

# plot results
pdf(file=paste(outdirectoryPlot,selectedstage,".pdf",sep=""),onefile=TRUE)
#tiff(file=paste(outdirectoryPlot,selectedstage,".tif",sep=""))
maxy =
ifelse(max(Indices$SimpleMean,na.rm=TRUE)>max(Indices$GLMIndex,na.rm=TRUE),ceil
ing(max(Indices$SimpleMean,na.rm=TRUE)/10)*10,ceiling(max(Indices$GLMIndex,na.rm
=TRUE)/10)*10)
plot(Indices$Year,Indices$GLMIndex,type='b',col="black",ylim=c(0,maxy),xlab="Year",yla
b=paste("Survey index (crabs.tow)",sep=""),main=selectedstage)
points(Indices$Year,Indices$SimpleMean,pch=16,col='red')

```

```

legend(2001,0.9*maxy,c("GLM Index","Simple Mean"),col=c('black','red'),pch=c(1,16,16))

dev.off()
graphics.off()

##### TO #####
infile<-"DE_Rdata, envgood.csv"

surveydata<-read.csv(paste(indirectory,infile,sep="))

#create data set that only has age 0
selectedstage<-"T0"
surveydata<-surveydata[surveydata$Stage==selectedstage,]

# Check you have the right data
head(surveydata)

Indices<-tapply(surveydata$Count,surveydata$Year,mean)
Year<-as.numeric(rownames(Indices))
Indices<-cbind(Year,Indices)
colnames(Indices)<-c('Year','SimpleMean')

head(Indices)
#Clean up survey data to subset how you wish
glmsdat <- surveydata[,-9]
head(glmsdat)

# C stands for continuous
# F stands for factor
#Column 1: response variable (must be a continuous variable)
#Column 2: [factor that will get jackknifed error estimates, e.g. year]
#Column 3: [2nd explanatory variable] (variables 2-p can be factors or continuous)
#: :
#: :
#Column p: [pth explanatory variable]
#
# cols.bin selects the numbers of the columns to be used inthe presence/absence
# cols.pos selects the numbers of the columns to be used in the abundance estimation - need
not be the same
#1= count
#2 = year
#3 = month
#4 = station
#5 = tow duration
#6 = depth
#7 = temp
#8 = salinity
DEindex<-
dglm(glmsdat,dist="gamma",types=c('C','F','F','F','C','C','C','C'),cols.bin=c(2,3,4,5,7),cols.pos
=c(2,3,4,5,6,7,8),minpos=5,write=F,J=FALSE)

```



```

GLM<-
as.data.frame(cbind(rownames(DEindex$deltaGLM.index),DEindex$deltaGLM.index))

#use if you are not jack knifing
colnames(GLM)<-c('Year','GLMIndex')
#use if you are jack knifing
#colnames(GLM)<-c('Year','GLMIndex','Jack.Mean','SE1','Jack.cv')
AIC[,1]<-deltagamma.summary$aic
Indices<-merge(Indices,GLM,by="Year",all.x=TRUE)

#write output
write.csv(Indices,file=paste(outdirectoryResults,selectedstage,"Indices.csv",sep=""),append=
FALSE)
write.csv(AIC,file=paste(outdirectoryResults,selectedstage,"AIC.csv",sep=""),append=FALS
E)

# plot results
pdf(file=paste(outdirectoryPlot,selectedstage,".pdf",sep=""),onefile=TRUE)
#tiff(file=paste(outdirectoryPlot,selectedstage,".tif",sep=""))
maxy =
ifelse(max(Indices$SimpleMean,na.rm=TRUE)>max(Indices$GLMIndex,na.rm=TRUE),ceiling(
max(Indices$SimpleMean,na.rm=TRUE)/10)*10,ceiling(max(Indices$GLMIndex,na.rm
=TRUE)/10)*10)
plot(Indices$Year,Indices$GLMIndex,type='b',col="black",ylim=c(0,maxy),xlab="Year",yla
b=paste("Survey index (crabs.tow)",sep=""),main=selectedstage)
points(Indices$Year,Indices$SimpleMean,pch=16,col='red')

legend(2001,0.9*maxy,c("GLM Index","Simple Mean"),col=c('black','red'),pch=c(1,16,16))

dev.off()
graphics.off()

```

Appendix B: R Code for Intervention Analyses

R code used to conduct analysis of the significance of reporting interventions on time series of commercial landings using Chesapeake Bay Maryland as an example.

```
rm(list=ls())

library(tseries)
library(forecast)

#read data file in
annualMD<-read.csv("C:/Users/Amanda/My Documents/CBL/bc stock assessment/data for
interventions/annual landings/MD_landings.csv", header=T, sep="," , dec=".")
year<-annualMD[,1]
pounds<-annualMD[,2]
tons<-annualMD[,3]

#create variables
tspounds<-ts(pounds,start=1950, end=2009, freq=1)
tstons<-ts(tons,start=1950, end=2009, freq=1)

#plot time series
x <- year
y1 <- tstons
y2 <- tspounds
par(mar=c(5,4,3,5)+.1)
plot(x,y1,type="l",col="black", ylim=c(0,30), xlab="Year", ylab="MT/1000")
par(new=TRUE)
plot(x, y2,type="l",col="",xaxt="n",yaxt="n",xlab="",ylab="",ylim=c(0,66138678.6))
axis(4)
mtext("Pounds",side=4,line=3)

#Difference Time Series
diftons<-diff(tstons)
mean(diftons)
sd(diftons)
ts.plot(diftons,type="l",col="black", ylim=c(-10,15), xlab="Year", ylab="MT/1000")

op<-par(mfrow=c(2,2))
acf(tstons, main="MD ACF")
pacf(tstons, main="MD PACF")
acf(diftons, main="MD Differenced ACF")
pacf(diftons, main="MD Differenced PACF")
par(op)

#use auto.arima function in order to know what order leads to best model
auto.arima(tstons,d=1,D=NA)

# fixed intervention at 1981
#create 0,1 vector
```

```

X1<-rep(1,60)
X1[32:length(tspounds)]<-0

#run intervention analysis
MDmodelxreg<-arima(tspounds,order=c(0,1,1),xreg=X1,method="ML")
summary(MDmodelxreg)
MDmodelxregt<-arima(tstons,order=c(0,1,1),xreg=X1,method="ML")
summary(MDmodelxregt)

fitt<-tstons+MDmodelxregt$residuals
fit<-tspounds+MDmodelxreg$residuals
adj<-MDmodelxreg$coef[2]*X1
corrected_ts<-tspounds-adj
corrected_tstons<-(corrected_ts*0.00045359237)/1000
mean(corrected_tstons)
sd(corrected_tstons)

#ARIMA model for corrected data
auto.arima(corrected_ts,d=1,D=NA)
MDauto<-arima(corrected_ts,order=c(0,1,1))
AIC(MDauto)
tsdiag(MDauto)
plot(corrected_ts,type='p', ylim=c(0,77161791.7))
fitauto<-corrected_ts+MDauto$residuals
lines(fitauto, col='blue')

#corrected with fit
par(mar=c(5,4,4,5)+.1)
x <- year
y1 <- corrected_tstons
y2 <- fitauto
par(mar=c(5,4,4,5)+.1)
plot(x,y1,type="p",col="black", ylim=c(0,35), xlab="Year", ylab="MT/1000")
par(new=TRUE)
plot(x, y2,type="l",col="black",xaxt="n",yaxt="n",xlab="",ylab="",ylim=c(0,77161791.7))
axis(4)
mtext("Pounds",side=4,line=3)

#raw and corrected with fit
x <- year
y1 <- tstons
y2 <- corrected_ts
par(mar=c(5,4,4,5)+.1)
plot(x,y1,type="p",col="black", ylim=c(0,35), xlab="Year", ylab="MT/1000")
lines(fitt)
par(new=TRUE)
plot(x, y2,type="p",col="gray47",xaxt="n",yaxt="n",xlab="",ylab="",ylim=c(0,77161791.7))
lines(fitauto,col="gray47")
axis(4)
mtext("Pounds",side=4,line=3)
abline("v"=c(1981),lty=c(2,2))

```

Appendix C: ADMB Codes and Data Sets

ADMB codes and data sets for a) Delaware Bay b) Chesapeake Bay c) coastal Maryland and Virginia d) North Carolina e) South Carolina f) Georgia g) Florida.

a) Delaware Bay

ADMB Code:

```
//Delaware Bay catch survey model
//A.R. Colton
//DATE 5/18/2011
//Delaware Bay catch survey model
```

TOP_OF_MAIN_SECTION

```
//increase number of estimated parameters
gradient_structure::set_NUM_DEPENDENT_VARIABLES(1000);
gradient_structure::set_GRADSTACK_BUFFER_SIZE(200040);
gradient_structure::set_CMPDIF_BUFFER_SIZE(1000000);
arrmbldsize = 10000000;
```

DATA_SECTION

```
//READ IN DATA HERE
init_int fyear //first year of model
init_int lyear //last year of model
```

//Catch Data

```
init_int ftcyear //first year of total catch
init_int ltcyear // last year of total catch
init_vector com_TC_obs(ftcyear,ltcyear) //total catch
```

//Delaware Survey Data

```
init_int fdeyear //first year of DE survey
init_int ldeyear //last year of DE survey
init_vector Ia_DEobs(fdeyear,ldeyear) //adult DE
init_vector Ir_DEobs(fdeyear,ldeyear) //juv. DE
init_number Ia_DEsd
init_number Ir_DEsd
```

//New Jersey Survey Data

```
init_int fnjyear //first year of NJ survey
init_int lnjyear //last year of NJ survey
init_vector Ia_NJobs(fnjyear,lnjyear) //adult NJ
init_vector Ir_NJobs(fnjyear,lnjyear) //juv. NJ
```

```

init_number Ia_NJsd
init_number Ir_NJsd

//Natural Mortality
init_number set_M //initial mortality for juveniles then adults

//proportion of recreational harvest
init_number p_rec

init_int test //EOF number

//Total Harvest including rec
init_vector TC_obs(ftcyear,ltcyear) //total catch
int y //looping variable for year

LOCAL_CALCS
if (test!=12345)
{
cout<<"Data not reading properly"<<endl;
cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
cout<<"ftcyear,ltcyear:"<<ftcyear<<","<<ltcyear<<endl;
cout<<"Total Catch"<<endl<<TC_obs<<endl;
cout<<"fdeyear,ldeyear:"<<fdeyear<<","<<ldeyear<<endl;
cout<<"fnjyear,lnjyear:"<<fnjyear<<","<<lnjyear<<endl;
cout<<"Adult DE survey indices"<<endl<<Ia_DEobs<<endl;
cout<<"Juv DE survey indices"<<endl<<Ir_DEobs<<endl;
cout<<"Adult NJ survey indices"<<endl<<Ia_NJjobs<<endl;
cout<<"Juv NJ survey indices"<<endl<<Ir_NJjobs<<endl;
cout<<"M:"<<set_M<<endl;
cout<<"EOF test:"<<test<<endl;
exit(1);
}

//Calculate Total Catch
TC_obs=com_TC_obs*(1.+p_rec); //commercial + rec catch

END_CALCS

PARAMETER_SECTION
init_bounded_number log_N(0.,20.,1) //log initial adult abundance
init_bounded_number log_mean_R(0.,20.,1) //log mean recruitment
init_bounded_dev_vector log_R_devs(fyear,lyear,-20.,20.,1) //log recruitment
deviations

```

```

number pen //penalty function for N
number qa_DE //Age 1+ catchability
number qr_DE //age-0 catchability
number qa_NJ //Age 1+ catchability
number qr_NJ //age-0 catchability

vector N(fyear,lyear)
vector R(fyear,lyear)
vector F(fyear,lyear)
vector C_est(fyear,lyear)
vector N_DE(fdeyear,ldeyear)
vector R_DE(fdeyear,ldeyear)
vector N_NJ(fnjyear,lnjyear)
vector R_NJ(fnjyear,lnjyear)
vector Ia_DEest(fdeyear,ldeyear) //index of DE adults
vector Ir_DEest(fdeyear,ldeyear) //index of DE recruits
vector Ia_NJest(fnjyear,lnjyear) //index of NJ adults
vector Ir_NJest(fnjyear,lnjyear) //index of NJ recruits
vector u(fyear,lyear)
number ubar

//Likelihoods
number La_DE
number Lr_DE
number La_NJ
number Lr_NJ
number u_prior
objective_function_value NegLL

LOCAL_CALCS
//Set initial parameter values
log_N=4.5;
log_mean_R=4.5;

END_CALCS
PROCEDURE_SECTION
//fill in recruitment
R=exp(log_mean_R+log_R_devs);

//Fill in first year of adult abundance
N(fyear)=exp(log_N);
//Fill in rest of years abundance
pen=.0;
for(y=fyear;y<lyear;y++)

```

```

{
  N(y+1)=((N(y)+R(y))*exp(-set_M/2.))-TC_obs(y))*exp(-set_M/2.);
  if (N(y+1)<=.0)
  {
    pen+=square(N(y+1));
    N(y+1)=1;
  }
}

for(y=fyear;y<=lyear;y++)
{
  u(y)=TC_obs(y)/((N(y)+R(y))*exp(-set_M/2.));
}
ubar=sum(u)/double(lyear-fyear+1);

//incorporate timing of the surveys
N_DE=(N*exp(-set_M/2.));
R_DE=(R*exp(-2.*set_M/3.));
N_NJ=(N(fnjyear,lnjyear)*exp(-set_M/2.));
R_NJ=(R(fnjyear,lnjyear)*exp(-set_M/2.));

//calculate catchability
qa_DE=exp(sum(log(Ia_DEobs)-log(N_DE))/double(ldeyear-fdeyear+1));
qr_DE=exp(sum(log(Ir_DEobs)-log(R_DE))/double(ldeyear-fdeyear+1));
qa_NJ=exp(sum(log(Ia_NJobs)-log(N_NJ(fnjyear,lnjyear)))/double(lnjyear-fnjyear+1));
qr_NJ=exp(sum(log(Ir_NJobs)-log(R_NJ(fnjyear,lnjyear)))/double(lnjyear-fnjyear+1));

//calculate indices
Ia_DEest=qa_DE*N_DE;
Ir_DEest=qr_DE*R_DE;
Ia_NJest=qa_NJ*N_NJ;
Ir_NJest=qr_NJ*R_NJ;

//calculate likelihood
//lognormal likelihood for indices of abundance
La_DE=double(ldeyear-fdeyear+1)*log(Ia_DEsd)+0.5*norm2(log(Ia_DEobs)-
log(Ia_DEest))/square(Ia_DEsd);
Lr_DE=double(ldeyear-fdeyear+1)*log(Ir_DEsd)+0.5*norm2(log(Ir_DEobs)-
log(Ir_DEest))/square(Ir_DEsd);
La_NJ=double(lnjyear-fnjyear+1)*log(Ia_NJsd)+0.5*norm2(log(Ia_NJobs)-
log(Ia_NJest))/square(Ia_NJsd);
Lr_NJ=double(lnjyear-fnjyear+1)*log(Ir_NJsd)+0.5*norm2(log(Ir_NJobs)-
log(Ir_NJest))/square(Ir_NJsd);

```

```

//implement beta distribution prior on u
//prior=-(alpha-1)*log(u)-(beta-1)*log(1-u)
u_prior=-(4.-1.)*log(ubar)-(4.-1.)*log(1.-ubar);

//calculate overall negative log likelihood
NegLL=La_DE+Lr_DE+La_NJ+Lr_NJ+u_prior+pen;

```

REPORT_SECTION

```

report << "Beginning of report section" << endl;
report << "Likelihood components" << endl;
report << "La_DE" << endl;
report << La_DE << endl;
report << "La_NJ" << endl;
report << La_NJ << endl;
report << "Lr_DE" << endl << Lr_DE <<endl;
report << "Lr_NJ" << endl << Lr_NJ <<endl;
report << "NegLL" << " " << NegLL <<endl;
report << "pen" << endl << pen <<endl;
report << endl;
report << "CVs for indices of abundance" << endl;
report <<Ia_DEsd << " " << Ir_DEsd << endl;
report <<Ia_NJsd << " " << Ir_NJsd << endl;
report << "M" << endl;
report << set_M << endl;
report << "Adult catchability" << endl;
report << qa_DE << " " << qa_NJ << endl;
report << "recruit catchability" << endl;
report << qr_DE << " " << qr_NJ << endl;
report << "Year Adult_N Rec_N u log_R_devs" << endl;
for(y=fyear;y<=lyear;y++)
{
  report << y << " " << N(y) << " " << R(y) << " " << u(y) << " " << log_R_devs(y) <<
endl;
}

report << "Year DEadult_est DEadult_obs DEjuv_est DEjuv_obs " << endl;
for(y=fdeyear;y<=ldeyear;y++)
{
  report << y << " " << Ia_DEest(y) << " " << Ia_DEobs(y) << " " << Ir_DEest(y) << "
" << Ir_DEobs(y) << endl;
}

report << "Year NJadult_est NJadult_obs NJjuv_est NJjuv_obs " << endl;
for(y=fnjyear;y<=lnjyear;y++)

```



```
{
  report << y << " " << Ia_NJest(y) << " " << Ia_NJobs(y) << " " << Ir_NJest(y) << " "
  << Ir_NJobs(y) << endl;
}
```

RUNTIME_SECTION

```
maximum_function_evaluations 5000, 25000, 20000, 20000, 20000, 20000
//leave empty line below here
```

Dataset:

#Data File

#Del. Bay stock assessment model

#uses 2 surves and 1 catch time series

#first, last year of model

1978 2008

#first year of total catch

1978

#last year of total catch

2008

#Total Commercial Catch (in millions of crabs)

0.8733584

1.5030455

5.14987734

2.3411212

2.38203544

2.827862

2.82706698

6.421395851

6.987045606

8.260991942

8.415398943

11.42443915

15.92609712

12.8696261

13.53733363

14.02895671

13.49463493

17.57317735

19.12402915

24.2715471

30.78114317

29.66026436

24.85336232

24.17562734

26.23762445

18.61861232

25.83152793

34.7559231
33.15481436
35.95982888
34.62286507

first year of DE survey
1978

last year of DE survey
2008

#Adult DE indices

2.088409766
1.584472413
2.879280892
2.235380553
0.468002847
0.323757932
1.283563038
3.141503006
4.785447203
3.001896586
3.767171655
6.979898878
4.438295444
3.274151226
7.953354305
4.643687491
10.32544121
7.351884636
3.103742291
4.840963568
5.80742655
4.353183313
3.745915795
3.482804628
7.939300563
0.937500886
1.67065431
2.062515699
1.455564703
3.335898814
2.589587826

#Juv DE indices

8.132304821
0.416688455
21.35010227
3.541861879
0.209602122
2.61004003

10.47094922
223.7332213
3.827374624
28.36271877
25.14727109
77.27246583
1.415974055
71.05471196
14.5643682
83.22147731
44.15626238
21.27794689
40.55169493
50.97499318
14.96208068
36.46274494
8.900551978
13.95556406
6.170230663
19.96166352
36.03282721
17.90602793
45.52775969
42.37413824
7.187182533

DE adult SD, juv SD
0.15 0.33

first year of NJ survey
1991

Last year of NJ survey
2008

#adult NJ indices
0.56128244
1.333836958
1.256189394
2.42574893
2.828910377
1.417694204
3.194956426
4.303387013
2.553910364
3.261880749
5.035614357
2.943578359
0.464632084
1.754069355
5.136946195

3.832762573
5.454252546
4.423986308

#juv NJ indices

3.209046697
2.062053791
7.309427268
4.730727162
8.478536073
5.308130992
10.60391697
9.222064069
6.74707607
5.616531576
8.083881491
4.307010215
0.931190408
0.874239791
12.64145096
12.2029834
13.06628825
6.597742075

NJ SD adults, juv

0.27 0.3

M

0.8

proportion of rec harvest

0.12

#EOF number

12345

b) Chesapeake Bay

ADMB code:

```
//Chesapeake Bay catch survey model
//A.R. Colton
//DATE 6/9/2011
//Chesapeake Bay catch survey model

TOP_OF_MAIN_SECTION
//increase number of estimated parameters
gradient_structure::set_NUM_DEPENDENT_VARIABLES(1000);
gradient_structure::set_GRADSTACK_BUFFER_SIZE(200040);
gradient_structure::set_CMPDIF_BUFFER_SIZE(1000000);
arrmblsize = 10000000;

DATA_SECTION
//READ IN DATA HERE
init_int fyear //first year of model
init_int lyear //last year of model

//Catch Data
init_int ftcyear //first year of total catch
init_int ltcyear // last year of total catch
init_vector com_TC_obs(ftcyear,ltcyear) //total catch

//Virginia Survey Data
init_int fvayear //first year of VA survey
init_int lvayear //last year of VA survey
init_vector Ia_VAobs(fvayear,lvayear) //adult VA
init_vector Ir_VAobs(fvayear,lvayear) //juv. VA
init_number Ia_VAsd
init_number Ir_VAsd

//Maryland Survey Data
init_int fmdyear //first year of MD survey
init_int lmdyear //last year of MD survey
init_vector Ia_MDobs(fmdyear,lmdyear) //adult MD
init_vector Ir_MDobs(fmdyear,lmdyear) //juv. MD
init_number Ia_MDsd
init_number Ir_MDsd

//WinterDredge Survey Data
init_int fwdyear //first year of winter dredge survey
init_int lwdyear //last year of winter dredge survey
init_vector Ia_WDobs(fwdyear,lwdyear) //adult winter dredge
init_vector Ir_WDobs(fwdyear,lwdyear) //juv. winter dredge
init_number Ia_WDsd
init_number Ir_WDsd
init_number qa_WD

//ChesMMAP Survey Data
```

```

init_int fchesyear //first year of ChesMMAP survey
init_int lchesyear //last year of ChesMMAP survey
init_vector Ia_chesobs(fchesyear,lchesyear) //adult CHesMMAP
init_number Ia_chessd

//Natural Mortality
init_number set_M

//proportion of recreational harvest
init_number p_rec

init_int test //EOF number

//Total Harvest including rec
init_vector TC_obs(ftcyear,lscyyear) //total catch

int y //looping variable for year

LOCAL_CALCS
if (test!=12345)
{
cout<<"Data not reading properly"<<endl;
cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
cout<<"ftcyear,lscyyear:"<<ftcyear<<","<<lscyyear<<endl;
cout<<"Total Catch"<<endl<<TC_obs<<endl;
cout<<"fvayear,lvayear:"<<fvayear<<","<<lvayear<<endl;
cout<<"fnjyear,lnjyear:"<<fmdyear<<","<<lmdyear<<endl;
cout<<"Adult VA survey indices"<<endl<<Ia_VAobs<<endl;
cout<<"Juv VA survey indices"<<endl<<Ir_VAobs<<endl;
cout<<"Adult MD survey indices"<<endl<<Ia_MDobs<<endl;
cout<<"Juv MD survey indices"<<endl<<Ir_MDobs<<endl;
cout<<"Adult dredge survey indices"<<endl<<Ia_WDobs<<endl;
cout<<"Juv dredge survey indices"<<endl<<Ir_WDobs<<endl;
cout<<"Adult ChesMMAP survey indices"<<endl<<Ia_chesobs<<endl;
cout<<"M:"<<set_M<<endl;
cout<<"EOF test:"<<test<<endl;
exit(1);
}

//Calculate Total Catch
TC_obs=com_TC_obs*(1.+p_rec); //commercial + rec catch
//cout<<"0"<<endl;
END_CALCS

PARAMETER_SECTION
init_bounded_number log_N(0.,20.,1) //log initial adult abundance
init_bounded_number log_mean_R(0.,20.,1) //log mean recruitment
init_bounded_dev_vector log_R_devs(fyear,lyear,-20.,20.,1) //log recruitment deviations

number pen //penalty function for N
number qa_VA //Age 1+ catchability

```

```

number qr_VA //age-0 catchability
number qa_MD //Age 1+ catchabilty
number qr_MD //age-0 catchability
number qr_WD //age-0 catchability
number qa_ches //Age 1+ catchabilty

vector N(fyear,lyear)
vector R(fyear,lyear)
vector N_VA(fvayear,lvayear)
vector R_VA(fvayear,lvayear)
vector N_MD(fmdyear,lmdyear)
vector R_MD(fmdyear,lmdyear)
vector N_WD(fwdyear,lwdyear)
vector R_WD(fwdyear,lwdyear)
vector N_ches(fchesyear,lchesyear)
vector Ia_VAest(fvayear,lvayear) //index of VA adults
vector Ir_VAest(fvayear,lvayear) //index of VA recruits
vector Ia_MDest(fmdyear,lmdyear) //index of MD adults
vector Ir_MDest(fmdyear,lmdyear) //index of MD recruits
vector Ia_WDest(fwdyear,lwdyear) //index of dredge adults
vector Ir_WDest(fwdyear,lwdyear) //index of dredge recruits
vector Ia_chesest(fchesyear,lchesyear) //index of ChesMAPP adults
vector u(fyear,lyear)
number ubar

//Likelihoods
number La_VA
number Lr_VA
number La_MD
number Lr_MD
number La_WD
number Lr_WD
number La_CHES
number u_prior
objective_function_value NegLL

LOCAL_CALCS
//Set initial parameter values
log_N=6.;
log_mean_R=7.;

END_CALCS
PROCEDURE_SECTION
//fill in recruitment
R=exp(log_mean_R+log_R_devs);

//Fill in first year of adult abundance
N(fyear)=exp(log_N);
//Fill in rest of years abundance
pen=.0;
for(y=fyear;y<lyear;y++)

```

```

{
  N(y+1)=(N(y)+R(y))*exp(-(set_M/2.))-TC_obs(y))*exp(-(set_M/2.));
  if (N(y+1)<=.0)
  {
    pen+=square(N(y+1));
    N(y+1)=1;
  }
}
for(y=fyear;y<=lyear;y++)
{
  u(y)=TC_obs(y)/((N(y)+R(y))*exp(-set_M/2.));
}
ubar=sum(u)/double(lyear-fyear+1);

//incorporate timing of the surveys
N_VA=(N);
R_VA=(R);
N_MD=(N(fmdyear,lmdyear)*exp(-(set_M/2.)));
R_MD=(R(fmdyear,lmdyear)*exp(-(3*set_M/4.)));
N_WD=(N(fwdyear,lwdyear));
R_WD=(R(fwdyear,lwdyear));
N_ches=(N(fchesyear,lchesyear)*exp(-(set_M/2.)));

//calculate catchability
qa_VA=exp(sum(log(Ia_VAobs)-log(N_VA))/double(lvayear-fvayear+1));
qr_VA=exp(sum(log(Ir_VAobs)-log(R_VA))/double(lvayear-fvayear+1));
qa_MD=exp(sum(log(Ia_MDobs)-log(N_MD(fmdyear,lmdyear)))/double(lmdyear-
fmdyear+1));
qr_MD=exp(sum(log(Ir_MDobs)-log(R_MD(fmdyear,lmdyear)))/double(lmdyear-
fmdyear+1));
qr_WD=exp(sum(log(Ir_WDobs)-log(R_WD(fwdyear,lwdyear)))/double(lwdyear-
fwdyear+1));
qa_ches=exp(sum(log(Ia_chesobs)-log(N_ches(fchesyear,lchesyear)))/double(lchesyear-
fchesyear+1));

//calculate indices
Ia_VAest=qa_VA*N_VA;
Ir_VAest=qr_VA*R_VA;
Ia_MDest=qa_MD*N_MD;
Ir_MDest=qr_MD*R_MD;
Ia_WDest=qa_WD*N_WD;
Ir_WDest=qr_WD*R_WD;
Ia_chesest=qa_ches*N_ches;

//calculate likelihood
La_WD=0.;
Lr_WD=0.;
for(y=fwdyear;y<=lwdyear;y++)
{
  La_WD+=log(Ia_WDsd*Ia_WDest(y))+0.5*square(Ia_WDobs(y)-
Ia_WDest(y))/square(Ia_WDsd*Ia_WDest(y));
}

```



```

    Lr_WD+=log(Ir_WDsd*Ir_WDest(y))+0.5*square(Ir_WDobs(y)-
Ir_WDest(y))/square(Ir_WDsd*Ir_WDest(y));
}

//lognormal likelihood for indices of abundance
La_VA=double(lvayear-fvayear+1)*log(Ia_VAsd)+0.5*norm2(log(Ia_VAobs)-
log(Ia_VAest))/square(Ia_VAsd);
Lr_VA=double(lvayear-fvayear+1)*log(Ir_VAsd)+0.5*norm2(log(Ir_VAobs)-
log(Ir_VAest))/square(Ir_VAsd);
La_MD=double(lmdyear-fmdyear+1)*log(Ia_MDsd)+0.5*norm2(log(Ia_MDobs)-
log(Ia_MDest))/square(Ia_MDsd);
Lr_MD=double(lmdyear-fmdyear+1)*log(Ir_MDsd)+0.5*norm2(log(Ir_MDobs)-
log(Ir_MDest))/square(Ir_MDsd);
La_CHES=double(lchesyear-fchesyear+1)*log(Ia_chesd)+0.5*norm2(log(Ia_chesobs)-
log(Ia_chesest))/square(Ia_chesd);
//cout<<"5"<<endl;
u_prior=-(4.-1.)*log(ubar)-(4.-1.)*log(1.-ubar);

//calculate overall negative log likelihood
NegLL=La_VA+Lr_VA+La_MD+Lr_MD+La_WD+Lr_WD+La_CHES+pen+u_prior;

REPORT_SECTION
report << "Beginning of report section" << endl;
report << "Likelihood components" << endl;
report << "La_VA" << endl;
report << La_VA << endl;
report << "La_MD" << endl;
report << La_MD << endl;
report << "La_WD" << endl;
report << La_WD << endl;
report << "La_ches" << endl;
report << La_CHES << endl;
report << "Lr_VA" << endl << Lr_VA <<endl;
report << "Lr_MD" << endl << Lr_MD <<endl;
report << "Lr_WD" << endl << Lr_WD <<endl;
report << "penalty" << endl;
report << "negLL" << endl << NegLL <<endl;
report << pen << endl;
report << endl;
report << "CVs for indices of abundance" << endl;
report <<Ia_VAsd << " " << Ir_VAsd << endl;
report <<Ia_MDsd << " " << Ir_MDsd << endl;
report <<Ia_WDsd << " " << Ir_WDsd << endl;
report <<Ia_chesd << endl;
report << "M" << endl;
report << set_M << endl;
report << "Adult catchability" << endl;
report << qa_VA << " " << qa_MD << " " << qa_WD << " " << qa_ches << endl;
report << "recruit catchability" << endl;
report << qr_VA << " " << qr_MD << " " << qr_WD << " " << endl;

```

```

report << "Year Adult_N Rec_N u" << endl;
for(y=fyear;y<=lyear;y++)
{
  report << y << " " << N(y) << " " << R(y) << " " << u(y) << " " << log_R_devs(y) <<
endl;
}

report << "Year VAadult_est VAadult_obs VAjuv_est VAjuv_obs " << endl;
for(y=fvayear;y<=lvayear;y++)
{
  report << y << " " << Ia_VAest(y) << " " << Ia_VAobs(y) << " " << Ir_VAest(y) << " "
<< Ir_VAobs(y) << endl;
}

report << "Year MDadult_est MDadult_obs MDjuv_est MDjuv_obs " << endl;
for(y=fmdyear;y<=lmdyear;y++)
{
  report << y << " " << Ia_MDest(y) << " " << Ia_MDobs(y) << " " << Ir_MDest(y) << " "
<< Ir_MDobs(y) << endl;
}

report << "Year WDadult_est WDadult_obs WDjuv_est WDjuv_obs " << endl;
for(y=fwdyear;y<=lwdyear;y++)
{
  report << y << " " << Ia_WDest(y) << " " << Ia_WDobs(y) << " " << Ir_WDest(y) << " "
<< Ir_WDobs(y) << endl;
}

report << "Year CHESadult_est CHESadult_obs CHESjuv_est CHESjuv_obs " << endl;
for(y=fchesyear;y<=lchesyear;y++)
{
  report << y << " " << Ia_chesest(y) << " " << Ia_chesobs(y) << endl;
}

```

RUNTIME_SECTION

```

maximum_function_evaluations 5000, 25000, 20000, 20000, 20000, 20000
//leave empty line below here

```

Dataset:

```

# Data File
#Chesapeake Bay stock assessment model
# uses 4 surveys and catch time series

```

```

# first year last year for model
1968 2008
# first year for total catch
1968

```

```

# last year for total catch
2008

```

Total Commercial Catch (in millions of crabs)

353.2649993
359.9548462
389.573118
409.4467322
406.0101668
346.970454
372.4924462
350.9267686
310.4507618
354.8006154
332.690882
370.8803657
362.8139262
402.3281932
373.1398442
387.4893563
385.7836057
393.8614898
353.5517168
325.0414361
337.1333044
363.8055438
403.9210756
393.8681015
274.801405
350.9034322
259.2563982
244.290027
242.5932991
275.2581305
207.2059382
217.9344792
175.0880675
170.220234
171.3021589
155.0371594
184.702237
179.032453
158.9912147
133.1260409
143.1395714

first year of VA survey

1968

last year of VA survey

2008

Adult VA indices (crabs)

3.12

1.65
7.85
10.91
5.7
1.54
1.77
1.55
1.61
2.49
1.79
5.47
3.68
12.93
11.7
11.73
3.9
10.09
5.81
4.67
6.79
8.07
20.9
9.62
3.97
3.1
2.49
3.03
4
2.98
4.35
2.62
2.46
4.12
4.1
1.61
2.61
1.03
1.93
2.42
5.64
Age 0 VA indices (crabs)
0.67
22.01
8.04
84.52
8.42
7.03
3.49
7.96
1.61
3.9

3.07
6.42
2.26
37.77
12.15
45.6
49.35
24.66
11.72
15.09
11.78
14.1
40.24
4.26
3.04
8.14
8.88
4.94
10.35
5.04
4.72
2.6
2
4.46
2.61
2.54
2.8
1.43
1.43
1.69
6.69

VA adult SD, juv SD
0.4 0.8

first year of MD survey
1977

Last year of MD survey
2008

adult indices for MD survey (crabs)
29.29
3.83
2.01
1.76
14.96
8.62
16.08
16.84
26.69

26.34
20.48
14.24
29.35
14.93
28.42
11.84
23.88
20.77
9.05
32.73
22.75
9.55
17.56
10.27
10.93
11.35
6.79
8.2
13.2
11.3
5.98
11.48

age 0 MD survey (crabs)

0.6
0.21
0.29
0.7
0.78
0.36
1.94
6.27
2.57
4.13
1.92
5.23
3.79
14.73
1.32
10.62
4.92
1.16
1.88
2.7
0.93
2.02
4.75
1.78
2.62
2.53

1.93
6.77
6.34
4.67
0.24
5.25

#MD SD adults, juv
0.7 1.1

first year of dredge survey
1990

Last year of dredge survey
2008

adult indices for dredge survey (millions)

344.57872
485.8936
271.54624
366.6468
223.73054
195.14912
244.23328
174.07064
193.36784
90.64736
164.17464
106.67888
124.09584
216.82136
144.28368
163.6382916
124.49168
151.9051715
130.03344

age 0 dredge survey (millions)

468.47664
360.51128
105.78824
507.36792
306.18224
303.90616
512.81072
516.17536
166.94552
225.23296
137.5544
156.95056
196.03976

176.94048
143.29408
244.1617923
195.14912
111.9368564
165.85696

#dredge SD adults, juv
0.1 0.1

#q_WD
1

first year of ChesMAPP survey
2002

Last year of ChesMAPP survey
2008

adult indices for ChesMAPP survey
17.32
15.62
5.78
26.92
31.21
15.76
34.19

#ChesMAPP SD adults
0.4

M
0.9

proportion of rec harvest
0.08

#EOF number
12345

c) Coastal Maryland and Virginia

ADMB code:

```
//coast MD and VA catch survey model
//A.R. Colton
//DATE 6/9/2011
//coastal MD and VA catch survey model

TOP_OF_MAIN_SECTION
//increase number of estimated parameters
gradient_structure::set_NUM_DEPENDENT_VARIABLES(1000);
gradient_structure::set_GRADSTACK_BUFFER_SIZE(200040);
gradient_structure::set_CMPDIF_BUFFER_SIZE(1000000);
arrmblsize = 10000000;

DATA_SECTION
//READ IN DATA HERE
init_int fyear //first year of model
init_int lyear //last year of model

//Catch Data
init_int ftcyear //first year of total catch
init_int ltcyear // last year of total catch
init_vector com_TC_obs(ftcyear,ltcyear) //total catch

//Coast Seine Survey Data
init_int fsyear //first year of seine survey
init_int lsyear //last year of seine survey
init_vector Ia_sobs(fsyear,lsyear) //adults seine
init_vector Ir_sobs(fsyear,lsyear) //juv. seine
init_number Ia_ssd
init_number Ir_ssd

//Coast Trawl Survey Data
init_int ftyear //first year of trawl survey
init_int ltyear //last year of trawl survey
init_vector Ia_tobs(ftyear,ltyear) //adult trawl
init_vector Ir_tobs(ftyear,ltyear) //juv. trawl
init_number Ia_tsd
init_number Ir_tsd

//Natural Mortality
init_number set_M //inital mortality for juveniles then adults

//proportion of recreational harvest
init_number p_rec

init_int test //EOF number

//Total Harvest including rec
init_vector TC_obs(ftcyear,ltcyear) //total catch
```

```

int y //looping variable for year

LOCAL_CALCS
if (test!=12345)
{
cout<<"Data not reading properly"<<endl;
cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
cout<<"ftcyear,ltycyear:"<<ftcyear<<","<<ltcyear<<endl;
cout<<"Total Catch"<<endl<<TC_obs<<endl;
cout<<"fsyear,lsyear:"<<fsyear<<","<<lsyear<<endl;
cout<<"ftyear,ltyear:"<<ftyear<<","<<ltyear<<endl;
cout<<"Adult seine survey indices"<<endl<<Ia_sobs<<endl;
cout<<"Juv seine survey indices"<<endl<<Ir_sobs<<endl;
cout<<"Adult trawl survey indices"<<endl<<Ia_tobs<<endl;
cout<<"Juv trawl survey indices"<<endl<<Ir_tobs<<endl;
cout<<"M:"<<set_M<<endl;
cout<<"EOF test:"<<test<<endl;
exit(1);
}

//Calculate Total Catch
TC_obs=com_TC_obs*(1.+p_rec); //commercial + rec catch

END_CALCS

PARAMETER_SECTION
init_bounded_number log_N(0.,20.,1) //log initial adult abundance
init_bounded_number log_mean_R(0.,20.,1) //log mean recruitment
init_bounded_dev_vector log_R_devs(fyear,lyear,-20.,20.,1) //log recruitment deviations

number qa_s //Age 1+ catchability
number qr_s //age-0 catchability
number qa_t //Age 1+ catchability
number qr_t //age-0 catchability

number pen
vector N(fyear,lyear)
vector R(fyear,lyear)
vector N_s(fsyear,lsyear)
vector R_s(fsyear,lsyear)
vector N_t(ftyear,ltyear)
vector R_t(ftyear,ltyear)
vector Ia_sest(fsyear,lsyear) //index of seine adults
vector Ir_sest(fsyear,lsyear) //index of seine recruits
vector Ia_test(ftyear,ltyear) //index of trawl adults
vector Ir_test(ftyear,ltyear) //index of trawl recruits

vector u(fyear,lyear)
number ubar

//Likelihoods

```

```

number La_s
number Lr_s
number La_t
number Lr_t
number u_prior
objective_function_value NegLL

LOCAL_CALCCS
//Set initial parameter values
log_N=2.;
log_mean_R=2.5;

END_CALCCS
PROCEDURE_SECTION
//fill in recruitment
R=exp(log_mean_R+log_R_devs);

//Fill in first year of adult abundance
N(fyear)=exp(log_N);
//Fill in rest of years abundance
pen=0.;
for(y=fyear;y<lyear;y++)
{
  N(y+1)=((N(y)+R(y))*exp(-set_M/2.))-TC_obs(y)*exp(-set_M/2.);
  if (N(y+1)<=.0)
  {
    pen+=square(N(y+1));
    N(y+1)=1;
  }
}

//calculate u
for(y=fyear;y<=lyear;y++)
{
  u(y)=TC_obs(y)/((N(y)+R(y))*exp(-set_M/2.));
}
ubar=sum(u)/double(lyear-fyear+1);

//incorporate timing of the surveys
N_s=N*exp(-set_M/2.);
R_s=R*exp(-set_M/2.);
N_t=N*exp(-set_M/2.);
R_t=R*exp(-set_M/2.);

//calculate catchability
qa_s=exp(sum(log(Ia_sobs)-log(N_s))/double(lyear-fsyear+1));
qr_s=exp(sum(log(Ir_sobs)-log(R_s))/double(lyear-fsyear+1));
qa_t=exp(sum(log(Ia_tobs)-log(N_t))/double(ltyear-ftyear+1));
qr_t=exp(sum(log(Ir_tobs)-log(R_t))/double(ltyear-ftyear+1));

//calculate indices

```

```

Ia_sest=qa_s*N_s;
Ir_sest=qr_s*R_s;
Ia_test=qa_t*N_t;
Ir_test=qr_t*R_t;

//lognormal likelihood for indices of abundance
La_s=double(lsy-fsyear+1)*log(Ia_ssd)+0.5*norm2(log(Ia_sobs)-
log(Ia_sest))/square(Ia_ssd); //log likelihood
Lr_s=double(lsy-fsyear+1)*log(Ir_ssd)+0.5*norm2(log(Ir_sobs)-
log(Ir_sest))/square(Ir_ssd);
La_t=double(lty-ftyear+1)*log(Ia_tsd)+0.5*norm2(log(Ia_tobs)-
log(Ia_test))/square(Ia_tsd);
Lr_t=double(lty-ftyear+1)*log(Ir_tsd)+0.5*norm2(log(Ir_tobs)-
log(Ir_test))/square(Ir_tsd);
//cout<<"5"<<endl;
u_prior=-(4.-1.)*log(ubar)-(4.-1.)*log(1.-ubar);
//calculate overall negative log likelihood
NegLL=La_s+Lr_s+La_t+Lr_t+u_prior+pen;

REPORT_SECTION
report << "Beginning of report section" << endl;
report << "Likelihood components" << endl;
report << "La_s" << endl;
report << La_s << endl;
report << "La_t" << endl;
report << La_t << endl;
report << "Lr_s" << endl << Lr_s <<endl;
report << "Lr_t" << endl << Lr_t <<endl;
report << "NegLL" << endl << NegLL <<endl;
report << endl;
report << "CVs for indices of abundance" << endl;
report <<Ia_ssd << " " << Ir_ssd << endl;
report <<Ia_tsd << " " << Ir_tsd << endl;
report << "M" << endl;
report << set_M << endl;
report << "Adult catchability" << endl;
report << qa_s << " " << qa_t << endl;
report << "recruit catchability" << endl;
report << qr_s << " " << qr_t << endl;

report << "Year Adult_N Rec_N u" << endl;
for(y=fsyear;y<=lyear;y++)
{
  report << y << " " << N(y) << " " << R(y) << " " << u(y) << " " << log_R_devs(y) <<
endl;
}

report << "Year seineadult_est seineadult_obs seinejuv_est seinejuv_obs " << endl;
for(y=fsyear;y<=lsyear;y++)
{

```

```

    report << y << " " << Ia_sest(y) << " " << Ia_sobs(y) << " " << Ir_sest(y) << " " <<
    Ir_sobs(y) << endl;
  }

  report << "Year trawladult_est trawladult_obs trawljuv_est trawljuv_obs " << endl;
  for(y=ftyear;y<=ltyear;y++)
  {
    report << y << " " << Ia_test(y) << " " << Ia_tobs(y) << " " << Ir_test(y) << " " <<
    Ir_tobs(y) << endl;
  }

```

RUNTIME_SECTION

```

  maximum_function_evaluations 5000, 25000, 20000, 20000, 20000, 20000
  //leave empty line below here

```

DataSet:

```

#Data File
#coastal MD and VA stock assessment model
#uses 1 survey and 1 catch time series

```

```

#first, last year of model
1989 2008

```

```

#first year of total catch
1989

```

```

#last year of total catch
2008

```

```

#Total Commercial Catch (in millions of crabs)

```

```

1.255730438
0.81397934
0.431322641
0.190210909
0.535355498
0.96111018
1.034754
0.802213489
1.285556495
1.066005404
0.920063017
1.273059501
1.416938802
1.143012225
1.05242859
1.401854686
1.509276931
0.960284039
0.993683703
1.051124482

```

```

# first year of seine survey

```

1989

last year of seine survey
2008

#Adult seine indices

14.81264622
10.97121128
6.87077683
11.93467524
7.998839239
8.050989388
8.402164838
13.1089071
8.056086913
5.748555771
7.676744457
7.071638256
8.342543637
5.189979745
6.098174773
7.797921964
8.179316703
5.979799283
6.906486047
5.851970027

#Juv seine indices

32.93167815
9.407134127
9.86254335
11.4002345
19.42313631
14.30318239
10.71462929
8.584000257
7.948180965
15.27974074
15.42031259
15.84453196
11.56849523
10.06580376
8.667098611
8.940967449
9.950469913
8.387987509
8.797581978
5.66534827

seine adult SD, juv SD
0.21 0.22

first year of trawl survey
1989

Last year of trawl survey
2008

#adult trawl indices

5.864967692
8.452417629
6.472109169
6.318818158
7.344587068
10.0319083
11.09577621
12.83330556
7.16110663
5.431676071
7.423611525
8.420751524
9.957423585
7.919534291
10.38017393
10.53520327
11.888821
3.12936708
0.892648532
0.567293179

#juv trawl indices

10.99842548
6.30079455
5.366934483
7.083740181
15.39314448
20.37268796
16.01299781
12.11648165
10.97460982
8.034525803
8.820363766
9.655274348
6.442922584
13.16058735
8.050967392
8.187565158
10.86311705
2.570448909
1.787305405
0.292007103

coast SD adults, juv
0.2 0.2

M
0.9

proportion of rec harvest
0.08

#EOF number
12345

d) North Carolina

ADMB code:

```
//North Carolina catch survey model
//A.R. Colton
//DATE 6/2/2011
//North Carolina catch survey model

TOP_OF_MAIN_SECTION
//increase number of estimated parameters
gradient_structure::set_NUM_DEPENDENT_VARIABLES(1000);
gradient_structure::set_GRADSTACK_BUFFER_SIZE(200040);
gradient_structure::set_CMPDIF_BUFFER_SIZE(1000000);
arrmblsize = 10000000;

DATA_SECTION
//READ IN DATA HERE
init_int fyear //first year of model
init_int lyear //last year of model

//Catch Data
init_int ftcyear //first year of total catch
init_int ltcyear // last year of total catch
init_vector com_TC_obs(ftcyear,ltcyear) //total catch

//North Carolina Survey Data
init_int fncyear //first year of NC survey
init_int lncyear //last year of NC survey
init_vector Ia_NCobs(fncyear,lncyear) //adult NC
init_vector Ir_NCobs(fncyear,lncyear) //juv. NC
init_number Ia_NCsd
init_number Ir_NCsd

//Natural Mortality
init_number set_M //inital mortality for juveniles then adults

//proportion of recreational harvest
init_number p_rec

init_int test //EOF number

//Total Harvest including rec
init_vector TC_obs(ftcyear,ltcyear) //total catch
int y //looping variable for year

LOCAL_CALCS
if (test!=12345)
{
cout<<"Data not reading properly"<<endl;
cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
cout<<"ftcyear,ltcyear:"<<ftcyear<<","<<ltcyear<<endl;
```

```

cout<<"Total Catch"<<endl<<TC_obs<<endl;
cout<<"fncyear,lnyear:"<<fncyear<<","<<lnyear<<endl;
cout<<"Adult NC survey indices"<<endl<<Ia_NCObs<<endl;
cout<<"Juv NC survey indices"<<endl<<Ir_NCObs<<endl;
cout<<"M:"<<set_M<<endl;
cout<<"EOF test:"<<test<<endl;
exit(1);
}

//Calculate Total Catch
TC_obs=com_TC_obs*(1.+p_rec); //commercial + rec catch

END_CALCS

PARAMETER_SECTION
init_bounded_number log_N(0.,20.,1) //log initial adult abundance
init_bounded_number log_mean_R(0.,20.,1) //log mean recruitment
init_bounded_dev_vector log_R_devs(fyear,lyear,-20.,20.,1) //log recruitment deviations

number pen //penalty function for N
number qa_NC //Age 1+ catchability
number qr_NC //age-0 catchability
vector N(fyear,lyear)
vector R(fyear,lyear)
vector N_NC(fncyear,lnyear)
vector R_NC(fncyear,lnyear)
vector Ia_NCest(fncyear,lnyear) //index of NC adults
vector Ir_NCest(fncyear,lnyear) //index of NC recruits

vector u(fyear,lyear)
number ubar

//Likelihoods
number La_NC
number Lr_NC
number u_prior
//number Lc
objective_function_value NegLL

LOCAL_CALCS
//Set initial parameter values
log_N=5.;
log_mean_R=6.;

END_CALCS
PROCEDURE_SECTION
//fill in recruitment
R=exp(log_mean_R+log_R_devs);

//Fill in first year of adult abundance
N(fyear)=exp(log_N);

```

```

//Fill in rest of years abundance
pen=.0;
for(y=fyear;y<lyear;y++)
{
  N(y+1)=((N(y)+R(y))*exp(-(set_M/2.))-TC_obs(y))*exp(-(set_M/2.));
  if (N(y+1)<=.0)
  {
    pen+=square(N(y+1));
    N(y+1)=1;
  }
}

//calculate u
for(y=fyear;y<=lyear;y++)
{
  u(y)=TC_obs(y)/((N(y)+R(y))*exp(-set_M/2.));
}
ubar=sum(u)/double(lyear-fyear+1);

//incorporate timing of the surveys
N_NC=(N);
R_NC=(R);

//calculate catchability
qa_NC=exp(sum(log(Ia_NCobs)-log(N_NC)))/double(lncyear-fncyear+1);
qr_NC=exp(sum(log(Ir_NCobs)-log(R_NC)))/double(lncyear-fncyear+1);

//calculate indices
Ia_NCest=qa_NC*N_NC;
Ir_NCest=qr_NC*R_NC;

//lognormal likelihood for indices of abundance
La_NC=double(lncyear-fncyear+1)*log(Ia_NCsd)+0.5*norm2(log(Ia_NCobs)-
log(Ia_NCest))/square(Ia_NCsd);
Lr_NC=double(lncyear-fncyear+1)*log(Ir_NCsd)+0.5*norm2(log(Ir_NCobs)-
log(Ir_NCest))/square(Ir_NCsd);

//implement beta distribution prior on u
//prior=-(alpha-1)*log(u)-(beta-1)*log(1-u)
u_prior=-(4.-1.)*log(ubar)-(4.-1.)*log(1.-ubar);

//calculate overall negative log likelihood
NegLL=La_NC+Lr_NC+pen+u_prior;

REPORT_SECTION
report << "Beginning of report section" << endl;
report << "Likelihood components" << endl;
report << "La_NC" << endl;
report << La_NC << endl;
report << "Lr_NC" << endl << Lr_NC << endl;
report << "penalty" << " " << pen << endl;

```

```

report << "u_prior" << " " << u_prior << endl;
report << "NEGLL" << " " << NegLL << endl;
report << endl;
report << "CVs for indices of abundance" << endl;
report << Ia_NCsd << " " << Ir_NCsd << endl;
report << "M" << endl;
report << set_M << endl;
report << "Adult catchability" << endl;
report << qa_NC << endl;
report << "recruit catchability" << endl;
report << qr_NC << endl;

report << "Year Adult_N Rec_N u" << endl;
for(y=fyear;y<=lyear;y++)
{
  report << y << " " << N(y) << " " << R(y) << " " << u(y) << " " << log_R_devs(y) <<
endl;
}

report << "Year NCadult_est NCadult_obs NCjuv_est NCjuv_obs " << endl;
for(y=fncyear;y<=lncyear;y++)
{
  report << y << " " << Ia_NCest(y) << " " << Ia_NCobs(y) << " " << Ir_NCest(y) << " " <<
Ir_NCobs(y) << endl;
}

RUNTIME_SECTION
  maximum_function_evaluations 5000, 25000, 20000, 20000, 20000, 20000
//leave empty line below here

DataSet:
#Data File
#North Carolina stock assessment model
#1 survey and 1 catch time series

#first, last year for model
1978 2008

#first, last year for total catch
1978 2008

#Total Commercial Catch (in millions of crabs)
67.64640606
77.47366061
101.1851333
113.7423758
113.4296788
102.282703
97.0106
87.9104
71.07474545

```

96.94073636
105.8893455
103.8617939
114.5744576
125.7750848
122.0914939
131.985103
159.9715679
139.6466273
202.0373789
168.6545579
186.066463
173.238384
122.1626497
96.3345374
113.0537406
128.3861055
102.7271016
76.77076566
76.54629186
64.69411183
99.43208315

#first, last year of NC survey
1978 2008

#Adult NC indices

0.914912538
1.525000129
1.152582468
2.192013031
1.898866992
1.399733677
1.61057996
2.129761359
1.509043795
1.366566362
1.461547659
0.74262998
1.827956727
1.6204293
1.129674623
0.888388519
1.256589387
1.204690557
2.469296428
1.649314856
1.35775037
2.56535607
1.276281349
1.264667707

1.790884633
0.763980034
1.816547839
0.952481049
1.52800682
0.67031337
1.608120499

#Age 0 NC indices

2.533380722
2.878488624
3.366388485
5.836850833
5.419294188
4.997892094
5.582331583
5.95419426
2.941629145
5.144781766
5.616085123
2.75811171
3.762420027
2.337096006
2.460793412
4.369226558
4.340990772
4.957548562
7.320624432
5.829072018
3.084145891
6.156426237
2.454515677
4.048424979
6.005449438
2.960141088
5.66345448
3.966640278
4.230760939
3.539749943
5.124939706

#NC adult, recruit SD

0.14 0.31

#M (from stock assessment)

0.87

proportion of rec harvest

0.01

#EOF number

12345

e) South Carolina

ADMB code:

```
//South Carolina catch survey model
//A.R. Colton
//DATE 6/2/2011
//South Carolina catch survey model

TOP_OF_MAIN_SECTION
//increase number of estimated parameters
gradient_structure::set_NUM_DEPENDENT_VARIABLES(1000);
gradient_structure::set_GRADSTACK_BUFFER_SIZE(200040);
gradient_structure::set_CMPDIF_BUFFER_SIZE(1000000);
arrmblsize = 10000000;

DATA_SECTION
//READ IN DATA HERE
init_int fyear //first year of model
init_int lyear //last year of model

//Catch Data
init_int ftcyear //first year of total catch
init_int ltcyear // last year of total catch
init_vector com_TC_obs(ftcyear,ltcyear) //total catch

//North Carolina Survey Data
init_int fscyear //first year of SC survey
init_int lscyear //last year of SC survey
init_vector Ia_SCobs(fscyear,lscyear) //adult SC
init_vector Ir_SCobs(fscyear,lscyear) //juv. SC
init_number Ia_SCsd
init_number Ir_SCsd

//Natural Mortality
init_number set_M

//proportion of recreational harvest
init_number p_rec

init_int test //EOF number

//Total Harvest including rec
init_vector TC_obs(ftcyear,ltcyear) //total catch
int y //looping variable for year

LOCAL_CALCS
if (test!=12345)
{
cout<<"Data not reading properly"<<endl;
cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
```

```

cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
cout<<"Total Catch"<<endl<<TC_obs<<endl;
cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
cout<<"Adult SC survey indices"<<endl<<Ia_SCobs<<endl;
cout<<"Juv SC survey indices"<<endl<<Ir_SCobs<<endl;
cout<<"M:"<<set_M<<endl;
cout<<"EOF test:"<<test<<endl;
exit(1);
}

//Calculate Total Catch
TC_obs=com_TC_obs*(1+p_rec); //commercial + rec catch
END_CALCS

PARAMETER_SECTION
init_bounded_number log_N(0.,20.,1) //log initial adult abundance
init_bounded_number log_mean_R(0.,20.,1) //log mean recruitment
init_bounded_dev_vector log_R_devs(fyear,lyear,-20.,20.,1) //log recruitment deviations

number pen //penalty function for N
number qa_SC //Age 1+ catchability
number qr_SC //age-0 catchability
vector N(fyear,lyear)
vector R(fyear,lyear)
vector N_SC(fyear,lyear)
vector R_SC(fyear,lyear)
vector Ia_SCest(fyear,lyear) //index of SC adults
vector Ir_SCest(fyear,lyear) //index of SC recruits
vector u(fyear,lyear)
number ubar

//Likelihoods
number La_SC
number Lr_SC
number u_prior
objective_function_value NegLL

LOCAL_CALCS
//Set initial parameter values
log_N=4.5;
log_mean_R=5.;

END_CALCS

PROCEDURE_SECTION
//fill in recruitment
R=exp(log_mean_R+log_R_devs);

//Fill in first year of adult abundance
N(fyear)=exp(log_N);

```



```

//Fill in rest of years abundance
pen=.0;
for(y=fyear;y<lyear;y++)
{
  N(y+1)=((N(y)+R(y))*exp(-set_M/2.))-TC_obs(y))*exp(-set_M/2.);
  if (N(y+1)<=.0)
  {
    pen+=square(N(y+1));
    N(y+1)=1;
  }
}

//calculate u
for(y=fyear;y<=lyear;y++)
{
  u(y)=TC_obs(y)/((N(y)+R(y))*exp(-set_M/2.));
}
ubar=sum(u)/double(lyear-fyear+1);

//incorporate timing of the surveys
N_SC=(N*exp(-(set_M/2.)));
R_SC=(R*exp(-(set_M/2.)));

//cout<<"2"<<endl;
//calculate catchability
qa_SC=exp(sum(log(Ia_SCobs)-log(N_SC))/double(lscyear-fscyear+1));
qr_SC=exp(sum(log(Ir_SCobs)-log(R_SC))/double(lscyear-fscyear+1));

//calculate indices
Ia_SCest=qa_SC*N_SC;
Ir_SCest=qr_SC*R_SC;

//calculate likelihood
//lognormal likelihood for indices of abundance
La_SC=double(lscyear-fscyear+1)*log(Ia_SCsd)+0.5*norm2(log(Ia_SCobs)-
log(Ia_SCest))/square(Ia_SCsd);
Lr_SC=double(lscyear-fscyear+1)*log(Ir_SCsd)+0.5*norm2(log(Ir_SCobs)-
log(Ir_SCest))/square(Ir_SCsd);

//implement beta distribution prior on u
//prior=-(alpha-1)*log(u)-(beta-1)*log(1-u)
u_prior=-(4.-1.)*log(ubar)-(4.-1.)*log(1.-ubar);

//calculate overall negative log likelihood
NegLL=La_SC+Lr_SC+u_prior+pen;

REPORT_SECTION
report << "Beginning of report section" << endl;
report << "Likelihood components" << endl;
report << "La_SC" << endl;
report << La_SC << endl;

```

```

report << "Lr_SC" << endl << Lr_SC <<endl;
report << "pen" << endl << pen << endl;
report << "u_prior" << endl << u_prior << endl;
report << "negLL" << endl << NegLL << endl;
report << endl;
report << "CVs for indices of abundance" << endl;
report <<Ia_SCsd << " " << Ir_SCsd << endl;
report << "M" << endl;
report << set_M << endl;
report << "Adult catchability" << endl;
report << qa_SC<< endl;
report << "recruit catchability" << endl;
report << qr_SC << endl;

report << "Year Adult_N Rec_N u" << endl;
for(y=fyear;y<=lyear;y++)
{
  report << y << " " << N(y) << " " << R(y) << " " <<u(y) << " " << log_R_devs(y) << endl;
}

report << "Year SCadult_est SCadult_obs SCjuv_est SCjuv_obs " << endl;
for(y=fscopy;y<=lscopy;y++)
{
  report << y << " " << Ia_SCest(y) << " " << Ia_SCobs(y) << " " << Ir_SCest(y) << " " <<
Ir_SCobs(y) << endl;
}

RUNTIME_SECTION
  maximum_function_evaluations 5000, 25000, 20000, 20000, 20000, 20000
//leave empty line below here

DataSet:
#Data File
#South Carolina stock assessment model
#1 survey and 1 catch time series

#first, last year for model
1979 2008

#first, last year for total catch
1979 2008

#Total Commercial Catch (in millions of crabs)
15.46889799
12.43814999
12.24412999
12.62901299
11.19549399
8.473985991
8.912343992
12.05003799

```

10.85855799
13.81072999
11.53505599
10.45936199
11.00053999
14.50406999
12.53724199
14.39159599
14.09217599
11.87846349
12.46066599
15.10907999
13.15866949
11.51961999
11.05867549
9.037670494
8.756011493
9.361771493
8.904629993
8.459598995
8.312516492
8.992739494

#first, last year of NC survey
1979 2008

#Adult SC indices

9.460865643
6.145052703
13.58359762
5.230808442
5.106242168
9.225080948
11.46409617
21.16090567
24.8198927
17.10432121
10.08027096
14.8865067
13.83846405
25.28770754
13.47933312
14.39820858
9.18062924
15.48720242
7.18963477
3.749210059
6.7845775
12.20942087
15.07576887
0.809663225

1.380223777
5.006404597
5.44099695
4.390805235
4.181245817
4.50577166

#Age 0 SC indices

1.420229067
1.876212885
2.611416521
1.15507631
1.528667537
1.076462911
3.42839139
5.768099464
4.75307813
4.027711218
2.635755141
2.863858619
2.562006357
3.32104457
4.018019428
6.184525865
1.740677471
5.267269825
2.463409016
0.562780599
0.833957862
0.59114174
1.003702508
1.209846612
1.307788514
2.134979865
2.492860205
2.285368947
1.703888042
1.586887404

#SC adult, recruit SD

0.16 0.21

#M (from stock assessment)

0.8

proportion of rec harvest

0.12

#EOF number

12345

e) Georgia

ADMB code:

```
//Georgia catch survey model
//A.R. Colton
//DATE 6/11/2011
//Georgia catch survey model

TOP_OF_MAIN_SECTION
//increase number of estimated parameters
gradient_structure::set_NUM_DEPENDENT_VARIABLES(1000);
gradient_structure::set_GRADSTACK_BUFFER_SIZE(200040);
gradient_structure::set_CMPDIF_BUFFER_SIZE(1000000);
armblsize = 10000000;

DATA_SECTION
//READ IN DATA HERE
init_int fyear //first year of model
init_int lyear //last year of model

//Catch Data
init_int ftcyear //first year of total catch
init_int ltcyear // last year of total catch
init_vector com_TC_obs(ftcyear,ltcyear) //total catch

//Georgia Survey Data
init_int fgayear //first year of GA survey
init_int lgayear //last year of GA survey
init_vector Ia_GAobs(fgayear,lgayear) //adult GA
init_vector Ir_GAobs(fgayear,lgayear) //juv. GA
init_number Ia_GAsd
init_number Ir_GAsd

//Natural Mortality
init_number set_M //inital mortality for juveniles then adults

//proportion of recreational harvest
init_number p_rec

init_int test //EOF number

//Total Harvest including rec
init_vector TC_obs(ftcyear,ltcyear) //total catch
int y //looping variable for year

LOCAL_CALCS
if (test!=12345)
{
```

```

cout<<"Data not reading properly"<<endl;
cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
cout<<"ftcyear,lctyear:"<<ftcyear<<","<<lctyear<<endl;
cout<<"Total Catch"<<endl<<TC_obs<<endl;
cout<<"SD of catch:"<<C_sds<<endl;
cout<<"fgayear,lgayear:"<<fgayear<<","<<lgayear<<endl;
cout<<"Adult GA survey indices"<<endl<<Ia_GAobs<<endl;
cout<<"Juv GA survey indices"<<endl<<Ir_GAobs<<endl;
cout<<"M:"<<set_M<<endl;
cout<<"starting values for alpha, beta:"<<salph<<","<<sbeta<<endl;
cout<<"EOF test:"<<test<<endl;
exit(1);
}

//Calculate Total Catch
TC_obs=com_TC_obs*(1.+p_rec); //commercial + rec catch
//cout<<"0"<<endl;
END_CALCS

PARAMETER_SECTION
init_bounded_number log_N(0.,20.,3) //log initial adult abundance
init_bounded_number log_mean_R(0.,20.,2) //log mean recruitment
init_bounded_dev_vector log_R_devs(fyear,lyear,-20.,20.,1) //log recruitment deviations

number pen //penalty function for N
number qa_GA //Age 1+ catchability
number qr_GA //age-0 catchability
vector N(fyear,lyear)
vector R(fyear,lyear)
vector N_GA(fgayear,lgayear)
vector R_GA(fgayear,lgayear)
vector Ia_GAest(fgayear,lgayear) //index of GA adults
vector Ir_GAest(fgayear,lgayear) //index of GA recruits
vector u(fyear,lyear)
number ubar

//Likelihoods
number La_GA
number Lr_GA
number u_prior
objective_function_value NegLL

LOCAL_CALCS
//Set initial parameter values
log_N=3.;
log_mean_R=3.5;

END_CALCS

PROCEDURE_SECTION
//fill in recruitment

```

```

R=exp(log_mean_R+log_R_devs);

//Fill in first year of adult abundance
N(fyear)=exp(log_N);
//Fill in rest of years abundance
pen=.0;
for(y=fyear;y<lyear;y++)
{
  N(y+1)=((N(y)+R(y))*exp(-set_M/2.))-TC_obs(y))*exp(-set_M/2.);
  if (N(y+1)<=.0)
  {
    pen+=10.*square(N(y+1));
    N(y+1)=1;
  }
}

//calculate u
for(y=fyear;y<=lyear;y++)
{
  u(y)=TC_obs(y)/((N(y)+R(y))*exp(-set_M/2.));
}
ubar=sum(u)/double(lyear-fyear+1);

//incorporate timing of the surveys
N_GA=(N*exp(-(set_M/2.)));
R_GA=(R*exp(-(set_M/2.)));

//calculate catchability
qa_GA=exp(sum(log(Ia_GAobs)-log(N_GA))/double(lgayear-fgayear+1));
qr_GA=exp(sum(log(Ir_GAobs)-log(R_GA))/double(lgayear-fgayear+1));

//calculate indices
Ia_GAest=qa_GA*N_GA;
Ir_GAest=qr_GA*R_GA;

//calculate likelihood
//lognormal likelihood for indices of abundance
La_GA=double(lgayear-fgayear+1)*log(Ia_GAsd)+0.5*norm2(log(Ia_GAobs)-
log(Ia_GAest))/square(Ia_GAsd);
Lr_GA=double(lgayear-fgayear+1)*log(Ir_GAsd)+0.5*norm2(log(Ir_GAobs)-
log(Ir_GAest))/square(Ir_GAsd);

//implement beta distribution prior on u
//prior=-(alpha-1)*log(u)-(beta-1)*log(1-u)
u_prior=-(4.-1.)*log(ubar)-(4.-1.)*log(1.-ubar);

//calculate overall negative log likelihood
NegLL=La_GA+Lr_GA+u_prior+pen;

/*****
****

```

```
//Functions to write report files
//*****
****
```

REPORT_SECTION

```
report << "Beginning of report section" << endl;
report << "Likelihood components" << endl;
report << "La_GA" << endl;
report << La_GA << endl;
report << "Lr_GA" << endl << Lr_GA <<endl;
report << "pen" << endl << pen << endl;
report << "u_prior" << endl << u_prior << endl;
report << "NegLL" << endl << NegLL << endl;
report << endl;
report << "CVs for indices of abundance" << endl;
report <<Ia_GAsd << " " << Ir_GAsd << endl;
report << "M R_sd prop_spawn part_recruit" << endl;
report << set_M << " " << rec_sd << " " << sp_time << " " << rf << endl;
report << "Adult catchability" << endl;
report << qa_GA<< endl;
report << "recruit catchability" << endl;
report << qr_GA << endl;

report << "Year Adult_N Rec_N u" << endl;
for(y=fyear;y<=lyear;y++)
{
  report << y << " " << N(y) << " " << R(y) << " " <<u(y) << " " << log_R_devs(y) << endl;
}

report << "Year GAadult_est GAadult_obs GAjuv_est GAjuv_obs " << endl;
for(y=fgayear;y<=lgayear;y++)
{
  report << y << " " << Ia_GAest(y) << " " << Ia_GAobs(y) << " " << Ir_GAest(y) << " "
<< Ir_GAobs(y) << endl;
}


```

RUNTIME_SECTION

```
maximum_function_evaluations 5000, 25000, 20000, 20000, 20000, 20000
//leave empty line below here
```

DataSet:

```
#Data File
#Georgia stock assessment model
#1 survey and 1 catch time series
```

```
#first, last year for model
1985 2008
```

```
#first, last year for total catch
```


1985 2008

#Total Commercial Catch (in millions of crabs)

16.69839087
13.30093981
12.62549425
17.0031262
14.79425134
14.38533366
14.01321746
17.61227449
16.47190025
17.88644354
18.84961368
11.91077228
14.12510835
10.50797269
8.087680999
6.713845145
5.613685019
6.597317644
3.855361128
6.30563131
8.916414217
8.230972081
9.040676871
8.578557583

#first, last year of NC survey

1985 2008

#Adult GA indices

6.281725934
8.034428589
5.995407795
9.721357095
5.092599619
5.708004918
4.63810924
9.493007751
6.560214164
4.207931262
3.595007926
3.885617415
2.913674969
1.636420345
2.241295038
2.221124848
2.041584531
0.147208435
0.096448915

2.673231379
2.819084789
3.738765369
4.963668995
2.768682344

#Age 0 GA indices

0.639931731
0.703061839
0.546776762
0.238798515
0.282058184
0.316149784
0.244964915
0.528018403
0.179740434
0.236334801
0.297569908
0.143841783
0.110801449
0.031631611
0.035328315
0.012062514
0.012597541
0.002916105
0.016622783
0.099668841
0.101999525
0.072474793
0.040155748
0.056795611

#GA adult, recruit SD

0.2 0.4

#M (from stock assessment)

0.9

proportion of rec harvest

0.1

#proportion of year before adult/juv GA

0.5 0.5

#EOF number

12345

f) Florida

ADMB code:

```
//Florida catch survey model
//A.R. Colton
//DATE 6/20/2011
//Florida catch survey model

TOP_OF_MAIN_SECTION
//increase number of estimated parameters
gradient_structure::set_NUM_DEPENDENT_VARIABLES(1000);
gradient_structure::set_GRADSTACK_BUFFER_SIZE(200040);
gradient_structure::set_CMPDIF_BUFFER_SIZE(1000000);
arrmbysize = 10000000;

DATA_SECTION
//READ IN DATA HERE
init_int fyear //first year of model
init_int lyear //last year of model

//Catch Data
init_int ftcyear //first year of total catch
init_int ltcyear // last year of total catch
init_vector com_TC_obs(ftcyear,ltcyear) //total catch

//IRM Survey Data
init_int fIRMyear //first year of IRM survey
init_int lIRMyear //last year of IRM survey
init_vector Ia_IRMobs(fIRMyear,lIRMyear) //adult IRM
init_vector Ir_IRMobs(fIRMyear,lIRMyear) //juv. IRM
init_number Ia_IRMsd
init_number Ir_IRMsd

//TQM Survey Data
init_int fTQMyear //first year of TQM survey
init_int lTQMyear //last year of TQM survey
init_vector Ia_TQMobs(fTQMyear,lTQMyear) //adult TQM
init_number Ia_TQMsd

//JXM Survey Data
init_int fJXMyear //first year of JXM survey
init_int lJXMyear //last year of JXM survey
init_vector Ia_JXMobs(fJXMyear,lJXMyear) //adult JXM
init_vector Ir_JXMobs(fJXMyear,lJXMyear) //juv. JXM
init_number Ia_JXMsd
init_number Ir_JXMsd
```

```

//Natural Mortality
init_number set_M

//proportion of recreational harvest
init_number p_rec

init_int test //EOF number

//Total Harvest including rec
init_vector TC_obs(ftcyear,ltyear) //total catch
int y //looping variable for year

LOCAL_CALCS
if (test!=12345)
{
cout<<"Data not reading properly"<<endl;
cout<<"fyear,lyear:"<<fyear<<","<<lyear<<endl;
cout<<"ftcyear,ltyear:"<<ftcyear<<","<<ltyear<<endl;
cout<<"Total Catch"<<endl<<TC_obs<<endl;
cout<<"fIRMyear,lIRMyear:"<<fIRMyear<<","<<lIRMyear<<endl;
cout<<"fTQMyear,lTQMyear:"<<fTQMyear<<","<<lTQMyear<<endl;
cout<<"Adult IRM survey indices"<<endl<<Ia_IRMobs<<endl;
cout<<"Juv IRM survey indices"<<endl<<Ir_IRMobs<<endl;
cout<<"Adult JXM survey indices"<<endl<<Ia_JXMobs<<endl;
cout<<"Juv JXM survey indices"<<endl<<Ir_JXMobs<<endl;
cout<<"Adult TQM survey indices"<<endl<<Ia_TQMobs<<endl;
cout<<"M:"<<set_M<<endl;
cout<<"EOF test:"<<test<<endl;
exit(1);
}

//Calculate Total Catch
TC_obs=com_TC_obs*(1.+p_rec); //commercial + rec catch
END_CALCS

PARAMETER_SECTION
init_bounded_number log_N(0.,20.,1) //log initial adult abundance
init_bounded_number log_mean_R(0.,20.,1) //log mean recruitment
init_bounded_dev_vector log_R_devs(fyear,lyear,-20.,20.,1) //log recruitment deviations

number pen //penalty function for N going below 0
number qa_IRM //Age 1+ catchabilty
number qr_IRM //age-0 catchability
number qa_JXM //Age 1+ catchabilty
number qr_JXM //age-0 catchability
number qa_TQM //Age 1+ catchabilty

vector N(fyear,lyear)
vector R(fyear,lyear)
vector N_IRM(fIRMyear,lIRMyear)
vector R_IRM(fIRMyear,lIRMyear)

```

```

vector N_JXM(fJXMyear,lJXMyear)
vector R_JXM(fJXMyear,lJXMyear)
vector N_TQM(fTQMyear,lTQMyear)
vector Ia_IRMest(fIRMyear,lIRMyear) //index of IRM adults
vector Ir_IRMest(fIRMyear,lIRMyear) //index of IRM recruits
vector Ia_JXMest(fJXMyear,lJXMyear) //index of JXM adults
vector Ir_JXMest(fJXMyear,lJXMyear) //index of JXM recruits
vector Ia_TQMest(fTQMyear,lTQMyear) //index of TQM adults
vector u(fyear,lyear)
number ubar

//Likelihoods
number La_IRM
number Lr_IRM
number La_JXM
number Lr_JXM
number La_TQM
number u_prior
objective_function_value NegLL

LOCAL_CALCCS
//Set initial parameter values
log_N=4.;
log_mean_R=4.5;

END_CALCCS
PROCEDURE_SECTION
//fill in recruitment
R=exp(log_mean_R+log_R_devs);

//Fill in first year of adult abundance
N(fyear)=exp(log_N);
//Fill in rest of years abundance
pen=.0;
for(y=fyear;y<lyear;y++)
{
  N(y+1)=((N(y)+R(y))*exp(-(set_M/2.))-TC_obs(y))*exp(-(set_M/2.));
  if (N(y+1)<=.0)
  {
    pen+=square(N(y+1));
    N(y+1)=1;
  }
}
for(y=fyear;y<=lyear;y++)
{
  u(y)=TC_obs(y)/((N(y)+R(y))*exp(-set_M/2.));
}
ubar=sum(u)/double(lyear-fyear+1);

//incorporate timing of the surveys
N_IRM=(N)*exp(-(set_M/2.));

```

```

R_IRM=(R)*exp(-(set_M/2.));
N_JXM=(N(fJXMyear,lJXMyear)*exp(-(set_M/2.)));
R_JXM=(R(fJXMyear,lJXMyear)*exp(-(set_M/2.)));
N_TQM=(N(fTQMyear,lTQMyear)*exp(-(set_M/2.)));

//calculate catchability
qa_IRM=exp(sum(log(Ia_IRMobs)-log(N_IRM))/double(lIRMyear-fIRMyear+1));
qr_IRM=exp(sum(log(Ir_IRMobs)-log(R_IRM))/double(lIRMyear-fIRMyear+1));
qa_JXM=exp(sum(log(Ia_JXMobs)-log(N_JXM))/double(lJXMyear-fJXMyear+1));
qr_JXM=exp(sum(log(Ir_JXMobs)-log(R_JXM))/double(lJXMyear-fJXMyear+1));
qa_TQM=exp(sum(log(Ia_TQMobs)-log(N_TQM))/double(lTQMyear-fTQMyear+1));

//calculate indices
Ia_IRMest=qa_IRM*N_IRM;
Ir_IRMest=qr_IRM*R_IRM;
Ia_JXMest=qa_JXM*N_JXM;
Ir_JXMest=qr_JXM*R_JXM;
Ia_TQMest=qa_TQM*N_TQM;

//calculate likelihood
//lognormal likelihood for indices of abundance
La_IRM=double(lIRMyear-fIRMyear+1)*log(Ia_IRMsd)+0.5*norm2(log(Ia_IRMobs)-
log(Ia_IRMest))/square(Ia_IRMsd);
Lr_IRM=double(lIRMyear-fIRMyear+1)*log(Ir_IRMsd)+0.5*norm2(log(Ir_IRMobs)-
log(Ir_IRMest))/square(Ir_IRMsd);
La_JXM=double(lJXMyear-fJXMyear+1)*log(Ia_JXMsd)+0.5*norm2(log(Ia_JXMobs)-
log(Ia_JXMest))/square(Ia_JXMsd);
Lr_JXM=double(lJXMyear-fJXMyear+1)*log(Ir_JXMsd)+0.5*norm2(log(Ir_JXMobs)-
log(Ir_JXMest))/square(Ir_JXMsd);
La_TQM=double(lTQMyear-fTQMyear+1)*log(Ia_TQMsd)+0.5*norm2(log(Ia_TQMobs)-
log(Ia_TQMest))/square(Ia_TQMsd);

u_prior=-(4.-1.)*log(ubar)-(4.-1.)*log(1.-ubar);

//calculate overall negative log likelihood
NegLL=La_IRM+Lr_IRM+La_JXM+Lr_JXM+La_TQM+pen+u_prior;

REPORT_SECTION
report << "Beginning of report section" << endl;
report << "Likelihood components" << endl;
report << "La_IRM" << endl;
report << La_IRM << endl;
report << "La_JXM" << endl;
report << La_JXM << endl;
report << "La_TQM" << endl;
report << La_TQM << endl;
report << "Lr_IRM" << endl << Lr_IRM <<endl;
report << "Lr_JXM" << endl << Lr_JXM <<endl;
report << "penalty" << endl;
report << pen << endl;
report << "NegLL" << " " << NegLL << endl;

```

```

report << endl;
report << "CVs for indices of abundance" << endl;
report <<Ia_IRMsd << " " << Ir_IRMsd << endl;
report <<Ia_JXMsd << " " << Ir_JXMsd << endl;
report <<Ia_TQMsd << endl;
report << "M" << endl;
report << set_M << endl;
report << "Adult catchability" << endl;
report << qa_IRM << " " << qa_JXM << " " << qa_TQM << endl;
report << "recruit catchability" << endl;
report << qr_IRM << " " << qr_JXM << endl;

report << "Year Adult_N Rec_N u" << endl;
for(y=fyear;y<=lyear;y++)
{
  report << y << " " << N(y) << " " << R(y) << " " << u(y) << " " << log_R_devs(y) <<
endl;
}

report << "Year IRMadult_est IRMadult_obs IRMjuv_est IRMjuv_obs " << endl;
for(y=fIRMyear;y<=lIRMyear;y++)
{
  report << y << " " << Ia_IRMest(y) << " " << Ia_IRMobs(y) << " " << Ir_IRMest(y) << "
" << Ir_IRMobs(y) << endl;
}

report << "Year JXMadult_est JXMadult_obs JXMjuv_est JXMjuv_obs " << endl;
for(y=fJXMyear;y<=lJXMyear;y++)
{
  report << y << " " << Ia_JXMest(y) << " " << Ia_JXMobs(y) << " " << Ir_JXMest(y) << "
" << Ir_JXMobs(y) << endl;
}

report << "Year TQMadult_est TQMadult_obs TQMjuv_est TQMjuv_obs " << endl;
for(y=fTQMyear;y<=lTQMyear;y++)
{
  report << y << " " << Ia_TQMest(y) << " " << Ia_TQMobs(y) << endl;
}

```

RUNTIME_SECTION

```

maximum_function_evaluations 5000, 25000, 20000, 20000, 20000, 20000
//leave empty line below here

```

DataSet:

```

# Data File
#Florida stock assessment model
# uses 3 surveys and catch time series

```

```

# first year last year for model
1990 2008

```

first year for total catch
1990

last year for total catch
2008

Total Commercial Catch (in millions of crabs)

14.23922649
9.316500033
13.71080367
7.983921576
11.03058355
7.050359708
11.31029833
11.7450948
9.266277769
9.273184707
9.78675596
5.526055997
4.699412235
4.208369183
7.677717111
8.480592143
6.602753814
8.556471347
7.053237782

first year of IRM survey
1990

last year of IRM survey
2008

Adult IRM indices

0.15687685
1.587296719
1.53649083
0.398880369
0.84158309
0.516661014
0.488161402
0.479635616
1.385172307
0.723503497
0.75031142
0.363532415
0.265953844
0.343996467
0.673071421
1.149053841
0.464930252

0.458115095
0.341384685

Age 0 IRM indices

0.009850746
0.440672931
0.168770327
0.127961701
0.088947406
0.089671481
0.045969936
0.105722655
0.916475789
0.173722839
0.318210117
0.192073212
0.041715603
0.234790885
0.192759011
0.247771304
0.848196724
0.651645158
0.240427345

IRM adult SD, juv SD

0.25 0.46

first year of TQM survey

1997

Last year of TQM survey

2008

adult indices for TQM survey

0.489716454
0.617292099
0.313038927
0.37303557
0.541617823
0.127567826
0.464253581
0.696561134
0.665656284
1.308710394
0.64657315
0.355431982

#TQM SD adults

0.24

first year of JXM survey

2001

Last year of JXM survey
2008

adult indices for JXM survey
0.446438932
0.45661138
0.308133996
0.751493146
0.555676682
0.903383255
1.054895094
0.695820517

age 0 JXM survey
0.093353378
0.083129901
0.132571152
0.168007215
0.130280677
0.124346249
0.114476483
0.08607648

#dredge SD adults, juv
0.33 0.23

M
1

proportion of rec harvest
0.18 #from tagging study

#EOF number
12345

Appendix D: R Code for Principal Component Analysis

```
rm(list=ls())
library(stats)
library(lattice)

# read in data and create variables
compiled1974<-read.csv("P:/Colton/thesis data/data 1974-2008/landings_by_bay.csv",
header=T, sep=",", dec=".")
matrixdata<-compiled1974[,2:10]
year<-compiled1974[,1]
yearlab<-year-1900
yearlab<-ifelse(yearlab>99,yearlab-100,yearlab)

head(matrixdata)

# look at correlation plots
splom(matrixdata, aspect="fill", panel=function(x,y,...) panel.xyplot(x,y,...),
panel.lmline(x,y,...))
cor(matrixdata)

#run PCA
PCAmode1<-princomp(matrixdata, cor=TRUE)
summary(PCAmode1)
loadings <- PCAmode1$rotation
scores<- PCAmode1$x
plot(PCAmode1,main="Scree Plot")
biplot(PCAmode1,scale=1, xlab=yearlab)

#calculate PCA correlation distance vector
PCAdist<-dist(as.matrix(PCAmode1$loadings[,1:2]))

#convert vector into a matrix of distances
dist2full <- function(dis)
{
  n <- attr(dis, "Size")
  full <- matrix(0, n, n)
  full[lower.tri(full)] <- dis
  full + t(full)
}
PCAmatdist<-dist2full(PCAdist)
```

Appendix E: Matlab Code for Calculating Geographic Distance Between Regions

```
function [Result] = Eucdist1(X,Y)

N = length(X);
for i = 1:N
    for j = 1:N
        if i == j
            Result(i,j)=0;
        else
            Result(i,j) = (((X(i)-X(j))^2)+((Y(i)-Y(j))^2))^0.5;
        end
    end
end
end
```

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