

**Informing U.S. Caribbean fisheries management through simulation modeling: a
case of length-based mortality estimation models**

by:

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ABSTRACT

Length-based stock assessment models estimating mortality rates are attractive choices for assessing fisheries with data deficiencies. The U.S. Caribbean is exploring using these models and trying to optimize their commercial sampling program for such a model.

A simulation model was constructed to compare two length-based mortality estimators, the Beverton-Holt and Gedamke-Hoenig models. The simulations also tested aspects of the Gedamke-Hoenig model previously not thoroughly addressed, such as the effects of varied life history parameters, violating the assumptions of constant growth and recruitment, sample sizes (n), and sampling program length (Y_s) on total mortality rate estimates (Z).

Given the scenarios investigated, the Beverton-Holt model produced consistently biased, but more stable results when n was low, variation was high for both growth and recruitment, and sampling began after the change in Z took place. The Gedamke-Hoenig model was generally less biased and detected changes in Z , but produced variable results of the current Z , especially with low sample sizes and high variability. In those situations, both models can be carefully interpreted together for management advice.

In the Gedamke-Hoenig model results, a clear pattern emerged in the mean accuracy and precision of the model where after an asymptote was reached, increasing n did not improve the means. The variance of the model improved with both increasing n and increasing Y_s . Outliers were predictable and could be accounted for on a case-by-case basis.

The model developed here can be a tool for guiding future stock assessment model choice and sample design in the U.S. Caribbean and other regions.

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LIST OF ABBREVIATIONS

Beverton-Holt mean-length mortality estimator (B-H model)
Caribbean Fisheries Management Council (CFMC)
Exclusive Economic Zone (EEZ)
Food and Agricultural Organization of the United Nations (FAO)
Gedamke-Hoenig mean-length mortality estimator (G-H model)
Magnuson-Stevens Fisheries Conservation and Management Act (MSRA)
National Marine Fisheries Service (NMFS)
Puerto Rico Department of Natural and Environmental Resources (PRDNER)
St. Thomas/St. John (STT/STJ)
St. Croix (STX)
Small-scale fisheries (SSF)
Southeast Data and Assessment Review (SEDAR)
Southeast Fisheries Science Center (SEFSC)
United States Virgin Islands (USVI)

CHAPTER 1—U.S. CARIBBEAN FISHERIES AND STOCK ASSESSMENT

Introduction

Effective fisheries management is highly dependent on science-based fishery information (FAO 2003). A critical component of the science-based input is stock assessment (Smith et al. 1999; National Research Council 2004). A stock assessment provides information on both the trends and status of a fishery and can also be the baseline for evaluating the potential impacts of alternative management actions. The information used in stock assessments comes from data collected directly from a fishery or from research outside of the fishery.

In the latest reauthorization of the Magnuson-Stevens Fisheries Conservation and Management Act (MSRA), Congress mandated that all overfishing end in U.S. waters by 2010 (U.S. Department of Commerce 2007). This task is delegated to the eight regional fisheries management councils. This and other critical fisheries management tasks such as allocating catch and defining catch regulations are dependent on stock assessments (U.S. Department of Commerce 2007). Without stock assessments, these decisions are made in the absence of critical information, which adds considerable uncertainty into the management process.

While a difficult task for all Councils, the mandate is particularly problematic for Councils whose fisheries are smaller in scale and where data are lacking to properly conduct the stock assessments used to inform management decisions. The Caribbean Fisheries Management Council (CFMC) falls into this category and their jurisdiction includes the waters of Puerto Rico, St. Thomas, St. John, and St. Croix, also known as the U.S. Caribbean (Figure 1.1). While effort has been made to collect data in the U.S. Caribbean, the inconsistent data collection, quantity, and quality of data over the years, typical of small-scale fisheries, have made it difficult to complete informative stock assessments and thus inform management. While the CFMC has made efforts to complete the best management possible, adequate data are lacking and a greater commitment to consistent data collection is necessary to allow for informative stock assessments. Simply improving data collection methods will not instantly allow for improved

management because consistent data collection over a time-series is required as input for most informative stock assessments.

Small-Scale Tropical Fisheries

Many reasons exist for the insufficient data and lack of comprehensive stock assessments available in the U.S. Caribbean. The small-scale nature of the fisheries is one major component. Several unique characteristics are common among small-scale tropical fisheries, such as those in the U.S. Caribbean. These characteristics were defined in the 2004 CoastFish meeting that focused on coastal fisheries in Latin America and the Caribbean (Salas et al. 2007):

- 1) Fishers are not very specialized, with many species targeted using several gear types.
- 2) There is low capital investment by fishers.
- 3) Fishing and processing methods are labor-intensive.
- 4) Several landing sites are utilized across areas in small communities.
- 5) Seasonal fishing occurs.
- 6) Fishers have other sources of income.
- 7) Fishers receive few, if any, health and employment benefits.

Special data problems arise when dealing with tropical small-scale fisheries (SSFs) because of these characteristics. Among the most prominent problems is the limited amount of fisheries management agencies' funding and personnel, making it more difficult to collect data needed for stock assessments (Salas et al. 2007). Stock assessments are difficult in many tropical SSFs because of one or more of the following (Salas et al. 2007):

- 1) There is limited funding for sampling programs.
- 2) No standardization occurs in sampling programs over years or areas.
- 3) Research is only done on the most valuable species.
- 4) Cost limits the number and duration of studies independent of fishery catch.
- 5) Those completing research or sampling lack the necessary skills or training
- 6) There is a lack of trust in the management process from fishers.

- 7) Catch data are questionable because of inconsistent data recording formats, limited continuity, and limited personnel.
- 8) Single species assessments are difficult when data is collected from multi-species groupings

The U.S. Caribbean fits virtually all of these characteristics and faces many of the same fisheries management and assessment challenges as other tropical SSFs.

U.S. Caribbean Fisheries

The profile of a typical commercial fisher from each of the two main island districts, Puerto Rico and the U.S. Virgin Islands (USVI; includes St. Thomas, St. John, and St. Croix), illustrates many SSF characteristics. Fishers target multiple species, using multiple gear types, with very few specializing (Griffith et al. 2007). Most fishers, while considering themselves full-time fishers, must supplement their income outside of fishing (Kojis 2004; Griffith et al. 2007). Fishers on all islands typically have one boat less than 25 feet in length (Kojis 2004; Griffith et al. 2007). Technology used on the boats for fishing, navigation, and recording is limited with only one-third having GPS, and one-half having depth finders (Kojis 2004).

Nearly 180 fish species are caught commercially in the U.S. Caribbean (SEDAR 2004). The species represent a wide range of life history traits, from fast-growing, short-lived species such as dolphinfish to long-lived, slow-growing fish such as tuna. Most of the species caught are reef-assemblage fish such as parrotfish, although some pelagic species are commonly caught as well. Among all the species caught, queen conch (*Strombus gigas*), spiny lobster (*Panulirus argus*), and yellowtail (*Ocyurus chryurus*), silk (*Lutjanus vivanus*), queen (*Etelis oculatus*), and lane (*Lutjanus synagris*) snappers make up much of the catch and are the most economically important species in the region (Matos-Caraballo et al. 2007).

In Puerto Rico, the largest of the U.S. Caribbean islands, the catch is brought into one of 100 official landings sites from around the island and sold locally in small fish markets, called pescaderias (Griffith et al. 2007). The islands in the USVI, on the other hand, are much smaller in size and have fewer places to pull in a boat due to geographic and oceanographic limitations.

As a result, fewer landings sites are recorded on St. Thomas/St. John (3-4 sites), and St. Croix (4 sites).

Fisheries management in the U.S. Caribbean is accomplished on two levels with separate rules and regulations for territorial and federal waters. Puerto Rico and the USVI each have their own territorial fisheries management rules and regulations within their territorial seas. The USVI territorial sea goes from shore to three miles out and Puerto Rico's territorial sea extends from shore to nine miles out (Figure 1.1). From the edge of the territorial seas to 200 miles out, the fisheries are under federal law and under the jurisdiction of the CFMC.

U.S. Caribbean Fisheries Management and the Caribbean Fisheries Management Council

The CFMC is different from most other federal fisheries management councils set up under the MSA because of the small-scale nature of the U.S. Caribbean fisheries and the variety of the number of species caught. The CFMC has 179 fish stocks under their control (SEDAR 2004). Although the CFMC faces somewhat unique challenges, they still must follow the same rules and mandates as other councils. The Council is made up of ten members (seven voting and three non-voting) representing territorial government agencies, federal government agencies and the commercial, recreational, and charterboat sectors of the fisheries.

As part of the law dictating fisheries management in the United States, the MSA was recently reauthorized, directing the regional fisheries management councils to end overfishing in the exclusive economic zones (EEZ; Figure 1.1) by 2010 (U.S. Department of Commerce 2007). Members of the Council and advisory groups set up by the Council look at current and past data to determine how best to accomplish this goal. These data come from fishery landings reports from fishers and port samplers, research outside of the fishery, and other expert knowledge and opinions. Ideally, management councils rely on stock assessments derived from these data, but unfortunately, informative stock assessments are not available to the CFMC due to limited sampling, few studies completed independent of fisheries landings, inconsistent data collection protocols, conflicting data records, and the multiple-species/multiple-gear nature of the fishery,

problems other similar SSFs face as well. These problems are seen in both the commercial and recreational sectors.

Commercial Catch

Commercial fishers in the U.S. Caribbean are required to have a license and to submit their landings information to the territorial fish and wildlife agency and the National Marine Fisheries Service (NMFS). In Puerto Rico, responsibility for collection of commercial catch data rests with the Puerto Rico Department of Environmental and Natural Resources (PRDNER). Puerto Rico has recorded commercial catch since the late 1800s. Fishers in Puerto Rico were not required to report their landings prior to 2004; however, many did so voluntarily (SEDAR 2007). The total landings for the island were estimated using an expansion factor accounting for those who did not voluntarily report (SEDAR 2007). Now, expansion factors are still used to account for non-reporting and mis-reporting but fishers not submitting their landings data can have their license revoked.

The USVI has required landings reports since 1973, which are reported to the USVI Division of Fish and Wildlife on a monthly basis, with punishments similar to Puerto Rico's if reports are not submitted (Department of Planning and Natural Resources 2004; SEDAR 2007c). In addition, all fishermen must agree to have their fish measured by port samplers at least four times every year.

Each territorial fishery management organization submits the raw data collected from the commercial fishery to the NMFS Southeast Fisheries Science Center (SEFSC) for analysis (Matos-Caraballo 2007). Detailed commercial catch data, despite the long history of the fishery, are not available for the years prior to the early 1970s for both Puerto Rico and the USVI (SEDAR 2004).

Recreational Catch

In addition to commercial catch, recreational catch also is important. While recreational catch is suspected to be a relatively large component of fishing pressure in the U.S. Caribbean, the

magnitude of this impact is difficult to measure (SEDAR 2009, 2007b, 2007c). Recreational fishing is likely increasing over time, both in the numbers of fish caught, as well as the percentage of the total fish caught. Recreational fishers, while subject to the rules and regulations of the territories and the U.S., are not required to report their catches. In the U.S. Caribbean, currently no recreational marine fishing license system exists, although a law allowing the system to exist was recently passed. Without knowledge of who is fishing, the job of collecting data on the recreational catch is difficult at best and ultimately, stock assessments require information from both the commercial and recreational sectors.

Commercial Data Availability

Stock assessments rely on two main types of data: fishery-dependent and fishery-independent. Fishery-dependent data are collected directly from the fishery as they normally operate. Fishery-independent data, in contrast, are collected outside of the fishery from designed research studies.

Fishery-dependent catch data from the commercial fisheries of the U.S. Caribbean are collected using two primary methods. The first method is the Trip Interview Program (TIP) and the second is the self-reported landings data.

Trip Interview Program (TIP)

The TIP dataset is a collaborative effort between the territorial governments and the NMFS SEFSC to collect size frequency data. To gather data, fisheries officials or port samplers intercept fishers at landing sites, markets, road side stands, or individual's houses and gather trip information and biological samples of a fishers' catch. Data are collected on the size and species composition of the catch and also on effort information such as trip time, gear types and amounts of gear types used by fishers (see Figure 1.2 for the Puerto Rico TIP reporting form from 2008). The Puerto Rican TIP data contained information on 29,000 trips from 1980-2003 (SEDAR 2004). Biological samples, such as otoliths can also be collected at this time to determine age composition or diet of selected species

Landings

The landings data comes directly from fishers' self-reported landings. Fishers are required to submit reports to the territorial fisheries management agencies in order to maintain active fishing licenses (Commonwealth of Puerto Rico 2004; Department of Planning and Natural Resources 2004). The exact information collected varies by island, but usually includes the date, species or species group caught, gear type, and trip duration (see Figure 1.3 for the Puerto Rico reporting form from 2008).

Data Problems

Both datasets have flaws. Problems with the data collected in both the TIP and landings data collection programs have led to considerable questioning of the data and the ability to rely on the data for stock assessments. The U.S. Caribbean specifically faces problems because essential data are lacking and conflicting information is relatively common. Additional problems arise from the multi-species and multi-gear nature of these fisheries.

Certain categories of data needed to run informative stock assessments are not collected in the current data collection system, or have not been collected consistently over a consecutive time series. If a fisher leaves out a piece of information in their landings report, such as the species caught, gear type, or distance from shore fished, the record is not included in analyses which depend on that specific information. For example, if no length information were recorded for the landings of a trip for the TIP, the trip entry would not be included in the analyses for a length-based stock assessment. When this problem consistently occurs, as it does in the current U.S. Caribbean data sources, then the quantity of data available for stock assessments decreases in an already data-poor situation.

The data collection forms for both the TIP and Landings data collection programs have also changed over the years, creating several problems. Not only has different information been collected over the years, but the names of the fields on the forms have also changed throughout the existence of the dataset (Figure 1.4). In some years the alternative answers to the question "Distance?" were either "yes" or "no," indicating whether the trip took place in or out of

territorial waters. In more recent years, a specific distance in miles was recorded, leading to some confusion on the proper unit of measurement to report and from what point to measure the distance from shore. Because of this, it has been difficult to ascertain whether fishing effort has shifted to new populations.

Another problem specific to the quality of the USVI fishery-dependent data is that, until very recently, the USVI only recorded species as species groups and recorded gear types by general gear type, rather than specific species or specific gear types (Figure 1.5, Figure 1.6, SEDAR 2007b, 2007c, SEDAR 2009). Multiple gear types or multiple species per trip also complicate the data. When not recorded or divided clearly, data listing the multiple gears and species become useless for certain assessments. For example, one trip entry in the landings data might have recorded “grouper” and “snapper” as the species caught and “diving” and “hook and line” as the gear types used, but it does not specify the species nor the type of diving nor which instrument was used for each fish. These problems make it more difficult to utilize the data and perform assessments based on species or gear type.

Perhaps the biggest problem for potential stock assessments is the questionable quality of the data. Data collected from a fishery will never be perfect, but some entries in the existing landings and TIP databases are particularly problematic. One field on the USVI landings reporting form, for example, clearly asks for the perpendicular distance from shore where the fishing occurred. While the shelf in St. Croix is not more than 12 miles long at its furthest point, before dropping off to over 100 fathoms, many fishers reported putting traps out 20, 30, and even over 100 miles perpendicular distance offshore and fishing for parrotfish. Similar situations appeared in the landings data for St. Thomas/St. John. To utilize this data a significant amount of time must be spent doing quality assurance and quality control.

Additional problems exist, such as underreporting, incorrect identification of caught fish, and the lack of information on non-licensed fishers. However, these issues are not problems involving the structure of the current required data submission form.

History of Caribbean SEDAR

Commercial data problems and other data issues pertaining to specific species or species groups have been officially reviewed as part of a process to improve the information available to the Councils. One in-depth process of synthesizing and evaluating known data, and conducting stock assessments is the Southeast Data, Assessment, and Review (SEDAR). The SEDAR process is a collaborative effort between the South Atlantic, Gulf of Mexico, and Caribbean Fisheries Management Councils, under the guidance of the SEFSC. The goal of the process is to provide critical information to the Councils to assist in their decision-making. SEDARs bring together experts to review available data on a species or species group, then develop and review relevant stock assessments. Several SEDARs have focused on U.S. Caribbean populations including mutton snapper (*Lutjanus analis*) (SEDAR 2007b), queen conch (SEDAR 2007c), yellowfin grouper (*Mycteroperca venenosa*) (SEDAR 2007a), yellowfin snapper (SEDAR 2005a), spiny lobster (SEDAR 2005b), and the deepwater snapper-grouper species group (SEDAR 2004). In January, 2009 a technical procedures workshop was held focusing specifically on Caribbean data; what was available, how it could possibly be used for stock assessment, and suggestions for the future (SEDAR 2009).

Although the specific results and recommendations from each U.S. Caribbean SEDAR have varied by species, none were able to successfully develop an informative stock assessment. The review panel for each SEDAR listed a number of data problems including data recording problems, and the lack of sufficient sample sizes. The queen conch, mutton snapper, and yellowfin grouper SEDARs in particular, noted these problems in the commercial landings data (SEDAR 2005b, 2007a, 2007b). For future assessments and management, a mixed-fishery approach was recommended by the yellowfin grouper and mutton snapper SEDARs. The technical procedures workshop reviewed the conclusions about stock assessments and data for the previously evaluated species, in addition to looking at data for other species and deciding whether stock assessments could be completed with their data. Specific stock assessment techniques attempted for each species group were also reviewed in each SEDAR.

Previous Stock Assessments

Because of the data problems described above, the SEDAR process has applied and reviewed a number of assessment methods, but had little success. Of the stock assessments attempted, the SEDAR review committees considered none successful because results were inconclusive.

Catch per unit effort (CPUE), a measure of the number of fish caught by a fixed amount of fishing intensity, can show changes in fishing effort and landings over time, which can help determine the general status of a fishery. CPUE was calculated for spiny lobster and queen conch using a Generalized Linear Model Approach (GLM) (Valle-Esquivel 2002; SEDAR 2005). The GLM incorporated explanatory variables relating to the fishery, such as year and place caught to standardize CPUE to estimate indices of abundance using only trips where the species of interest was caught. Densities for queen conch and mutton snapper were also calculated and compared across islands and habitats and then extrapolated to estimate populations (SEDAR 2007b, 2007c).

A non-equilibrium surplus production model (ASPIC software) was done on the queen conch landings from Puerto Rico (Valle-Esquivel 2002). The model used removal information and CPUE indices to estimate outputs such as the biomass which will produce the maximum sustainable yield (B_{MSY}), the fishing mortality to achieve maximum sustainable yield at B_{MSY} (F_{MSY}), and yield available given F_{MSY} ($Y.(F_{MSY})$). The ASPIC models, which seemed to fit the data, did not produce realistic results and therefore, the model was questioned.

The Gedamke-Hoenig mean-length mortality estimator (Gedamke and Hoenig 2006) was attempted for Caribbean data in 2008. However, there was not enough data to support the use of the model for Mutton snapper in Puerto Rico because initial evaluation of spatial patterns of fishing indicated that fishing location might have shifted, possibly violating an assumption of fishing from only one population (Gedamke et al. 2009).. Other fisheries were not thoroughly analyzed using the method for these same reasons.

Exploitation status was also estimated for coral reef fish in Puerto Rico based on length information from fishery-dependent and fishery-independent data (Ault et al. 2008). The results indicated that most of snapper-grouper fish in Puerto Rico are being fished at unsustainable

levels, although stock sizes were not estimated (Ault et al. 2008). SEDAR 2009 found that the assumptions of the model were likely violated, sample sizes were low, and the life history data used were questionable. The group indicated that the Gedamke-Hoenig model showed more promise for use in the Caribbean.

Despite these attempts, the species-specific SEDARs reported that no definitive stock assessments could evaluate the current or past status of the populations as well as the possible impacts of alternate management. The conclusions of the technical procedures workshop in 2009 were the same as other SEDARs: stock assessment appropriate data does not currently exist for U.S. Caribbean fish stocks. It is clear that before adequate assessments can be completed, improved data on fish stocks must become available.

An additional consideration for stock assessments is the management area or stocks that they pertain to. The CFMC currently manages each island as a separate management group. Assessments based on information from Puerto Rico only are not helpful for determining the best management for the Virgin Island fisheries because each island in the U.S Caribbean has its own unique geographical and fisheries characteristics. Often more data is available from Puerto Rican fisheries, so the results of analyses of Puerto Rican data are extended to apply to USVI management, despite the differences between the islands. More island-specific data are needed to run assessments that would allow for island-specific management.

Potential Stock Assessment Techniques

In order to effectively manage sustainable fisheries, managers need current information on the levels of fishing effort, the types of gear, and the amount of catch (Booth and Quinn 2006). This information serves as input for stock assessments evaluating past trends and the potential impacts of alternative management decisions on a fishery. The list of potentially applicable stock assessment methods is long and varied, depending on the quantity, quality, and types of data available and the output required from the assessment. Given the lack of sufficient data to perform stock assessments on important fish stocks in the past, the challenge in the U.S. Caribbean is to look to the future and see what assessment methods are possible given the likely availability of additional data.

Specifically from a commercial fishery, the following categories of data can potentially be collected (Sparre and Venema 1998):

1. Total catch
 - i. By species
 - ii. By area
 - iii. By gear type
2. Effort
 - i. By area
 - ii. By gear type
3. Length-frequencies
 - i. By species
 - ii. By sex
4. Age-frequencies
 - i. By species
 - ii. By sex
5. Biological data (ex: length-weight relationship, length-age relationship)
6. Gear data (ex: size of traps)

Ideally in the U.S. Caribbean, we would hope to collect total catch, effort, length-frequencies, and gear data with an improved data collection program. Otolith analysis in tropical species can be a long, difficult and/or expensive process, meaning attempts to do analysis based on annually collected age data are less likely to succeed (Gulland 1983, Sparre and Venema 1998). Given this information, length-based models have been an attractive choice for SSFs, as length data are relatively simple and inexpensive to collect and the age-growth relationships based on otolith analyses only need to be completed once (Pauly 1983, Jones 1984, Quinn and Deriso 1999).

Length-based stock assessment models

Several length-based models exist for use in stock assessment, including the Beverton-Holt (Beverton and Holt 1957), Ssentongo-Larkin (Ssentongo and Larkin 1973), Powell (Powell

1979), Ehrhardt-Ault (Ehrhardt and Ault 1992, Ault et al. 2008), and the Gedamke-Hoenig models (Gedamke and Hoenig 2006). These models can provide estimates of Z , which in turn, can help determine the level of overfishing in a population. If the natural mortality rate (M) is calculated, then it can be used several ways in conjunction with the estimate of Z . The difference between Z and M is attributed to the fishing mortality rate (F). Additionally, the natural mortality value approximates the fishing mortality rate at maximum sustainable yield (F_{MSY}). F can then be compared to F_{MSY} (F/F_{MSY}). If $F/F_{MSY} > 1$, then overfishing is occurring and the fishing mortality rate is above the rate that would achieve maximum sustainable yield. If an assessment can provide this type of information, then managers can adjust regulations, enforcement, and ACLs to ensure that F/F_{MSY} does not reach a level indicative of overfishing.

The Beverton-Holt model (B-H model) was among the first of the length-based models and is relatively simple in its methods and assumptions. The B-H is commonly suggested for use in data-poor situations, like those in the U.S. Caribbean. Using the mean lengths and the von Bertalanffy growth parameters of asymptotic length (L_{∞}), length at first capture into the fishery (L_c) and growth rate (K), the total mortality rate for a population can be solved (Equation 1) (Beverton and Holt 1956).

$$Z = \frac{K(L_{\infty} - \bar{L})}{\bar{L} - L_c} \quad (1)$$

A critical assumption of the model's estimates is that there is no change in the mortality rate of the population over the time of analysis. This assumption is often violated given changes that occur in fishing communities due to changes in technology, regulations, and environmental factors over periods of time. Other assumptions of the model include constant growth of individuals, constant recruitment over time, and L_{∞} and K remaining constant over time. These assumptions are broad and likely violated in a fishery over time.

The model has been tested in several situations using real and/or simulated data. Studies have consistently found that the Beverton-Holt model has low variance, but a sizeable bias compared to other length-based models (Wetherall et al. 1987, Ehrhardt and Ault 1992). Studies have varied in their testing and conclusions on violating assumptions or the impact of estimating key

growth parameters on the mortality estimation. Laurec and Mensil (1987) thoroughly tested the model and found that while it is robust to variability in growth parameters, problems can arise when there are several length samples close to the defined value of L_∞ . Wetherall et al. (1987) also mentioned that caution should be used when using the method when L_c and L_∞ are not well known. Because of this, and the likelihood of the assumption of constant mortality being violated, some have expressed the need for caution in using the B-H model for management situations (Ralston 1989, Gulland and Rosenberg 1992).

Many of the length-based models have built onto the simple B-H model and tried to account for some of its broad assumptions. One such model is the Gedamke-Hoenig mean-length mortality estimator (G-H model). The use of the model has been suggested by the CFMC, the CFMC's Scientific and Statistical Committee (SSC), and by the 2009 SEDAR working group (SEDAR 2009). Most length-based models, including the B-H model, require the population to be at equilibrium, whereas the G-H model does not. Instead, the model evaluates changes in mean lengths to estimate changes in total mortality rates and attributes those changes to changes in fishing mortality rates (Gedamke and Hoenig 2006). Since fishing behaviors in the U.S. Caribbean have been changing in recent years, the G-H model appears to be a good choice for a length-based stock assessment model. In addition, the model can be extended to look at multiple species in one assessment, another important component for potential stock assessment methods in the United States Caribbean.

Like the B-H model, the G-H model requires initial guesses for the von Bertalanffy growth parameters, K , L_∞ , and L_c , in addition to the mean length for each year of the sampling effort. Using these values, the model estimates the mortality rate before change (Z_1), the mortality rate after the change (Z_2) and the years since the change occurred (d) which leads to an estimate of the year of change (T_c). With this information and equation (2), you can solve for the parameters of interest using a likelihood function (Gedamke and Hoenig 2006).

$$\bar{L} = L_\infty - \frac{Z_1 Z_2 (L_\infty - L_c) \{Z_1 + K + (Z_2 - Z_1)^{[-(Z_2 + K)d]}\}}{(Z_1 + K)(Z_2 + K)[Z_1 + (Z_2 - Z_1)^{(-Z_2 d)}]} \quad (2)$$

However promising the model may be, the G-H model is relatively new in existence and the tradeoffs between it and other length-based models have not been rigorously tested. It was tested using real data from the goosefish fishery and also simulated data (Gedamke and Hoenig 2006). In this initial testing of the model, results indicated that it performed well compared to the Beverton-Holt model (B-H model), the simpler length-based model it is derived from (Gedamke and Hoenig 2006). Additional analyses for the model were based on real data with small sample sizes, where the actual values for critical parameters (e.g., Z_1 , Z_2) were not known. Evaluation using Caribbean data has even been attempted in the past. Unfortunately, the results were not used because of doubts as to whether or not fishing location had changed, which would violate spatial assumptions and because existing data were too limited (Gedamke 2007, Gedamke et al. 2009). More recently, the model with multiple changes in mortality has been used by Gaertner 2010 to evaluate Eastern Atlantic skipjack data. The study found that the model was able to detect multiple changes in mortality in the fishery and that the predicted changes of the model were similar to annually calculated Beverton-Holt estimates (Gaertner 2010).

While the G-H model has been used and tested in the few cases mentioned above and some others, there are still aspects of the model behavior that are not well understood. Most of the cases have utilized data directly from a fishery, where the actual total and fishing mortality rates are not known exactly. That makes it difficult to truly measure how accurate the estimates are. Simulations were utilized in the inaugural publication of the model, but the simulations were limited in scale, only looking at the possible implications of miscalculating K or L_∞ over one set change Z ($Z_1=0.3$, $Z_2=0.6$) for one species of fish (Gedamke and Hoenig 2006). Simulations have yet to be completed looking at different changes in Z or other life histories. Studies have also yet to thoroughly look at the implications of violating the model's assumptions, such as constant growth or recruitment. The model has also been put forward as ideal for data-poor fisheries, only requiring small sample sizes. However, it is unclear what the minimum sample size or number of years of a sampling program the model would need to get a realistic and informative estimates of the changes in total mortality rates.

Information Required to Improve Assessments

Before a stock assessment is completed and used to inform management, it needs to be well understood whether or not the model is appropriate for the data available and what the caveats are for using that model. Choosing the best model for the data involves understanding the assumptions, the inputs required, and the possible bias or uncertainty in estimations from that model. For some stock assessment methods, such as the G-H model, these things have yet to be thoroughly tested. Although groups involved in U.S. Caribbean fisheries would like to use the G-H model, before doing so this understanding of model behavior, the possible outcomes if assumptions are violated, and the amount of data required needs to be studied in more detail. After such testing occurs, not only will there be a better understanding of the types and quantities of data needed to improve assessments, but there will also be further scientific justification for the use of the model for management.

Even if a perfect length-based data collection protocol were established today and the tradeoffs of the model of choice were well understood, we would not have the capability to conduct a stock assessment for a number of years. The time it will take to successfully assess stocks will be dependent on the number of samples taken per year, the species in question, the pattern of exploitation, and the level of commitment to acquiring an appropriate quantity and quality of data. The time and amount of data it takes to gather necessary information and see change is not well understood by fishers. Fishers have seen new regulations implemented, restricting their catch, despite their cooperation within the management process. As a result, many feel their participation in the process is being used against them. Fishers, in general, are frustrated and impatient with the pace of any positive management decisions and have unrealistic expectations of timelines for change.

Council members and fishers have varying levels of sophistication in their understanding of the underlying theory and mathematics of stock assessment models used in management decisions. As a result, some do not understand the quantity, quality, or types of data needed in the process. Some also are unlikely to know that transitioning from current data collection methods to effective methods, and then producing sufficient data for an adequate stock assessment will likely take a minimum of five to ten years, even for so-called “data poor” methods. Even further complicating the issue is a lack of understanding of how experimental design and sample size

influence that timeline. Some stock assessment models claim to work well at “small sample sizes.” Yet the definition of “small” will vary depending on the species type, stock assessment model of choice, and overall sample design. It is important that all involved in the fisheries management process understand not only how long sampling needs to occur, but also at what magnitude per year and the relationship between the two variables. The challenge is to communicate the assessment needs to those at all levels of understanding. Long-term change is unlikely if the fishers and Council members expect results from modified data collection within one to two years and fewer than fifty samples in each of those years. Buy-in will decrease if parties involved feel the process is going too slowly because of unrealistic expectations of the time it takes to see results. If this occurs, the efforts to change methods might be for naught and data problems will likely plague future assessments as well. With budgets and personnel already limited in the region, it is also important for the management, Council, and other stakeholders to understand the monetary commitment it will take to collect the samples necessary to complete a stock assessment.

Simulation Modeling

Simulation models are useful tools that can determine the tradeoffs between the range of time and sample sizes it will take get enough information to complete a length-based stock assessment under improved data collection scenarios across a broad range of life history traits. They are particularly valuable tools when little real data are available. Simulation models can create populations of hypothetical fish (based on real fish populations) where everything about that population is known and then extract data from that population to test out theories, model behaviors, or experimental designs. This method of testing can help scientists, managers, and other stakeholders understand population dynamics, stock assessment models, and the implications of possible management actions in ways that would otherwise be expensive or difficult, if not impossible. A completed simulation model based on U.S. Caribbean fisheries can be a powerful tool for guiding sample design, stock assessment choice, and influencing expectations for the region both now and in the future.

Conclusions

Model selection can be a complex process, particularly in SSFs. Even models that seem to require relatively little amounts of data to complete analyses and are desired for use in the Caribbean, such as the Gedamke-Hoenig model, have assumptions and sensitivities that need to be understood and tested before their extended use is suggested. Using a simulation model, behaviors of such stock assessment models can be understood and used to compare and select models. Understanding the tradeoffs between the amount of time and sample sizes it might take to complete informative assessments is also critical so the Council can support, and can encourage fishers to support, the improved methods long enough to see the results necessary to improve management. This thesis developed such a simulation model for use in the U.S. Caribbean commercial data collection restructuring comparing the Beverton-Holt and Gedamke-Hoenig mean-length mortality estimators over a range of sample sizes and short sampling time series to evaluate the ability to get results in the near future.

Fisheries management in the U.S. Caribbean is challenging because of commercial fishery data problems and the resulting limitations they impose on stock assessments. The Council cannot complete management directives as mandated by national law because of this. Even the most basic of assessments, while technically possible, are not informative. In order for the Council to follow through with their mandates, the data collection and protocols of each island in the U.S. Caribbean need to be reviewed to suggest possible improvements. In addition, the Council and fishers on the islands need to understand the depth of commitment to the modified data collection method necessary to get enough data for stock assessment biologists to complete assessments to aid critical fisheries management decisions.

Improving data collection in small-scale, multi-species and multi-gear fisheries is a very important part of successful management (Berkes et al. 2001; FAO 2003). The “Improving the Collection and Use of Fisheries Data Study” by the Ocean Studies Board, under the National Research Council, encouraged NMFS and fishery management councils to put a high priority on improving fishery-dependent data because they are more useful in stock assessments than fishery-independent data (National Research Council 2000). Improvements and the understanding of data requirements and potential stock assessment models and their caveats are necessary to take management to the next level of science-based decision making and the CFMC

has made it a priority to do so. A group of scientists, managers, fishermen, and other stakeholders have been meeting since the SEDAR procedures workshop in 2009 to guide the improvements in data collection. My project has focused on creating a simulation model to be used as a tool by the group to inform them of the approximate number of samples and years of sampling necessary to use their model of choice, the Gedamke-Hoenig mean-length mortality estimator model, as well as presenting the possible caveats of using the model, including the tradeoffs between using it and the simpler Beverton-Holt model.

Literature Cited

- Ault, J.S., S.G. Smith, J. Luo, M.E. Monaco and R. Appeldoorn. 2008. Length-based assessment of sustainability benchmarks for coral reef fishes in Puerto Rico. *Environmental Conservation*. 35(3):221-231.
- Berkes, F., R. Mahon, P. McConney, R. Pollnac, and R. Pomeroy. 2001. *Managing small-scale fisheries: alternative directions and methods*. International Development Research Centre. Ottawa. 309 p.
- Beverton, R. J. H. and S. J. Holt. 1956. A review of methods for estimating mortality rates in fish populations, with special reference to sources of bias in catch sampling. *Rapports et Proces-verbaux des Reunions, Conseil International Pour L'Exploration de la Mer* 140: 67-83.
- Booth, A.J. and T.J. Quinn. 2006. Maximum likelihood and Bayesian approaches to stock assessment when data are questionable. *Fisheries Research* 80: 169-181.
- Commonwealth of Puerto Rico. 2004. *Puerto Rico fishing regulations (English version)*. Puerto Rico Department of Natural and Environmental Resources. San Juan. 43 p.
- Department of Planning and Natural Resources. 2004. *Commercial and recreational fisher's information booklet*. Division of Fish and Wildlife and Division of Environmental Enforcement. 33 p.
- Ehrhardt, N. M. and J. S. Ault. 1992. Analysis of two length-based mortality models applied to bounded catch length frequencies. *Transactions of the American Fisheries Society*. 121: 115-122.
- Food and Agricultural Organization of the United Nations (FAO). 2003. *Strategy for improving information on status and trends of capture fisheries*. Rome. 34 p.
- Gaertner, D. 2010. Estimates of historic changes in total mortality and selectivity for Eastern Atlantic skipjack (*Katsuwonus pelamis*) from length composition data. *Aquatic Living Resources*. 23: 3-11.
- Gedamke, T. and J. M. Hoenig. 2006. Estimating mortality from mean length data in nonequilibrium situations, with application to the assessment of goosfish. *Transactions of the American Fisheries Society* 135: 476-487.
- Gedamke, T. 2007. Estimation of Mutton Snapper total mortality rate from length observations. SEDAR 14 Caribbean Yellowfin Grouper, Mutton Snapper, Queen Conch. North Charleston, SC. SEDAR14-AW-05.
- Griffith, D., Valdes Pizzini, M., and C. Garcia Quijano. 2007. *Entangled communities: Socioeconomic profiles of fishers, their communities and their responses to marine protective*

measures in Puerto Rico (Volume 2: Regional Profiles). NOAA Technical Memorandum NMFS-SEFSC-5562007. NOAA Series on U.S. Caribbean Fishing Communities. 190 p.

Gulland, J. A. 1983. Fish stock assessment: A manual of basic methods. FAO/Wiley Series on Food and Agriculture, Vol. I.

Gulland, J. A. and A. A. Rosenberg. 1992. A review of length-based approaches to assessing fish stocks. FAO Fisheries Technical Paper. No. 323. Rome, FAO. 100 p.

Hilborn, R. and C.J. Walters. 1992. Quantitative Fisheries Stock Assessment: Choice, Dynamics and Uncertainty. Chapman & Hall. New York.

Jentoft, S. 1989. Fisheries co-management: delegating government responsibility to fishermen's organizations. Marine Policy (2): 137-154.

Jones, R. 1984. Assessing the effects of changes in exploitation pattern using length composition data. FAO Fisheries Technical Paper. No. 256, Rome, 118 p.

Kojis, B. 2004. Census of the marine commercial fishers of the U.S. Virgin Islands. Report to the Caribbean Fisheries Management Council. San Juan. 78 p.

Laurec, A. and B. Mesnil. 1987. Analytical investigations of errors in mortality rates estimated from length distribution of catches. In Pauly, D. and G. R. Morgan (eds.). Length-based Methods in Fisheries Research. ICLARM Conference Procedures, 13: 239-281.

Matos-Caraballo, D., León, J., López, H.Y., Mercado-Porrata, A., Rivera, L.A., and L.T. Vargas. 2007. Puerto Rico's small-scale fisheries statistics 2004-2006. Report: Proceedings of the 60th Gulf and Caribbean Fisheries Institute Meeting, November 5-9th, 2007. Punta Cana, Dominican Republic.

McCarthy, K. and T. Gedamke. 2009. United States Virgin Islands fisheries description and available data: preliminary evaluation. SFD-2009-002, 13 p.

Munro, J. L. and R. Thompson. 1973. The biology, ecology, exploitation and management of Caribbean reef fishes. Part II. The Jamaican fishing industry, the area investigated and the objectives and methodology of the ODA/UWI Fisheries Ecology Research Project. Research Report 3, University of the West Indies Zoology Department. 44 p.

National Research Council. 1998. Improving Fish Stock Assessments. National Academies Press, Washington D.C. 177 p.

National Research Council. 2000. Improving the Collection and Use of Fisheries Data Study. National Academies Press, Washington D.C. 222 p.

National Research Council. 2004. Improving the Use of the “Best Scientific Information Available” Standard in Fisheries Management. National Academies Press, Washington D.C. 119 p.

Pauly, D. 1983. Some simple methods for the assessment of tropical fish stocks. FAO Fisheries Technical Papers No. 234, Rome, 52 p.

Powell, D. G. 1979. Estimation of mortality and growth parameters from the length frequency of a catch. *Rapports et Proces-verbaux des Reunions, Conseil International Pour L’Exploration de la Mer* 175: 167-169.

Quinn, T.J. and R. B. Deriso. 1999. *Quantitative Fish Dynamics*. Oxford University Press. New York. 542 p.

Salas, S., R. Chuenpagdee, J. C. Seijo, A. Charles. 2007. Challenges in the assessment and management of small-scale fisheries in Latin America and the Caribbean. *Fisheries Research* 87: 5-16.

SEDAR. 2009. Caribbean Fisheries Data Evaluation. SEDAR Procedures Workshop 3. North Charleston, SC. 183 p.

SEDAR. 2007a. Stock Assessment Report 1: Caribbean Yellowfin Grouper. SEDAR 14-SAR1. North Charleston, SC. 164 p.

SEDAR. 2007b. Stock Assessment Report 2: Caribbean Mutton Snapper. SEDAR 14-SAR2. North Charleston, SC. 194 p.

SEDAR. 2007c. Stock Assessment Report 3: Caribbean Queen Conch. SEDAR 14-SAR3. North Charleston, SC. 171 p.

SEDAR. 2005a. Assessment Report I: Caribbean Yellowtail Snapper. SEDAR 8-Stock Assessment Report 1. Charleston, SC. 179 p.

SEDAR. 2005b. Assessment Report 2: Caribbean Spiny Lobster. SEDAR 8-Stock Assessment Report 2. Charleston, SC. 195 p.

SEDAR. 2004. Data Report of SEDAR 4, Atlantic and Caribbean Deepwater Snapper-Grouper, Caribbean Species. SEDAR4-SAR2. Charleston, SC. 196 p.

Sparre, P. and S. C. Venema. 1998. Introduction to tropical fish stock assessment Part 1: Manual. FAO Fisheries Technical Paper No. 306.1, Rev. 2. Food and Agriculture Organization of the United Nations. Rome. 407 p.

Ssentongo, G. W. and P. A. Larkin. 1973. Some simple methods of estimating mortality rates of exploited fish populations. *Journal of the Fisheries Research Board of Canada*. 30: 698-698.

U.S. Department of Commerce. 2007. Magnuson-Stevens Fishery Conservation and Management Act. National Oceanic and Atmospheric Administration. National Marine Fisheries Service. Public Law 94-265. May. 170 p.

Valle-Esquivel, M. 2002. Standardized catch rates and preliminary assessment scenarios for queen conch (*Strombus gigas*) in the U.S. Caribbean. NOAA National Marine Fisheries Service Southeast Fisheries Science Center. Sustainable Fisheries Division Contribution No. SFD-02/03-184. 63 p.

Wetherall, J. A., J. J. Polovina and S. Ralston. 1987. Estimating growth and mortality in steady-state fish stocks from length-frequency data. In Pauly D. and G.R. Morgan (eds.). Length-based methods in fisheries research. ICLARM Conference Proceedings, 13:53–74.

Figure 1.1 Map of the U.S. Caribbean from the Caribbean Fisheries Management Council website (www.caribbeanfmc.com).

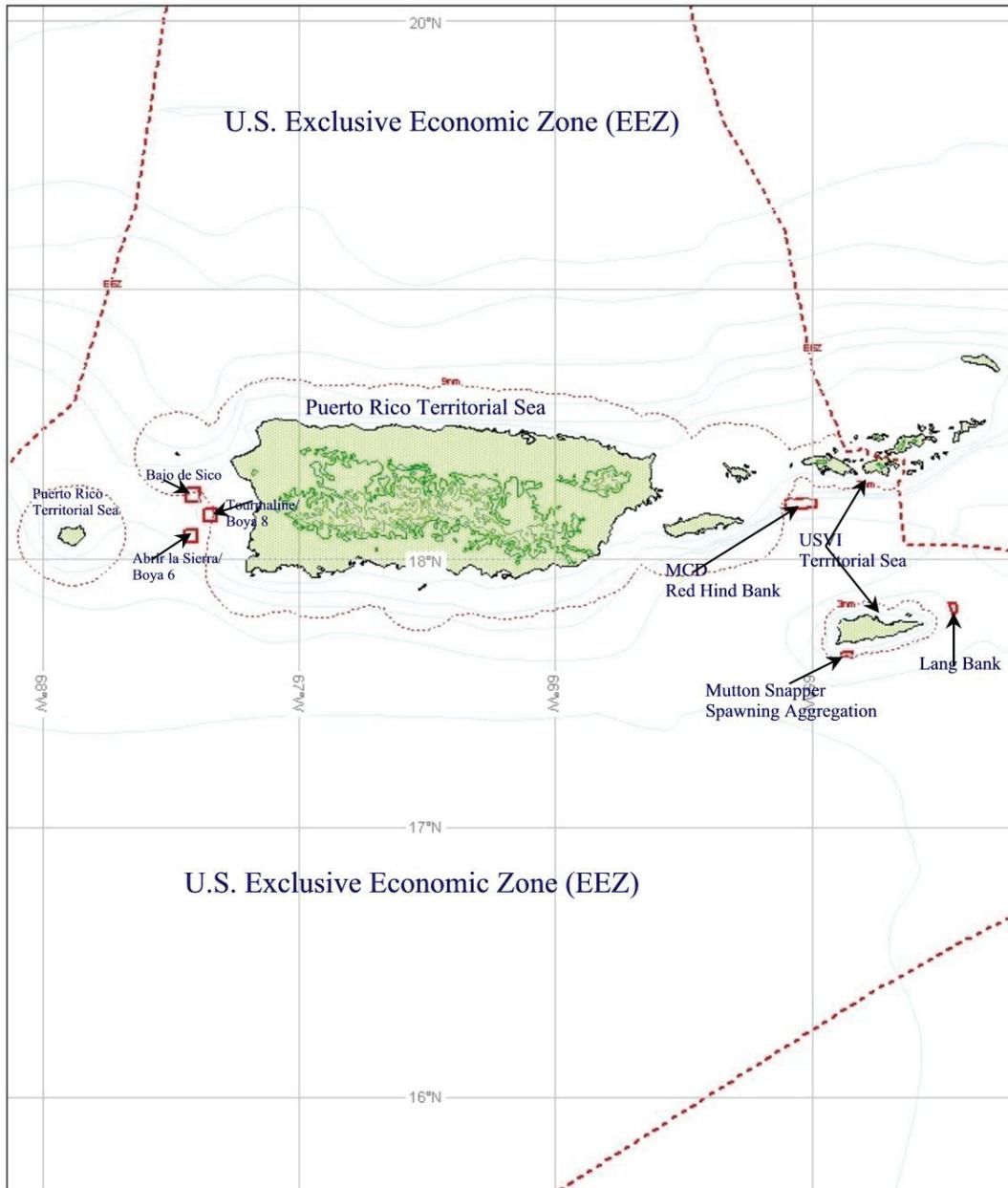


Figure 1.2 Page one of the 2008 Puerto Rico TIP form.

REPORTING FORM FOR THE TRIP INTERVIEW PROGRAM (TIP)												
Next Row is for Data Entry Personnel Use Only												
PC Data Entry by:		Date:		Batch		Interview #:						
SECTION I												
Interview Number												
Fishery Codes	CP	RF	OP		IN	ML	BF		EG	MX	SL	
Trip Type	030	100	200	300	400	600	675	676	735	900		
Agent Code or Name	OR											
Date of Interview	Month		Day		Year							
Reporting Area of Landings	Reporting State				Reporting County				Reporting Area Zipcode			
Sampling Site	State		County		Zipcode		Sampling Location Code (Dealer or MRFSS)					
Start / End Date of Trip	Start Month		Start Day		Start Year		End Month		End Day		End Year	
Information Source	SR	LB	CI	SS		SI	OD		SO			
	Sales Records	Logs		Site Sampling		Recs and Int	Observer Data		Recs and Observ			
Fishing Mode	CM	CP		HB		PR	TR		SS			
	Commercial	Charter/Party		Head Boat		Private Rec	Tournament		Scientific Survey			
Time of Data Collection -24hr	Begin	:		End	:							
	Hour	Minutes		Hour	Minutes							
Bias Type	NB		SB		EB		SE		NI			
	No Bias		Size Bias		Effort Bias		Size & Effort		No Information			
Interview Type	FS		DS		TS		AT					
	Fisherman Sample		Dealer Sample		Trip Survey		Angler Trip					
Landings Type	CL		IL		NL		NF					
	Complete Landings (weight)		Incomplete Landings		No Landings		No Fish Caught					
Crew Size	(The number of crew including the captain)											
Total Effort	---	---	UK	NR	WR	EQ	NF	SA	WI	OB	QR	
	Days Out	Days Fished	Termination Code									
Vessel Information	Vessel ID				Vessel Length (feet)				Vessel Name			
SECTION II												
Gear Information						Effort / Location						
Code	Number	Quantity	Other			Soak Time (Hours)	Area Fished	Depth Range (Fathoms)				
---	-----	-----	-----			-----	-----	---/---				
---	-----	-----	-----			-----	-----	---/---				
---	-----	-----	-----			-----	-----	---/---				
---	-----	-----	-----			-----	-----	---/---				
---	-----	-----	-----			-----	-----	---/---				

Figure 1.3 Page one of the 2008 Puerto Rico landings form.



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**PROGRAMA DE ESTADÍSTICAS PESQUERAS
 SISTEMA DE UN BOLETO POR VIAJE**

Fecha de desembarco ____/____/____
 Mes Día Año

Pueblo _____

Centro de desembarco _____ Uso Oficial _____

Número de teléfono _____ Número de horas pescando _____

Nombre del pescador 1 _____

Número licencia del pescador 1 _____ Fecha de Exp. _____

Nombre del pescador 2 _____

Número licencia del pescador 2 _____ Fecha de Exp. _____

Nombre del pescador 3 _____

Número licencia del pescador 3 _____ Fecha de Exp. _____

Profundidad máxima en brazas _____ Profundidad mínima en brazas _____

Area donde capturó la pesca: Lat _____ Min _____ Long _____ Min _____

Pesca capturada a una distancia de la costa:

Mayor de 10 millas _____ Menor de 10 millas _____

CLASE DE PESCADO	PESO	PRECIO POR LIBRA	ARTE	CANTIDAD O TAMAÑO DE ARTE
(226) ATUN ALETA AMARILLA				
(228) BONITO				
(230) VACA				
(229) BACORA				
(225) ATUNES				
(055) BALAJU				
(155) BOQUICOLORADO				
(189) CAPITAN				
(256) CHAPINES				
(128) DORADO				
(064) GALLOS				
(199) JAREA				
(155) COJINUA				

LISTA DE PESCADO Y MARISCO CONTINUA AL REVERSO DE ESTA HOJA

CLASE DE PESCADO	PESO	PRECIO POR LIBRA	ARTE	CANTIDAD O TAMAÑO DE ARTE
(116) GUAYMEN AMARILLO				
(118) JUREL				
(109) QJON				
(192) JURELES				
(192) LOROS				

Figure 1.4 Changes in the USVI reporting form over time.

1	2	3	4	5
OLD FORM (1) (1974-1985)	OLD FORM (2) (1986-1999)	OLD FORM (3) (Short) (1988-1992)	OLD FORM (4) (1992-1999)	NEW FORM (Revised) (1994-2003)
1. ID#	1. LOCATION	1. ID CODE	1. ID CODE	1. GEAR TYPE
2. LAST NAME	2. FISHERMEN #	2. CLASS	2. FISHED (yes/no)	2. GEAR NO.
3. FIRST NAME	3. VESSEL #	3. ISLE: St. Croix St. Thomas/ St. John	3. TRIP DATE	3. AREA FISHED
4. BOAT LICENSE	4. DATE	4. TRIP DATE	4. POT FISH	4. HOURS FISHED
5. FISHING LICENSE	5. POTFISH	5. FISH CODE: Bait (B), Conch (C)	5. POTS	5. GROUPED
6. DATE	6. NETFISH	6. GEAR CODE:	6. HOOK FISH	6. SNAPPER
7. # OF HELPERS	7. HOOKFISH	Finfish (S), Lobster (L), Whelk (W), Other(Z)	7. NET FISH	7. GRUNT
8. POT FISH SNAPPER GROUPER	8. SPEAR GUN	7. NO. POTS	8. SPEARGUN	8. JACK
9. POT FISH ALL OTHERS	9. POT LOBSTER	8. NO. SPEAR GUNS (S_G)	9. POT LOBSTER	9. SURGEON
10. NET FISH SNAPPER GROUPER	10. DIVED LOBSTER	9. NO. OTHER GEAR	10. DIVED LOBSTER	10. PARROT
11. NET FISH ALL OTHERS	11. CONCH	10. FISH AREA	11. CONCH	11. SHELLFISH
12. HOOK FISH SNAPPER GROUPER	12. WHELK	Diving (D), Hook& Line (H) Net (N), Pot or trap (P).	12. WHELK	12. TRIGGER
13. HOOK FISH ALL OTHERS			13. BAITFISH	13. BARRA
14. SPEAR/GUN FISH SNAPPER GROUPER			14. FISH AREA	14. GOAT
15. SPEAR/GUN FISH ALL OTHERS			15. DISTANCE FROM SHORE (> 3 miles)	15. MACKEREL
16. LOBSTER BY POT			16. TUNA	16. OFFSHORE (D/T/W)
17. LOBSTER BY HAND			17. DORADO	17. FAD
18. OTHER KINDS CONCH, WHELK, OCTOPUS, SQUID, CLAM, OYSTERS			18. WAHOO	18. BAITFISH
19. AREA				19. LOBSTER
20. NOTES				20. CONCH MEAT
				21. WHELK MEAT
				22. DISTANCE FR LAND

Figure 1.5 Data availability of landings data and species groups in St. Thomas and St. John from commercial fishermen's logbooks. From McCarthy and Gedamke 2009.

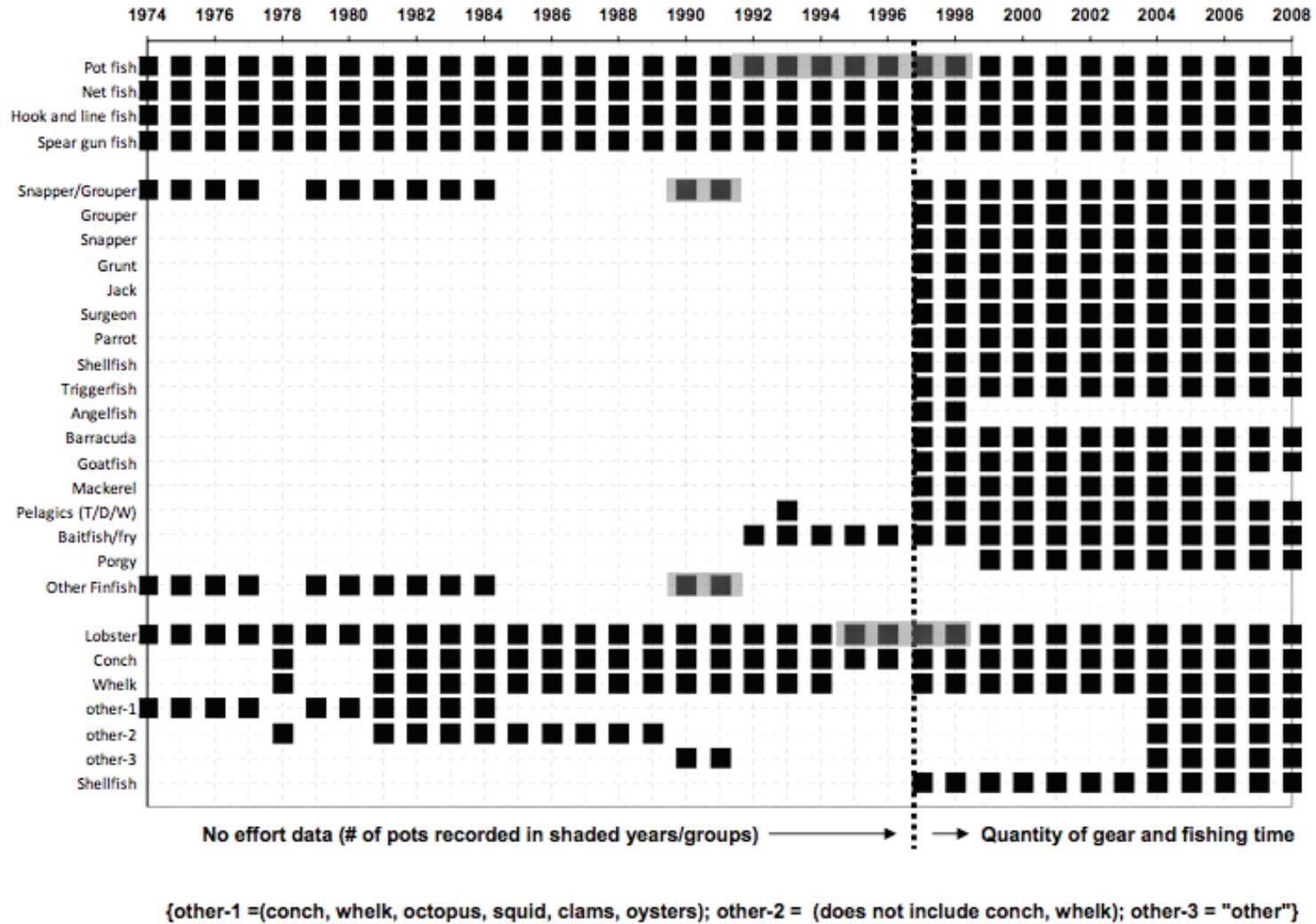
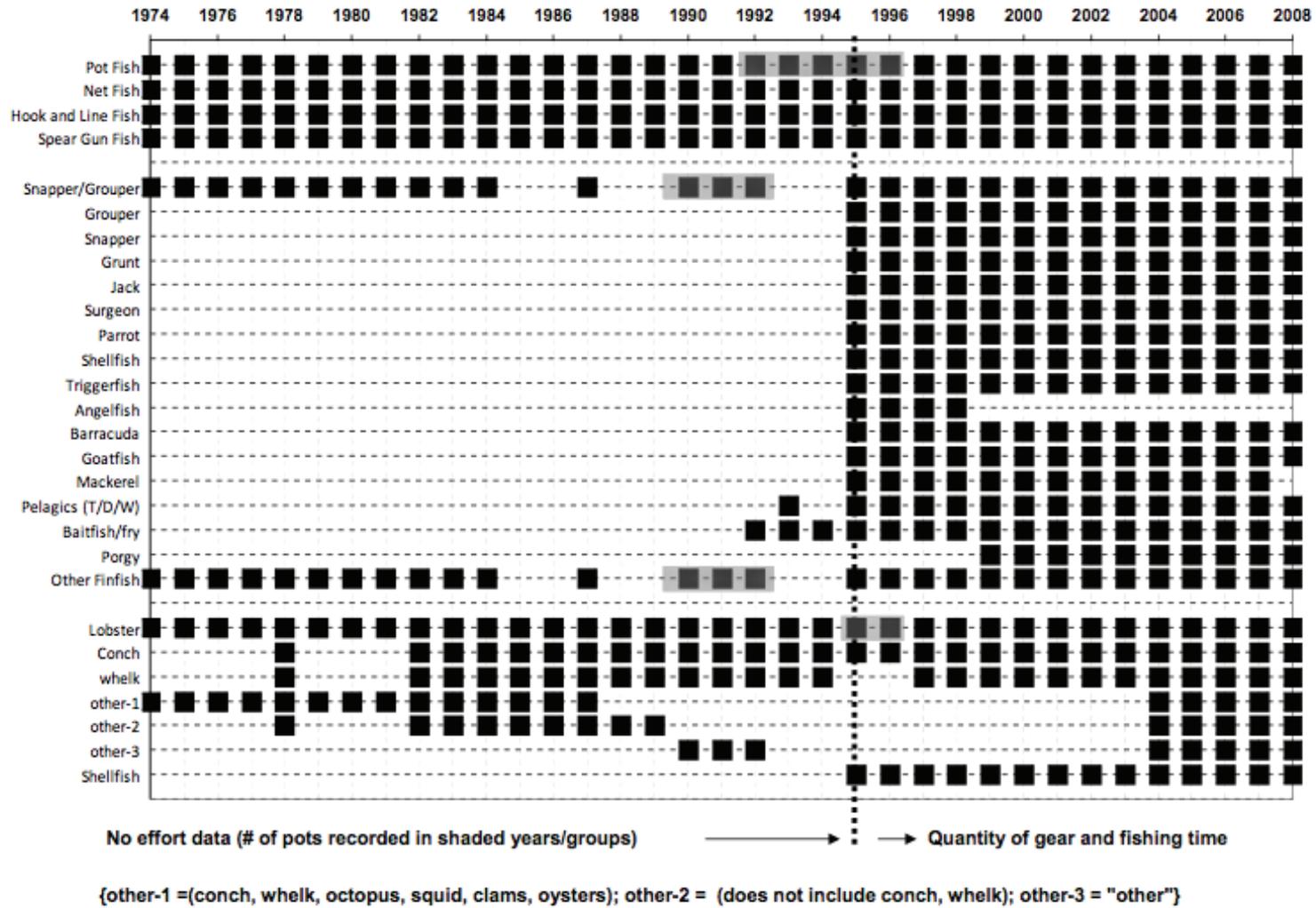


Figure 1.6 Data availability of landings data and species groups in St. Croix from commercial fishermen's logbooks. From McCarthy and Gedamke 2009.



CHAPTER 2—COMPARING TWO LENGTH-BASED MORTALITY ESTIMATORS USING SIMULATION MODELING

Introduction

Length-based stock assessment models are attractive choices for assessing fisheries with limited data. The models require only length data over time and the von Bertalanffy growth parameters derived from an age-growth relationship. This information is relatively cheap and easy to collect compared to many other biological samples. They are especially attractive in data-poor tropical fisheries, because aging tropical fish is not only expensive, but can be difficult as well (Gulland 1983, Sparre and Venema 1998). One tropical region exploring the use of length-based methods for stock assessment is the U.S. Caribbean.

As a small-scale tropical fishery, the U.S. Caribbean (consisting of the islands of Puerto Rico, St. Thomas, St. John, and St. Croix) has had several issues collecting data appropriate for stock assessments. The fisheries are often artisanal in nature, spread out over many landing sites, and fishermen and managers often do not have a relationship of trust and cooperation (Griffith et al. 2007). In addition to the social and economical challenges, the data previously collected has not been species-specific in the United States Virgin Islands (USVI) part of the region (St. Thomas, St. John, and St. Croix). In the entire region, it has also been difficult to determine where fishing is occurring across a broad range of habitats, and the multi-gear, multi-species catches were difficult to sort apart (Gedamke et al. 2009). Fishing pressure has also likely changed in the past few years with the passing of new fishery management plans and the banning of some of the gears. With all of these factors in mind, the U.S. Caribbean has been trying to improve data quality for stock assessment, but time and money resources are limited. The Caribbean Fishery Management Council (CFMC), its Scientific and Statistical Committee (SSC), and the 2009 Caribbean Data technical procedures Southeast Data, Assessment, and Review (SEDAR) Workshop have all expressed a desire to use the Gedamke-Hoenig mean-length mortality estimator (G-H model) to evaluate their fisheries, once enough quality data are available (SEDAR 2009).

While several length-based methods exist, most require the assumption of a population in a state of equilibrium with constant mortality rates for at least as long a time period as the longevity of the species being analyzed. The G-H model does not require the assumption of constant mortality. Since fishing behaviors in the U.S. Caribbean have been changing in recent years due to changing regulations on all islands and the banning of gill nets in the USVI, the G-H model appears to be a good choice for a length-based stock assessment model. However, the G-H model is relatively new and the statistical tradeoffs between it and other length-based models have not been rigorously tested. It was initially tested using real data from the goosefish fishery in the northeast and also simulated data (Gedamke and Hoenig 2006). Initial testing of the model found that it performed well compared to the Beverton-Holt model (B-H model), the simpler length-based model from which it is derived (Gedamke and Hoenig 2006). However, those analyses did not look at species with several different life history types, did not incorporate yearly variability in growth or recruitment in their simulated data and did not investigate the effects of sample sizes. Understanding the performance of the G-H model in comparison to the B-H model requires knowledge of the effects of these factors.

As part of a stock assessment simulation modeling project for the U.S. Caribbean, the performance of two models (the B-H and G-H models) was further explored to provide guidance in interpreting results in order to better inform management, scientists, and fishermen in the region about the mortality rates in their fisheries and help determine how best to modify their commercial data collection to get stock assessment appropriate data. Both models have similar data requirements, yet the assumption of a population at equilibrium in the B-H model is likely violated given the history of fishing in the region. The thorough testing of the robustness and possible bias of length-based models that depart from the assumption of equilibrium has been strongly encouraged before deciding on their use as stock assessment tools in developing countries or other data-poor fisheries (Csirke et al. 1987). As a result, the goal of this portion of the project was to determine how well the Gedamke-Hoenig model performed compared to the Beverton-Holt model, in terms of accuracy and variance, using a simulation model for U.S. Caribbean fishery-dependent sampling. This simulation model allowed for everything about the population of fish to be known and helped to analyze the behavior of the Gedamke-Hoenig

model in ways previous simulations had not, including: using information from several different species covering several different life history parameters, varying growth and recruitment yearly, and looking at the impact of sample sizes.

Length-Based Mortality Estimators

Length-based stock assessment models, such as the Beverton-Holt mortality estimator model (B-H model) are commonly suggested for use in data-poor situations, like those in the U.S. Caribbean (Pauly 1983, Jones 1984, Quinn and Deriso 1999). Using the mean lengths and the von Bertalanffy growth parameters of asymptotic length (L_{∞}), length at first capture into the fishery (L_c) and growth rate (K), the total mortality rate for a population can be solved using the B-H model (Equation 1) (Beverton and Holt 1956).

$$Z = \frac{K(L_{\infty} - \bar{L})}{\bar{L} - L_c} \quad (1)$$

A critical assumption of the model's estimates is that the population is at an equilibrium mean length, meaning that the oldest animal in the population has only been subject to a single total mortality rate. This assumption is often violated given changes that occur in fishing communities due to changes in technology, regulations, and environmental factors over periods of time. Other assumptions of the model include constant growth of individuals and constant recruitment over time. These assumptions are broad and likely violated in a fishery over time. Because of this, some have expressed the need for caution in using the B-H model for management situations (Ralston 1989).

In contrast, the Gedamke-Hoenig model (G-H model) not only allows for, but estimates changes in mortality rates over time. The model's methods evaluate changes in average length to estimate changes in total mortality rates. Like the B-H model, it requires the von Bertalanffy growth parameters, K , L_{∞} , and the length at full vulnerability (L_c). In addition, the model requires the mean length of the samples for each year of sampling effort. Using these values, the model estimates the mortality rate before change (Z_1), the mortality rate after the change (Z_2) and the years since the change occurred (d) which leads to an estimate of the year of change (T_c).

With this information and equation (2), you can solve for the parameters of interest using a likelihood function (Gedamke and Hoenig 2006).

$$\bar{L} = L_{\infty} - \frac{Z_1 Z_2 (L_{\infty} - L_c) \{Z_1 + K + (Z_2 - Z_1)^{-(Z_2 + K)d}\}}{(Z_1 + K)(Z_2 + K)[Z_1 + (Z_2 - Z_1)^{-Z_2 d}]} \quad (2)$$

While having similar data requirements as the B-H model, the G-H model accounts for changes in the mortality of the population (Z_1 to Z_2) (Gedamke and Hoenig 2006). Obviously, this is a necessary development in stock assessment because fishing behavior does change over time and needs to be considered in the calculation of important biological reference points often used to evaluate the fishery and guide regulations. Assuming the natural mortality rate does not change over time, the differences in total mortality rates are attributed to changing fishing mortality rates.

The G-H model has been applied to other data-poor situations, such as goosefish (Gedamke and Hoenig 2006). Studies indicated the model performed well, especially when it came to determining a pattern of exploitation (Gedamke and Hoenig 2006). The G-H model with multiple changes in mortality has also been used by Gaertner 2010 to evaluate Eastern Atlantic skipjack data. The study found that the model was able to detect multiple changes in mortality in the fishery and that the predicted changes of the model were similar to annually calculated Beverton-Holt estimates (Gaertner 2010). The use of the G-H model is desired in the Caribbean and evaluation using Caribbean data has even been attempted in the past. Unfortunately, the results were not used because of doubts as to whether or not fishing location had changed, which would violate spatial assumptions (Gedamke 2007, Gedamke et al. 2009).

Methods

For comparing the two models, a simulation study was conducted with five major modules. The first was the population generation, used to develop a population of fish where all lengths of fish were known throughout the years. The second was the random sampling of fish from the generated population. Next, the samples were used to estimate total mortality rates using both the B-H and G-H mean-length mortality estimators. For each simulation's estimations, results

were calibrated to account for a concern over the optimization function in the programming language used for the model and differences between the population generation and estimation steps of the model. Finally, results for both calibrated model estimates were compared and analyzed to evaluate AIC values and performances in accuracy and variance. Each of these steps is outlined in detail below.

Population Generation

The simulation model was developed using the R statistical programming language with a simulated population of fish where life history parameters and total mortality rate histories were known exactly (R Development Core Team 2010). Each population was initialized with 1000 individuals per each 1 cm length interval over the length distribution from the length of first catch (L_c) to the length at infinity (L_∞). The population was then projected forward by converting the lengths at time t (L_t) to ages (Equation 3a) and then increasing the age one time step (Equation 3b), before converting the ages back to lengths (Equation 3c). Any length bins remaining without individuals after each time step were filled with recruits. Recruits were either constant between each year, with 1000 individuals per empty length bin, or varied each year, depending on the scenario.

$$Age_t = \frac{-\log\left(1 - \left(\frac{L_t}{L_\infty}\right)\right)}{K} \quad (3a)$$

$$Age_{t+1} = Age_t + 1 \quad (3b)$$

$$L_{t+1} = L_\infty(1 - e^{-K(Age_{t+1})}) \quad (3c)$$

This was done for a seventy year time period to ensure the population had reached a stable length distribution. At year seventy ($T_c=70$), mortality rate of the simulated population changed (from Z_1 to Z_2 , where Z_1 designates the total mortality before the change and where Z_2 designates the total mortality after the change) with the direction and magnitude of that change varying by scenario. For each scenario, 2500 simulations were run.

Several different scenarios, with 2500 simulations each, were run where several parameters varied. The total mortality rate (Z_1 and Z_2), the direction and magnitude of the change in total

mortality rate were two factors that varied: in half of the scenarios, total mortality rates increased (from 0.5 yr⁻¹ to 1.0 yr⁻¹) and in the rest total mortality decreased (from 1.0 yr⁻¹ to 0.5 yr⁻¹). Other factors included the year of the change in total mortality rate occurred in relation to the year in which sampling began (T_c) as well as the overall length of the time series (Y_s). Three commonly caught species in the U.S. Caribbean covering different Von Bertalanffy growth parameter values (K, L_c, L_∞) were the basis for the simulated populations and included: Yellowtail snapper (*Ocyurus chrysurus*), red hind (*Epinephelus guttatus*), and redbtail parrotfish (*Sparisoma chrysopterus*). The growth parameter information came from Claro (2001) and analyses of existing U.S. Caribbean data by Todd Gedamke were used to calculate L_c (T. Gedamke, Southeast Fisheries Science Center, personal communication).

The consequences of violating the assumptions of constant mortality and growth have not been thoroughly studied for the G-H model, although we know some variation and uncertainty for these parameters are likely to occur in real data. To account for uncertainty and variability in the population, in some scenarios recruitment and growth rates (R and K; respectively) were randomly chosen from lognormal distributions, mimicking stochastic environmental changes on a year-to-year basis. The lognormal distribution was chosen because negative values of both growth and recruitment rates are impossible. For each rate, one of three levels of variability was chosen (none, low, or high) and all possible combinations were analyzed (Table 1). For the recruitment rate, the base number of recruits was 1000 and that was multiplied times a random number from a lognormal distribution centered around one with a standard deviation for the low level at 0.2 and while at the high level was 0.4 (Equation 4a; Equation 4b; Figure 1). The variability of the growth rate was centered at a multiplier of one, with the standard deviations at 0.25 and 0.5 for the low and high levels respectively (Equation 5a; Equation 5b; Figure 2).

$$\text{Recruitment} = f(x) = 1000 \left(\frac{e^{-((\ln x)^2 / 2(0.2^2))}}{x(0.2)\sqrt{2\pi}} \right) \quad (4a)$$

$$\text{Recruitment} = f(x) = 1000 \left(\frac{e^{-((\ln x)^2 / 2(0.4^2))}}{x(0.4)\sqrt{2\pi}} \right) \quad (4b)$$

$$\text{Growth rate} = f(x) = K \left(\frac{e^{-((\ln x)^2 / 2(0.25^2))}}{x(0.25)\sqrt{2\pi}} \right) \quad (5a)$$

$$\text{Growth rate} = f(x) = 1000 \left(\frac{e^{-((\ln x)^2 / 2(0.5^2))}}{x(0.5)\sqrt{2\pi}} \right) \quad (5b)$$

Little is known about the variability of growth and recruitment of the fish stocks in the U.S. Caribbean, so values were chosen so that at the low standard deviations there was approximately an equal probability of having a rate that was half of the mean as it was double the mean. Standard deviations for the high levels of variability were chosen so that there was approximately an equal probability of having no recruitment or growth, as there was of the recruitment rate equaling four times the mean. For this study, the species chosen purposefully covered several possible life histories to determine the sensitivity of the model to differences in life history parameters. Given the uncertainty in the amount of annual in growth and recruitment rates, understanding some of the possible impacts of breaking the critical assumptions of constant growth and recruitment over the period of sampling on our results is more important at the present time than knowing impacts at specific magnitudes of the variation.

The selected growth rate value (K) was chosen as described above, but in addition, the von Bertalanffy equation was modified to account for this change (Equation 6). This determined the new length class for individuals by taking the old length the previous year and accounting for the change in K by calculating the new length with the new growth rate (K.var) and subtracting what the old length would have been with the new growth rate. By varying K this way, in certain scenarios the population went above L_{∞} .

$$L_{t+1} = L_{\infty}(1 - e^{(-K(Age_t))}) + L_{\infty}(1 - e^{(-K.var(Age_{t+1}))}) - L_{\infty}(1 - e^{(-K.var(Age_t))}) \quad (6)$$

Sampling

For each of the 2500 simulations, a set of length measurement samples was taken from the population in the last few years of the simulated population. These samples represented length samples that could be taken by port samplers at the dock. A range of samples sizes was analyzed (n=10, 25, 50, 100, 250, and 500 length measurements per year). Different numbers of years

sampled were examined (Y_s), ranging from four consecutive years of sampling to eight years of sampling for each scenario.

In addition, when the year sampling started (T_s) relative to the year of change in mortality rate (T_c) also varied by scenario. Three different scenarios were examined. In the first scenario, sampling started the year the total mortality rate changed ($T_s=T_c$). In the second scenario, sampling started two years before the change in Z occurred ($T_s=T_c-2$). In the third scenario, sampling began two years after the change in Z ($T_s=T_c+2$).

Looking at these possible T_s values is important because sampling does not always begin when a change in fishing mortality occurs and that can impact the model's ability to accurately and precisely estimate a change in mortality. In the case of the U.S. Caribbean, it is difficult to determine when these major changes occurred or will occur relative to when sampling will begin. Changes have likely occurred in the past due to changing regulations and have the possibility of occurring in the future. Given the relatively short sampling time frames examined in this study, it was important to understand the sensitivity of the model's estimates to all these possible scenarios.

Stock Assessment Model

For each set of length samples within a year, the mean length of the samples was calculated. This was done for each simulation, across all scenarios. These mean lengths were then used in both the B-H and G-H mean-length mortality estimators. The number of mean lengths used in each estimation was dependent on the length of Y_s (from three to seven). For the B-H model, the total mortality rate (Z) and variance (σ) was then calculated. The G-H model estimated Z_1 , Z_2 , T_c and variance (σ). While the G-H model is capable of estimating multiple changes in mortality, for this particular simulation model T_c was not estimated and only one change was simulated, to simplify and increase the speed of the simulations.

Adjustments

Several adjustments of the final estimation values were necessary given the programming language used and models chosen for this project. A concern has been raised about the reliability of the optimization function in R (M. Prager, Adjunct Faculty Member, Virginia Tech Department of Fisheries and Wildlife Sciences, personal communication). To mitigate the potential effect of poor optimization in R and standardize the simulations, an optimization study was completed with the simulation model. It compared the five main algorithms within the `optim()` function in R to determine which would be most appropriate for the model. For this study, I chose the limited-memory Broyden-Fletcher-Goldfarb-Shanno algorithm (LBFGS) with `par`scale option of the `optim()` function because it consistently gave results closest to the known values in the simulated population, it has more flexibility than the regular Broyden-Fletcher-Goldfarb-Shanno (BFGS) algorithm if major problems should arise in the future, and differences between the top two performing algorithms were generally negligible (Table 2.2).

The population simulation and estimation procedures had slightly different computational assumptions. The population simulation was developed using a discrete growth function, where the population distribution across lengths was not continuous. In contrast, the estimation method was developed based on a continuous population distribution. To address this, a correction factor was calculated by estimating parameters using mean length data from the entire simulated population (i.e. with no sampling and ‘perfect’ data) for both the B-H and G-H models. The difference between the parameters estimated using lengths from the entire simulated population and the known parameters (The simulated Z_1 and Z_2 for G-H model and the average Z for B-H model) was used as a correction factor that was applied to all results within a scenario to correct for this behavior. Separate correction factors were developed for each scenario.

Evaluation

After generating the population and estimating the parameters of interest, several filters were applied to the results. These filters took out estimations that were considered invalid because they produced values that were not numbers (e.g., NaN) or estimates were at the limit of a predetermined upper and lower bound within the optimization (lower bound=0.01 and upper bound=3). In a non-hypothetical analysis, only one set of parameter estimations would be

produced, because you would only have one mean length value per sampled year. For this study, 2500 possible outcomes per scenario are presented. If an invalid estimation result were to occur in a single analysis, little adjustments in the optimization and initial starting guesses could eliminate the error. In this study no such adjustments were done so that all of the results would be standardized.

In addition, the AICc values of the two models were compared. The Akaike information criterion (AIC) has traditionally played an important role in determining which model is most appropriate for the data presented. AIC was developed as a tool for model selection to measure the tradeoffs between parsimony and the information you could get out of the data. The calculation incorporates the number of model parameters (k), the number of samples (n), and the value of the likelihood objective function (Equation 6) (Akaike 1974).

$$AIC = 2k + n[\ln(\sum_{i=1}^n \hat{\epsilon}_i^2)] \quad (6)$$

The criterion has been shown as a viable tool to justify the use of a particular stock recruit curve (Wang and Liu 2006), and choose models in hypothetical situations using stock assessment tools such as stock synthesis (Helu, et al. 2000).

For each simulation and each model, an AICc value was calculated. AICc is an extension of the regular AIC calculation, taking into account small sample sizes, which were present in the range of samples examined here. As with the AIC calculation, n represents the sample size and k represents the number of model parameters (Equation 7). Regardless of sample size, the use of AICc has been supported over just AIC (Burnam and Anderson 2004).

$$AICc = AIC + \frac{2k(k+1)}{n-k-1} \quad (7)$$

Four different AICc comparisons were completed:

- 1) All of the results not hitting a bound, regardless of AICc value

- 2) Results where AICc strongly supported the use of the G-H model, the more complex model
- 3) Results where AICc strongly supported the use of the B-H model, the simpler model
- 4) Results where there was no difference between the AICc values for the two models.

For the second and third comparisons, an AICc score that was considered to strongly support the G-H model occurred only in those cases where the AICc value for the more complex model was much less than the B-H's or vice versa. A strongly supported difference was defined as a situation where the AICc value was more than five points less than the B-H AICc value. In the fourth comparison, no difference between the models occurred when the two model's scores were within five points of each other. As a measure of how often results were produced in each comparison, the number of simulations in each category out of the 2500 run for each scenario were counted.

By completing a simulation study, everything about the created population of fish could be known and compared to reality for each of our stock assessment models. Most of the results here focus on the accuracy (the difference between the estimated and known values of Z) and overall variability in each scenario (spread of results within a set of 2500 simulations) of the Z_2 estimates for the G-H model and Z estimates compared to the Z_2 estimates for the B-H model. While it is important to know the magnitude and direction of change over time, in many cases managers of the fishery are focused on knowing the current fishing mortality and current total mortality of the fishery. By knowing what is currently going on in the fishery, they can adjust regulations or enforcement to try to get the fishing mortality rate to the desired level. Results for estimates of Z_1 are not presented for all scenarios, but when they are available, they are an important tool for interpreting results of both models and providing management advice.

Results

When looking at those scenarios with no variability in growth or recruitment, several patterns appeared for the G-H model estimations. The spread, or overall variability of the individual simulation estimations around the median estimation within a set of 2500 simulations was broad

at smaller sample sizes and narrowed as the sample size increased (Figure 2.3; Figure 2.4; Figure 2.5). These overall variabilities were also consistently broader than the B-H overall variability, especially at small sample sizes (Figure 2.3; Figure 2.4; Figure 2.5). The median Z_2 estimate for the G-H model was closer than the median B-H estimate of Z to the actual Z_2 value, regardless of the time of the change in mortality, as expected (Figure 2.3; Figure 2.4, Figure 2.5). The magnitude of the difference between the known and estimated Z_2 values and pattern of the average estimation was dependent on T_s relative to T_c . When sampling occurred before the change in mortality rate ($T_s=T_c-2$), the average G-H estimates were underestimations of Z_2 (Figure 2.3). As sampling began to occur at or after the change in mortality, the median followed an asymptotic pattern, overestimating Z_2 at lower sample sizes, then leveling out at approximately the known value of Z_2 (Figure 2.4; Figure 2.5).

The B-H average Z estimate position relative to the known Z_2 value was highly dependent on when sampling began. When sampling began two years before the change ($T_s=T_c-2$), the estimate was much closer to the known value of Z_1 (Figure 2.3). As the window of sampling shifted along the mean length time series (T_s relative to T_c), the median of the estimates within a set of simulations shifted as well. For sampling beginning at the time of change ($T_s=T_c$), the B-H estimate was approximately halfway between the known values of Z_1 and Z_2 (Figure 2.4). Sampling two years after the change yielded a B-H estimate that was on average closer to Z_2 (Figure 2.5). The median stayed consistent across sample sizes, although the overall variability decreased.

As a commonly used tool for model selection, the AICc value was calculated for each model in each simulation. When none of the models' assumptions were violated other than the B-H assumption of constant mortality (no variation in growth or recruitment was present), the percent of supported results changed with the shift in T_s . When sample sizes were smaller than $n=100$, for all T_s scenarios, the majority of simulations had no strongly supported difference between the two models (Figure 2.6). As sample size increased, the number of times the information content of the data strongly supported the G-H model increased substantially to be supported in nearly every simulation (Figure 2.6). Little difference was seen in the accuracy and overall variability of Z_2 estimations whether all simulations were examined, only those simulations where AICc

showed strong support for the G-H model, and only those simulations where the difference between the two models was not strongly supported (Figure 2.7). However, the overall variability of the G-H Z_2 estimates was not dramatically affected by the use of the AIC criterion. This indicates that the use of AICc as a tool should be further investigated to see if AIC selection improves results in ways other than the overall variance, especially at small sample sizes.

As variability in growth and recruitment was incorporated into the simulations, The general patterns of accuracy and variance remained the same when growth and recruitment variability increased, although the size of the inter-quartile range of the overall variability increased for the G-H model at all sample sizes (Figure 2.8). Similar patterns were seen in the comparisons of AICc results as in previous comparisons, although the percent of simulations where AICc indicated support for the G-H model increased when $T_s=T_c-2$ and $T_s=T_c$ and decreased when $T_s=T_c+2$ (Figure 2.9, Figure 2.10).

When Z was decreasing from $Z_1=1.0$ to $Z_2=0.5$, G-H on average was more accurate, a similar result to those scenarios where Z was increasing from $Z_1=0.5$ to $Z_2=1.0$ (Figure 2.11). The asymptotic pattern of the mean was not as clearly seen with the G-H results because the Z_2 value was closer to the bound of zero, truncating the width of the bars and shifting the average upward (Figure 2.11). The B-H results remained consistent across sample sizes and followed a pattern of becoming more accurate when sampling occurred after the time of change. This pattern was expected because the degree that the B-H estimate median differs from the known Z_2 is very dependent on how much of the shape of the mean-length times series captured by the sampling data, regardless of the magnitude or direction in the changing Z values because the B-H estimate is an average of the annual Z s across the Y_s . Estimating Z_1 when $Z_1=0.5$ and $Z_2=1.0$ produced similar patterns to the estimations of Z_2 when $Z_1=1.0$ and $Z_2=0.5$, as expected (Figure 2.12).

The previous graphs focused on six years of sampling, a scenario that was halfway between the fewest number of years sampled (4) and the largest number of years sampled (8). The general pattern of B-H and G-H results remained consistent as the years of sampling changed from four years to eight years of sampling, although the width of the variance did seem to decrease slightly with increasing years of sampling and increasing sample size for both models (Figure 2.12).

Among the three species examined in this particular simulation study, yellowtail snapper and red hind had very similar results. This was expected as their growth rates were relatively close to each other with slower growth than the redbait parrotfish (Table 2.3). In contrast, the redbait parrotfish showed a shift in the patterns from the other species (Figure 2.13). When sampling began in the year of change, redbait parrotfish showed a similar pattern to sampling starting two years after the change for the other two species (Figure 2.15). When $T_s=T_c+2$, the median B-H estimate continued to shift upwards, going from an underestimate of Z_2 to an overestimate (Figure 2.15). The accuracy and variance of the G-H Z_2 estimate did not continue to shift upwards and increase at that point, but rather stayed about the same as when $T_s=T_c$ (Figure 2.15). This pattern was only seen when variability was high for both growth and recruitment and was not present when variability was not incorporated into the simulation (Figure 2.14). The exact reason for this unexpected pattern is unclear, and could be an artifact of the set up of the simulation model. Further investigation is warranted to verify results.

Discussion

Given the way in which the simulation model was constructed, the limited parameter space explored, and initial analyses of the results, there is no clear “best” choice for a model for estimating current mortality rates between the Beverton-Holt and Gedamke-Hoenig mean-length mortality estimators, nor does there need to be one choice. The scenarios in which an analysis would need to be done will change over time and so can the use of the two models. In our limited scenarios, the Beverton-Holt model produced stable and less overall variable results in situations where sample size was low, variation was high for both growth and recruitment, and sampling began after the change in Z took place. The Gedamke-Hoenig model was most accurate at larger sample sizes, when variation was low and sampling occurred before or at the same time as the change in Z occurred. The determining factors are a combination of sample size, length of sampling time, the level of recruitment variability and when sampling began relative to the time of change (T_s). Overall, on average, the G-H model was closer to the known Z_2 value and the spread of the 2500 results over each scenario was much broader for G-H than B-H, especially at smaller sample sizes.

The smaller overall variability in the B-H model relative to that of the G-H model can generally be expected because only two parameters were estimated, a total mortality rate and variance. With the G-H model, at least two additional parameters (Z_1 , Z_2 , T_c , and σ) are required, leading to more complex dynamics and potential variability in results due to more difficult optimization. Each additional parameter adds on a layer of complexity and removes a degree of freedom. In addition, the G-H model is trying to estimate parameters from a change between points, rather than an average among points, so the B-H model is able to use all of the data points to estimate two parameters, whereas the G-H model does not. It is also important to note that the spread of results for the G-H model represents summaries of all simulations and on a case-by-case basis, it would be apparent to an analyst that the outliers seen here were not credible. The outliers generally result when the mean length is still substantially changing at the end of the time series due to the time of change and the level of variability. A careful inspection of residuals and the use of both the B-H and G-H outputs is recommended when the mean length is still in transition. Larger sample sizes and sampling for longer periods provides more information for parameter estimation, but at smaller sample sizes both models can be used in concert to gain information about the mortality rates and trends.

The B-H model has several assumptions that appear to be restrictive, such as the assumptions of constant mortality and constant recruitment. However, though nearly all of the main assumptions of the model were purposely violated in this study, the B-H results were consistent in each case. However, since all of the simulated scenarios introduced a change in mortality, all B-H results are biased due to the violation of the assumption of constant mortality. This was evident in the fact that the main factor influencing how accurate the B-H estimate was compared to the known Z_2 value was when sampling occurred relative to the time of change. The B-H results became less biased as less transition in mean lengths was simulated.

Studies have consistently found that the Beverton-Holt model has low variance, but a sizeable bias compared to other length-based models, much like the results from this study (Wetherall et al. 1987, Ehrhardt and Ault 1992). Ehrhardt and Ault reached such conclusions about the robustness of B-H and consistent bias in 1992 and developed a model for a population at equilibrium to adjust for this and to account for a lack of availability of the larger, older animals

in the population. However, this developed model has not been widely used and still does not address populations in non-equilibrium conditions. In addition, the authors mentioned that the variance of their model was likely to be higher than that of the B-H model due to the addition of parameters, which would lead to a similar problem as seen here comparing the B-H and G-H models (Ehrhardt and Ault 1992).

The results from the scenarios run in this particular simulation model indicate caution is needed when using either model by itself in a data limited situation over a very short time series. With the B-H model, without knowing the initial Z_1 and Z_2 values and when a change occurred relative to the beginning of sampling, it would be difficult to know how biased an estimate would be, although it would be consistent. The comparatively lower variance is expected because only one parameter is being estimated and the entire sampling periods mean lengths are available to estimate that one parameter. Regarding the G-H model, on average it did well and given sufficient data, it not only provides information on the current fishing mortality of the fishery, but also on the recent history (Z_1 to Z_2 , T_c). This information is above and beyond what is possible for the B-H model and can be essential for management.

The results from the G-H model should be interpreted carefully at smaller sample sizes, particularly when the assumption of constant recruitment is believed to have been violated. The time series of length frequency data used to conduct a mean length analysis would give indications of whether highly variable recruitment is present, but additional information should be explored and more effort put into understanding recruitment patterns on an annual or seasonal basis (depending on the fishery). Several methods exist for obtaining information on recruitment variability: directly measuring recruitment through baseline assessments and monitoring, estimating recruitment through stock assessment models such as virtual population analysis or statistical catch at length models, or by utilizing recruitment data from similar species in other regions with more data.

One of the species simulated, yellowtail snapper, had some recruitment variation information available for a Florida Keys stock, with a variation level of $\sigma_R=0.15$ for 1-year old recruits (Muller et. al 2003). This might suggest that our simulations for yellowtail, at least, might have

included variability outside of the natural range. However, the independent peer review of that analysis found this number to be unusually low compared to other marine species and suggested that the numbers used to derive the variation level could be caused by ageing errors, a non-representative age-length key, or unrepresentative sampling (Francis 2003). The SEDAR report also noted that the number might be an underestimation because the same age-length key was used over several years (SEDAR 2003). Future work could use a value of 0.15 as a base case and sensitivities to higher values should be explored using any additional information available at that time. Using information from areas with more data and species similar to those in the U.S. Caribbean is a viable solution and should be explored further. An additional option is that a recruitment index could be calculated using the samples collected to supplement the understanding of recruitment (Gedamke 2008).

Implications for Management

Collecting additional recruitment information should be a priority for research in the area. However, until baseline data or supplementary data from other species are identified, effort should be given to collect large sample sizes over as many continuous years of sampling as possible in order to increase the probability of getting an accurate estimation of mortality rates using mean length mortality estimates.

While trends in fishery mortality can give managers a general idea of how fishing mortality has changed, it, by itself, is not a good means of detecting or determining overfishing. Overfishing occurs in a population when the fishing mortality rate is above the rate that would achieve maximum sustainable yield. Deciding whether overfishing is occurring in a stock is critical: as of 2010, the Magnuson-Stevens Fisheries Conservation and Management Act (MSRA; U.S. Department of Commerce 2007) requires that annual catch limits (ACLs) be in place for all fisheries undergoing overfishing and for all stocks by 2011. These limits need to be set at a level to ensure that overfishing is not occurring in a population. With a reliable estimate of Z , scientists and management can make approximations to help determine if overfishing is occurring.

Length-based methods, such as the B-H and G-H models, and the estimates of Z from these models, can help determine the level of overfishing. If the natural mortality rate (M) is calculated, then it can be used several ways in conjunction with the estimate of Z . The difference between Z and M is attributed to the fishing mortality rate (F). Additionally, the natural mortality value approximates the fishing mortality rate at maximum sustainable yield (F_{MSY}). F can then be compared to F_{MSY} (F/F_{MSY}). If $F/F_{MSY} > 1$, then overfishing is occurring. If an assessment can provide this type of information, then managers can adjust regulations, enforcement, and ACLs to ensure that F/F_{MSY} does not reach a level indicative of overfishing.

With the current course of management, it is critical for managers to understand how scientific uncertainty plays a role in required MSRA regulations and how model choice influences the level of scientific uncertainty that needs to be incorporated into setting ACLs. ACLs are based on several factors. The first factor is the overfishing limit (OFL), which is a level of catch above which $F/F_{MSY} > 1$ and overfishing is occurring. Anywhere at or below the OFL is the acceptable biological catch (ABC). The ABC is a level of catch that is set by each region's SSC to account for scientific uncertainty. From that point, the council sets the ACL, which is not allowed to exceed the ABC set by the SSC. In addition, the councils can set an annual catch target (ACT) at or below ACL to account for management uncertainty. If the ACLs are exceeded, then accountability measures are enacted to correct or mitigate for the excessive catch.

Stock assessment is in many ways subjective. In any analysis, all aspects of the fishery can not be accounted for, so it is important to have someone with knowledge about the system to look at other sources of information, explore patterns, and adjust the analysis to account for unique situations that occur in every system. The exclusion rules presented to limit the estimations used in the final analyses for the models discussed in this thesis are just the beginning of what can be explored. Analysts determine these rules based on their knowledge, and the values chosen can have a significant impact on results. These exclusion rules can be, and need to be, adjusted by each analyst to account for unique aspects of the system on a case-by-case basis. Other facets of fisheries information such as trends in recruitment, growth, and professional judgment can be used to inform these decisions. For example, analysis of residual values accounting for the difference in observed and estimated values of interest can help identify unusual patterns or

outliers in data that can have a major impact on parameter estimations. Adjustments can then be made to account for this information. However, it is important for managers to understand the implications of the choices of both the model used and the rules used to choose that model on levels of OFLs and ABCs. Furthermore, they should understand how scientific uncertainty affects SSC recommendations to buffer OFLs and ABCs, i.e., the greater the uncertainty, the larger the buffer must be. With some models, the buffer for scientific uncertainty will likely be larger than that of other models.

Specifically regarding the B-H and G-H models, these tradeoffs between the level of uncertainty and risk need to be considered on the part of the analyst when interpreting model results and on the part of the manager when organizing a sampling program. Within the limited parameter space presented here, the level of uncertainty (based on the variance) was dependent on the model used, the number of samples, and the number of years spent sampling. The level of risk was also dependent on these factors, but the measures were slightly different: a combination of accuracy, or how close to reality an estimate was, and variance, which gave an idea of the chance of getting an accurate (or inaccurate) estimation. Another important aspect of risk to consider is the direction of accuracy—within these scenarios the B-H model always produced an underestimation of the simulated Z_2 value when Z was increasing and overestimation of Z_2 when Z was decreasing. In an extreme case, this could mean that the analysis using that model indicates that overfishing is not occurring, when in reality it is. Deciding on a model that consistently underestimates mortality rates when mortality is increasing without accounting for that underestimation is, of course, much more risky than choosing a model that tends to overestimate fishing mortality rate when it is increasing.

Ultimately, the amount of risk and which type of risk in the form of the choice of how accurate and varied estimates of total mortality rates should be is a value judgment, with no right or wrong answer. Naturally, many aspects besides accuracy and variance of stock assessments play a role in management decisions (e.g., monitoring costs, stakeholder satisfaction, etc.). For example, fishermen might argue for the use of the B-H model over the G-H model, if both results were presented covering the same time period, because the B-H model provides an estimate that indicates less fishing is occurring and has a smaller variance, which would mean less restrictive

regulations and a smaller OFL to ABC buffer. To fishermen, both are valid models based on data collected, so the one hurting the fishermen the least should be used because the MSRA specifically mentions that economic impacts to fishery participants needs to be a consideration in fisheries management. However, using the B-H model when fishing pressure is increasing puts the council and SSCs at risk of suggesting limits that allow overfishing to occur, the prevention of which is the top priority of the MSRA. By better understanding the levels of risk based on model choice, sample size, and sample time, managers can develop more informed management decisions.

Unfortunately, there is no simple solution. This trade-off is highlighted by our results, which show that models can be both more risky in one way (e.g., B-H bias) and, at the same time, a less risky choice by another measure (e.g., B-H overall variability). A primary conclusion of this study is that in a data-poor situation, as many models as the data will allow should be explored and a careful interpretation of the results should be conducted. As sampling increases both in samples per year and number of years, the G-H model can be used to provide additional information on changes in Z over time and the time changes occurred. Knowing these exploitation patterns and the time of change can help management evaluate past management actions and improve suggestions for the future. The B-H model could be used to examine just a couple of years at a time in conjunction with G-H estimates over a longer period of time and the results compared. Both models provide important information about the fishing system and both should be explored in future analyses.

Caveats

For this particular study, full analyses were only done for the changes of $Z_1=0.5$ to $Z_2=1.0$ and $Z_1=1.0$ to $Z_2=0.5$. A much larger parameter space and further analyses on the impacts of recruitment and growth patterns needs to be explored before determining if the estimation patterns presented above would hold for many other fish stocks and changes in total mortality rates.

Another consideration should be the methods used to vary growth and recruitment. The exact levels of accuracy and variance and the differences between the different levels of stochastic

growth and recruitment are artifacts on the values chosen. In some cases, the values randomly chosen would not reflect a realistic pattern over time, as the values were randomly chosen from year to year and include some extremes of the distributions which were not based on other studies. If available, an analyst examining trends in growth and recruitment would be able to use these trends as auxiliary data. Some of these unrealistic patterns in growth and recruitment would account for some of the estimations presented here as outliers.

In addition, this study assumed that L_c and L_{inf} could be calculated for each fish stock. The issues regarding problems relating to properly calculating L_c and L_{inf} and the outcome of the B-H model have been looked at in the past (Laurec and Mesnil 1987, Ssentongo and Larkin 1973, Wetherall et al. 1987). The Gedamke and Hoenig 2006 paper also addressed this issue regarding their model (Gedamke and Hoenig 2006). Knowing or being able to closely approximate L_c and L_{inf} are critical to the estimations for both the B-H and G-H models. Although this study did not address the issue relating to sensitivities of these models to these parameters, it should be an important consideration before choosing a length-based model for stock assessment over other methods.

Literature Cited

- Akaike, Hirotugu (1974). A new look at the statistical model identification. *IEEE Transactions on Automatic Control*. 19(6): 716-723.
- Beverton, R. J. H., and S. J. Holt. 1956. A Review of Methods for Estimating Mortality Rates in Fish Populations, with Special Reference to Sources of Bias in Catch Sampling. *Rapports et Procès-verbaux des Réunions, Conseil International pour l'Exploration de la Mer*. 140: 67-83.
- Burnam, K. P., and D. R. Anderson. 2002. *Model Selection and Multimodel Inference: A Practical Information Theoretic Approach*, 2nd ed. Springer-Verlag.
- Claro, R., K. C. Lindeman, and L. R. Parenti (eds). 2001. *Ecology of the Marine Fishes of Cuba*. Smithsonian Institution Press, Washington, London. 253 p.
- Csirke, J., J. F. Caddy, and S. Garcia. 1987. Methods of size-frequency analysis and their incorporation in developing countries: FAP interest in receiving advice. In Pauly D. and G.R. Morgan (eds.). *Length-based methods in fisheries research*. ICLARM Conference Proceedings, 13:53-74.
- Ehrhardt, N. M. and J. S. Ault. 1992. Analysis of Two Length-Based Mortality Models Applied to Bounded Catch Length Frequencies. *Transactions of the American Fisheries Society*. 121: 115-122.
- Francis, R. I. C. C. 2003. Report on the 2003 Assessment of Yellowtail Snapper in the Southeast United States. National Institute of Water and Atmospheric Research. Client Report: WLG2003-54.
- Gaertner, D. 2010. Estimates of historic changes in total mortality and selectivity for Eastern Atlantic skipjack (*Katsuwonus pelamis*) from length composition data. *Aquatic Living Resources*. 23: 3-11.
- Gedamke, T. 2007. Estimation of Mutton Snapper Total Mortality Rate From Length Observations. SEDAR 14 Caribbean Yellowfin Grouper, Mutton Snapper, Queen Conch. North Charleston, SC. SEDAR14-AW-05.
- Gedamke, T. 2008. Total mortality rates of the barndoor skate, *Dipturus laevis*, from the Gulf of Maine and Georges Bank, United States, 1963-2005. *Fisheries Research*. 89(1): 17-25.
- Gedamke, T. and J. M. Hoenig. 2006. Estimating Mortality from Mean Length Data in Nonequilibrium Situations, with Application to the Assessment of Goosefish. *Transactions of the American Fisheries Society*. 135: 476-487.

Gedamke, T, S. Hudy and K. McCarthy. 2009. Preliminary Evaluation of Available U.S. Caribbean Fisheries Length-Frequency Data and Spatial Changes in the Fisheries. SFD-2009-001, 50 p.

Griffith, D., Valdes Pizzini, M., and C. Garcia Quijano. 2007. Entangled communities: Socioeconomic profiles of fishers, their communities and their responses to marine protective measures in Puerto Rico (Volume 2: Regional Profiles). NOAA Technical Memorandum NMFS-SEFSC-5562007. NOAA Series on U.S. Caribbean Fishing Communities. 190 p.

Gulland, J. A. 1983. Fish stock assessment: A manual of basic methods. FAO/Wiley Series on Food and Agriculture, Vol. I.

Helu, S. L., D. B. Sampson, and Y. Yin. 2000. Application of Statistical Model Selection Criteria to the Stock Synthesis Assessment Program. Canadian Journal of Fisheries and Aquatic Sciences. 57: 1784-1793.

Jones, R. 1984. Assessing the effects of changes in exploitation pattern using length composition data. FAO Fish. Tech. Pap. No. 256, Rome, 118 p.

Laurec, A. and B. Mesnil. 1987. Analytical Investigations of Errors in Mortality Rates Estimated From Length Distributions of Catches. In Pauly D. and G.R. Morgan (eds.). Length-based Methods in Fisheries Research. ICLARM Conference Procedures, 13:239-281.

Pauly, D. 1983. Some simple methods for the assessment of tropical fish stocks. FAO Fisheries Technical Papers No. 234, Rome, 52 p.

Quinn, T.J. and R. B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press. New York. 542 p.

R Development Core Team. 2010. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing. Vienna, Austria.

Muller, R.G., M. D. J. de Silva, and L. R. Barbieri. 2003. A Stock Assessment of Yellowtail Snapper, *Ocyurus chrysurus*, in the Southeast United States. FWC-FMRI Report: IHR 2003-10. 217 p.

SEDAR. 2009. Caribbean Fisheries Data Evaluation. SEDAR Procedures Workshop 3. North Charleston, SC. 183 p.

Sparre, P. and S. C. Venema. 1998. Introduction to tropical fish stock assessment Part 1: Manual. FAO Fisheries Technical Paper No. 306.1, Rev. 2. FAO. Rome. 407 p.

Ssentogo, G. W. and P. Larkin. 1973. Some Simple Methods of Estimating Mortality Rates of Exploited Fish Populations. Journal of Fisheries Research Board Canada. 30(5): 695-698.

U.S. Department of Commerce. 2007. Magnuson-Stevens Fishery Conservation and Management Act. National Oceanic and Atmospheric Administration. National Marine Fisheries Service. Public Law 94-265. May. 170 p.

Wang, Y. and Q. Liu. 2006. Comparison of Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) in Selection of Stock-Recruitment Relationships. *Fisheries Research*. 77: 220-225.

Wetherall, J. A., J. J. Polovina and S. Ralston. 1987. Estimating Growth and Mortality in Steady-state Fish Stocks From Length-frequency Data. In Pauly D. and G.R. Morgan (eds.). *Length-based Methods in Fisheries Research*. ICLARM Conference Procedures, 13: 53-74.

Table 2.1 A table of the combinations of levels of growth and recruitment variability scenarios. This set of scenarios was repeated for each species and change in Z.

	Recruitment Variation	Growth Variation
Scenario 1	None	None
Scenario 2	Low	None
Scenario 3	High	None
Scenario 4	None	Low
Scenario 5	None	High
Scenario 6	Low	Low
Scenario 7	Low	High
Scenario 8	High	Low
Scenario 9	High	High

Table 2.2 The results of the optimization study, showing which algorithm within the optim function in R that performed the best by the number of years sampled and the Z_2 known value when $Z_1=0.3$. Only the life history data for yellowtail snapper was used. The SANN, CG, and Nelder-Mead algorithms within optim were consistently unable to run within our model, both with and without parscale.

	$Z_2=0.1$	$Z_2=0.2$	$Z_2=0.3$	$Z_2=0.4$	$Z_2=0.5$	$Z_2=0.6$	$Z_2=0.7$	$Z_2=0.8$	$Z_2=0.9$	$Z_2=1.0$
$Y_s=2$	BFGS w/ parscale	LBFGS w/ parscale	LBFGS w/o parscale	BFGS w/ parscale	BFGS w/ parscale	BFGS w/ parscale	BFGS w/ parscale	Tie all BFGS	BFGS w/ parscale	Tie all BFGS
$Y_s=5$	LBFGS w/ parscale	LBFGS w/ parscale	LBFGS w/o parscale	BFGS w/ parscale	LBFGS w/ parscale	LBFGS w/ parscale	LBFGS w/ parscale	LBFGS w/ parscale	LBFGS w/ parscale	LBFGS w/ parscale
$Y_s=15$	BFGS w/ parscale	LBFGS w/o parscale	LBFGS w/o parscale	LBFGS w/ parscale	LBFGS w/ parscale	BFGS w/ parscale	Tie all w/o parscale	LBFGS w/ parscale	LBFGS w/ parscale	LBFGS w/ parscale
$Y_s=25$	BFGS w/ parscale	Tie all BFGS	LBFGS w/o parscale	LBFGS w/ parscale	LBFGS w/ parscale	Tie all BFGS and LBFGS	LBFGS w/ parscale	Tie all BFGS and LBFGS	LBFGS w/o parscale	Tie LBGS w/o parscale and BFGS w/ parscale

Table 2.3 The von Bertalanffy parameters used in the simulation model. Values were taken from Claro (2001) and analyses of existing U.S. Caribbean data by Todd Gedamke (T. Gedamke, Southeast Fisheries Science Center, personal communication)

	K	L_c (cm)	L_∞ (cm)
Yellowtail snapper	0.139	230	500
Red hind	0.085	300	558
Redtail parrotfish	0.79	255	400

Figure 2.1 Examples of histograms of 100 randomly chosen values of recruitment at the study designated “high” or “low” for this study.

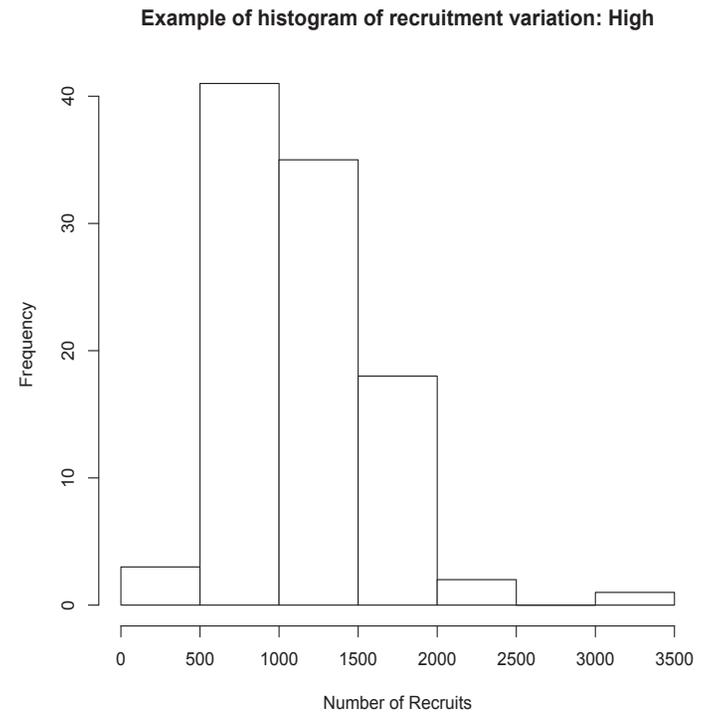
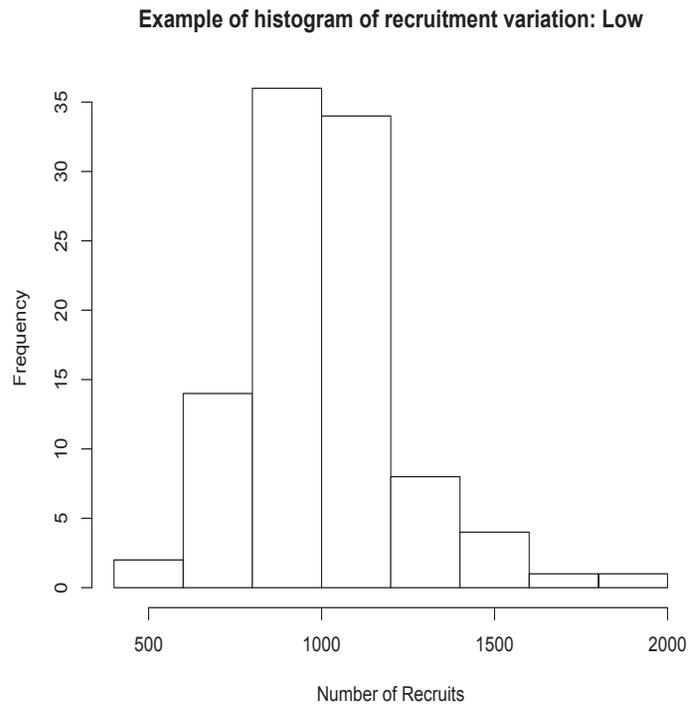


Figure 2.2 Examples of histograms of 100 randomly chosen growth rates (K) at the study designated “high” or “low” for this study.

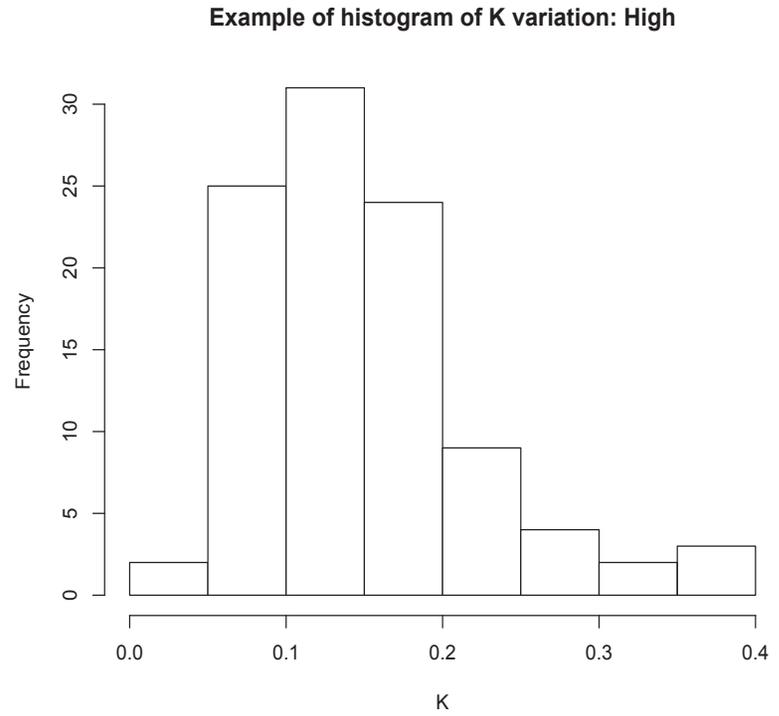
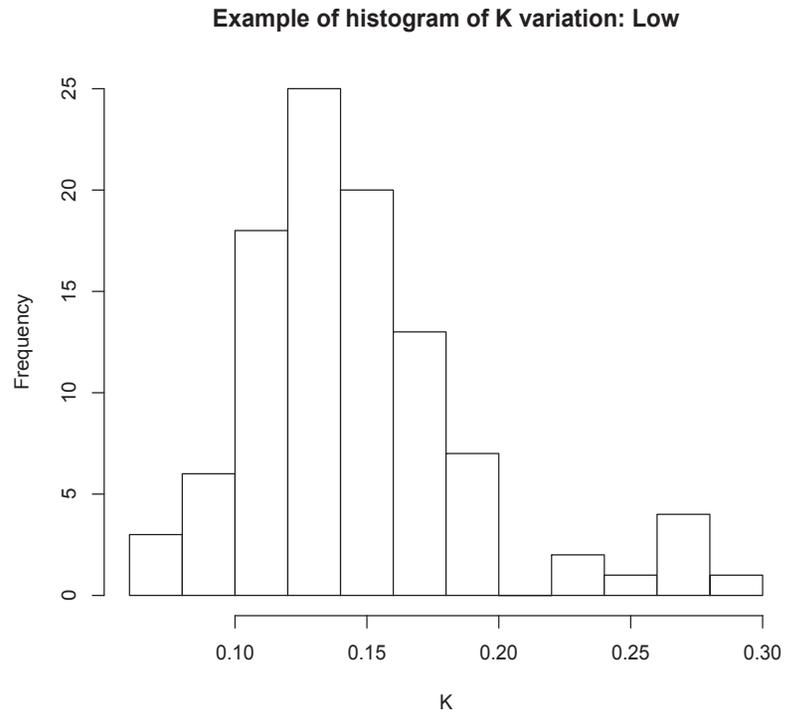


Figure 2.3 Tukey box plots comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound as sample sizes per year increased. Outliers represent values more than 1.5 the inter-quartile range. Estimations were for yellowtail snapper, $T_s=T_c-2$, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$ and no variability in growth or recruitment. The solid blue line represents the known value of Z_2 .

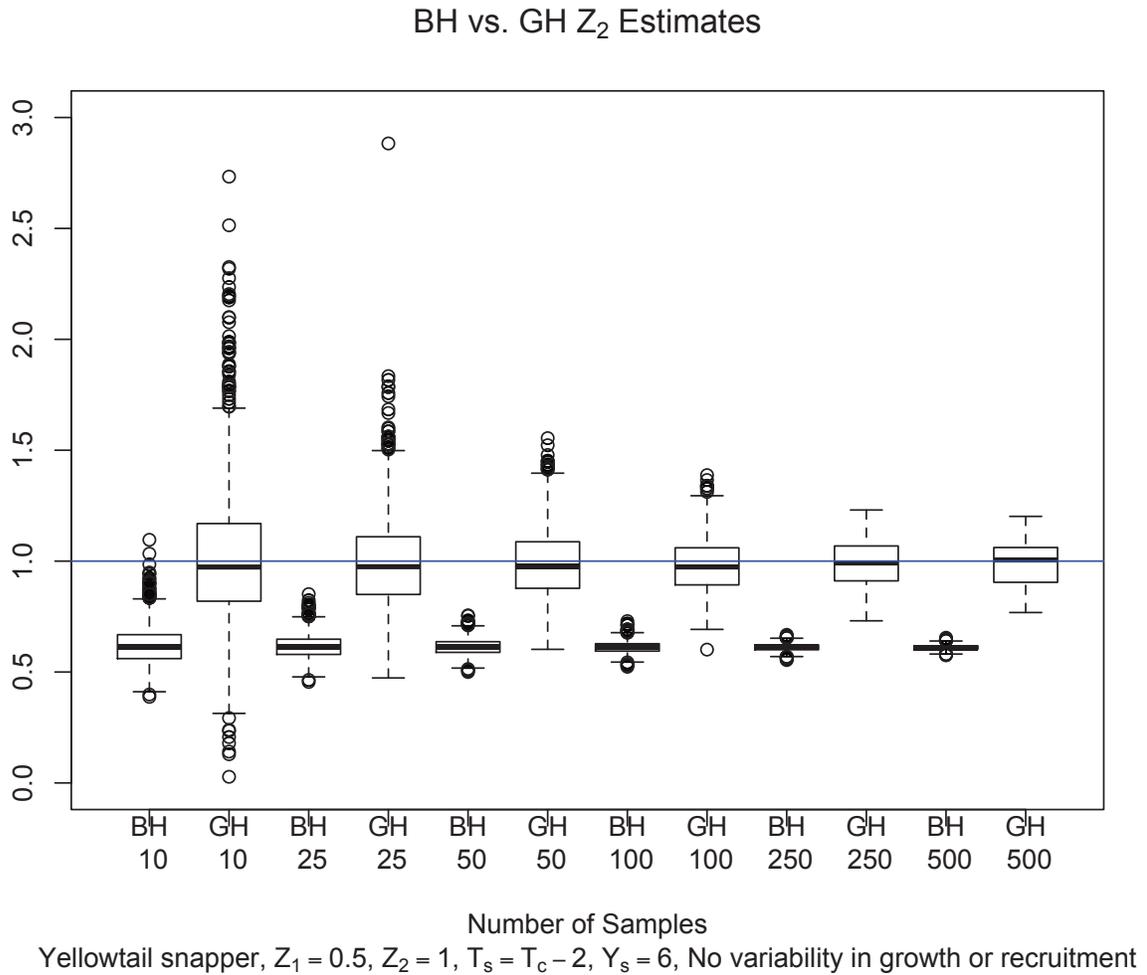


Figure 2.4 Tukey box plots comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound as sample sizes per year increased. Outliers represent values more than 1.5 the inter-quartile range. Estimations were for yellowtail snapper, $T_s=T_c$, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$ and no variability in growth or recruitment. The solid blue line represents the known value of Z_2 .

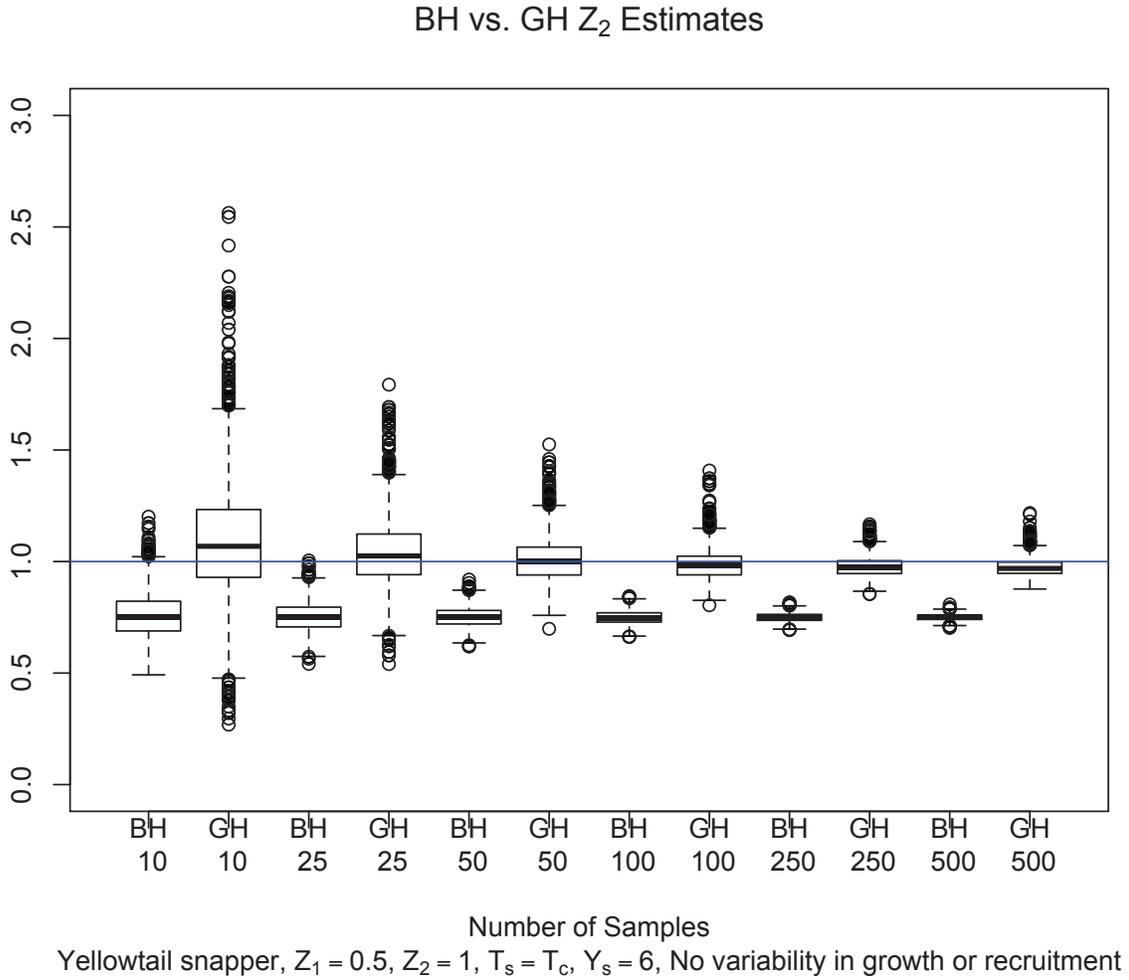


Figure 2.5 Tukey box plots comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound as sample sizes per year increased. Estimations were for yellowtail snapper, $T_s=T_c+2$, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$ and no variability in growth or recruitment. The solid blue line represents the known value of Z_2 .

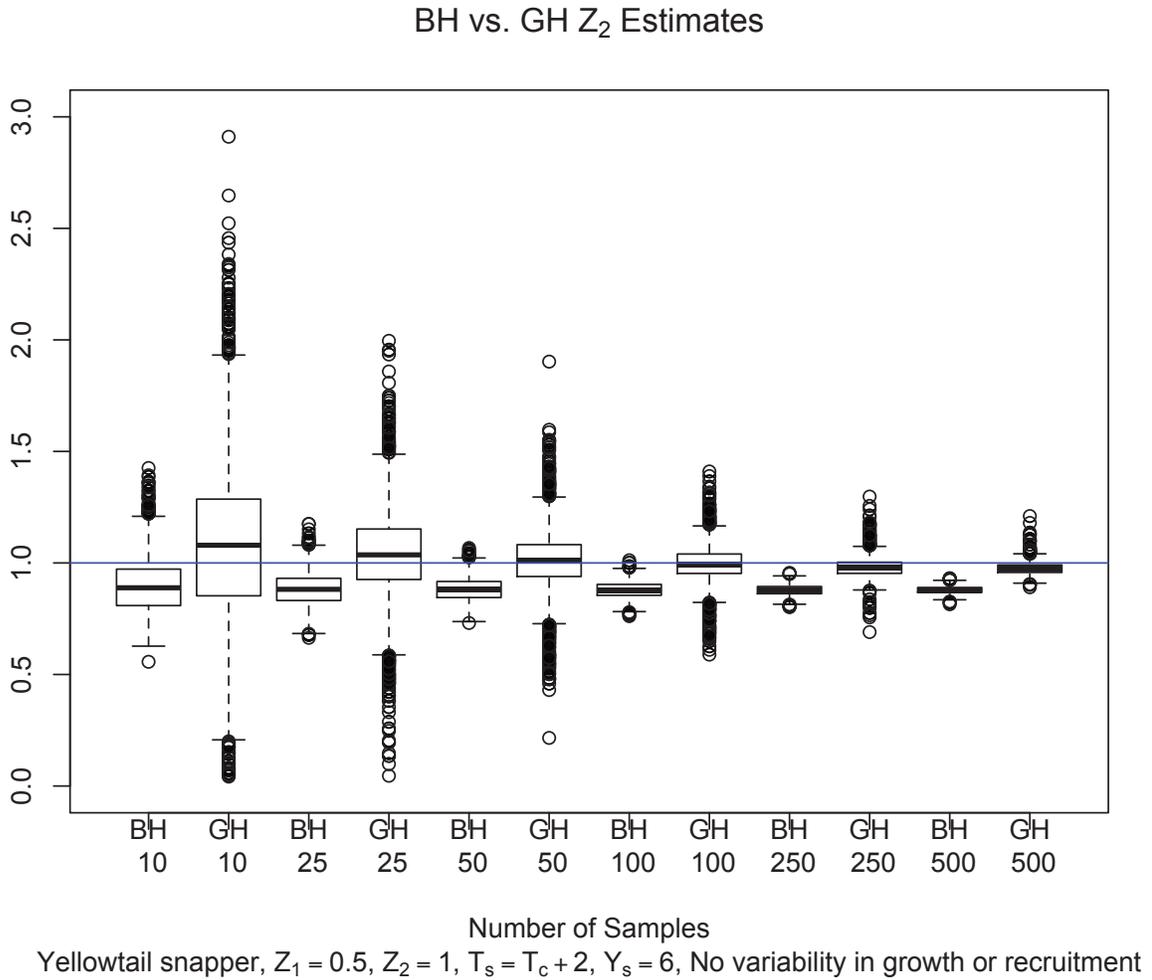


Figure 2.6 The percent of results where AIC values indicated support for one model strongly (more than five points less) over another, where there was no strong difference in the AIC values, and where values were excluded because they were estimated as NaNs or hit a pre-defined upper and lower bound in the optimization. Results are for yellowtail snapper, $Y_s=6$, $Z_1=0.5$, $Z_2=1.0$, and no variability in growth or recruitment.

Percent of AIC Supported Results Yellowtail snapper, $Y_s=6$, No variability in growth and recruitment

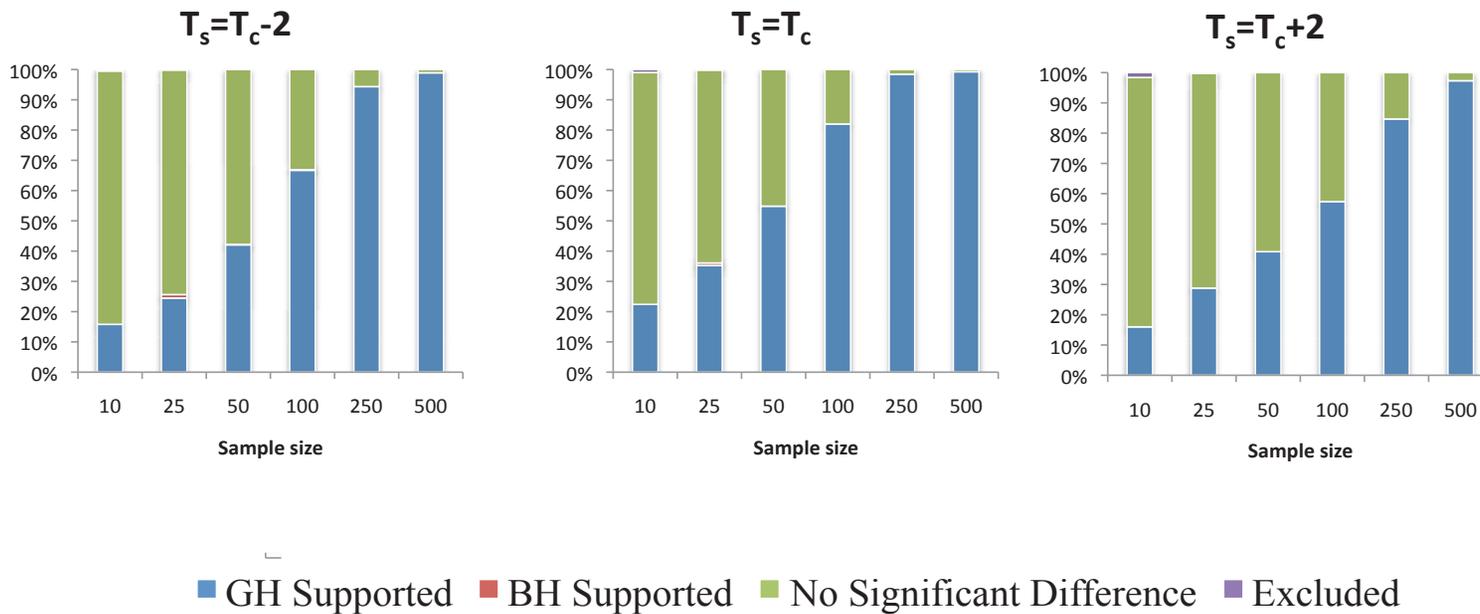


Figure 2.7 Tukey box plots comparing Z and Z_2 estimates for the B-H and G-H models respectively for simulations not hitting a bound or producing an NaN in three scenarios: 1. All simulations regardless of AIC value. 2. Simulations where G-H had an AIC value that strongly supported the use of the more complex model and 3. Simulations where the AIC values were not strongly different between the two models. Estimations were for yellowtail snapper, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$ and no variability for both growth and recruitment. The solid blue line represents the known value of Z_2 .

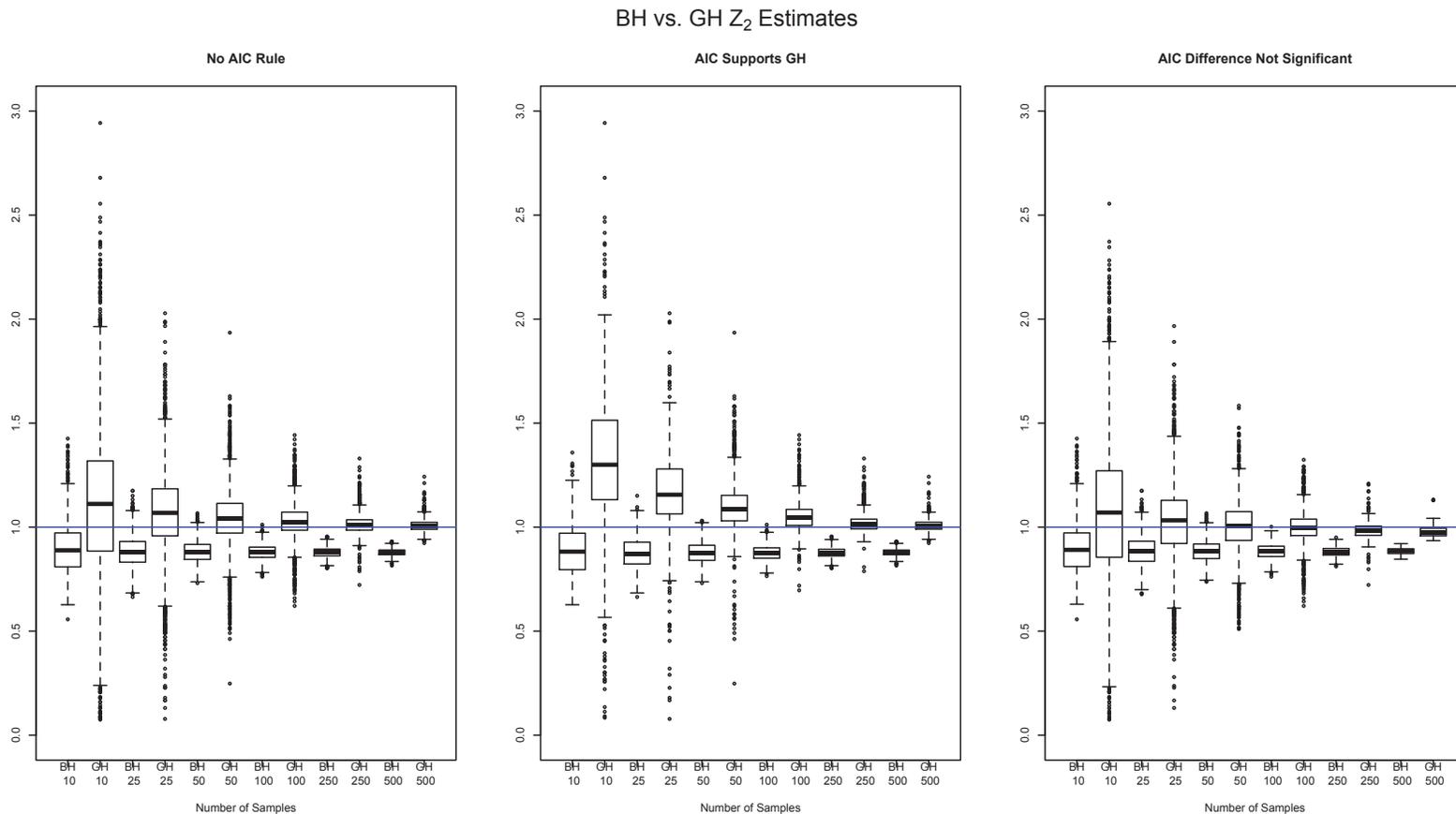


Figure 2.8 Tukey box plots comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound. Estimations were for yellowtail snapper, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$ and high variability for both growth and recruitment. The solid blue line represents the known value of Z_2 .

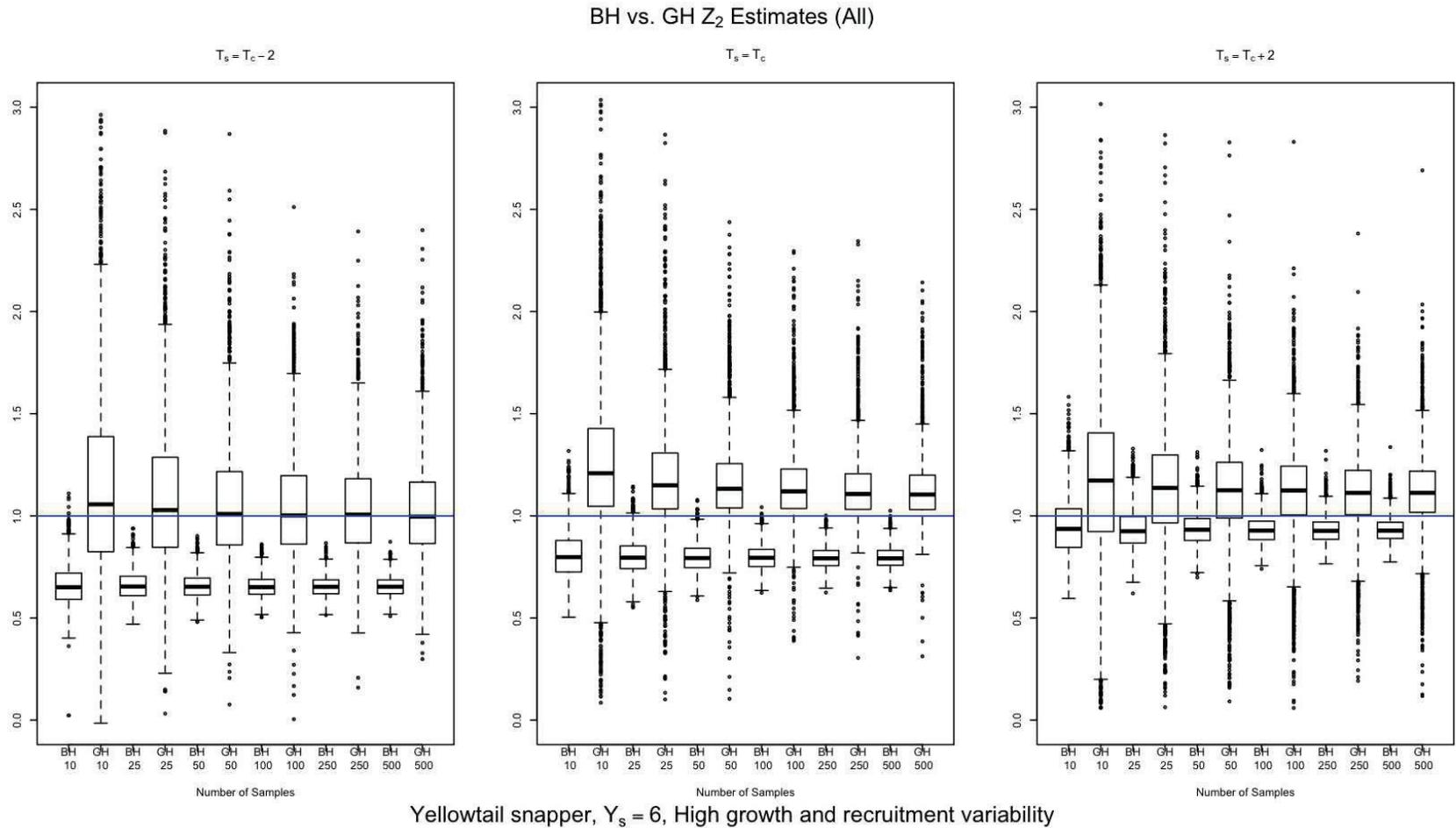


Figure 2.9 The percent of results where AIC values indicated support for one model strongly (more than five points less) over another, where there was no strongly supported difference in the AIC values, and where values were excluded because they were estimated as NaNs or hit a pre-defined upper and lower bound in the optimization. Results are for yellowtail snapper, $Y_s=6$, $Z_1=0.5$, $Z_2=1.0$, and high variability in growth or recruitment.

Percent of AIC Supported Results Yellowtail snapper, $Y_s=6$, High variability in growth and recruitment

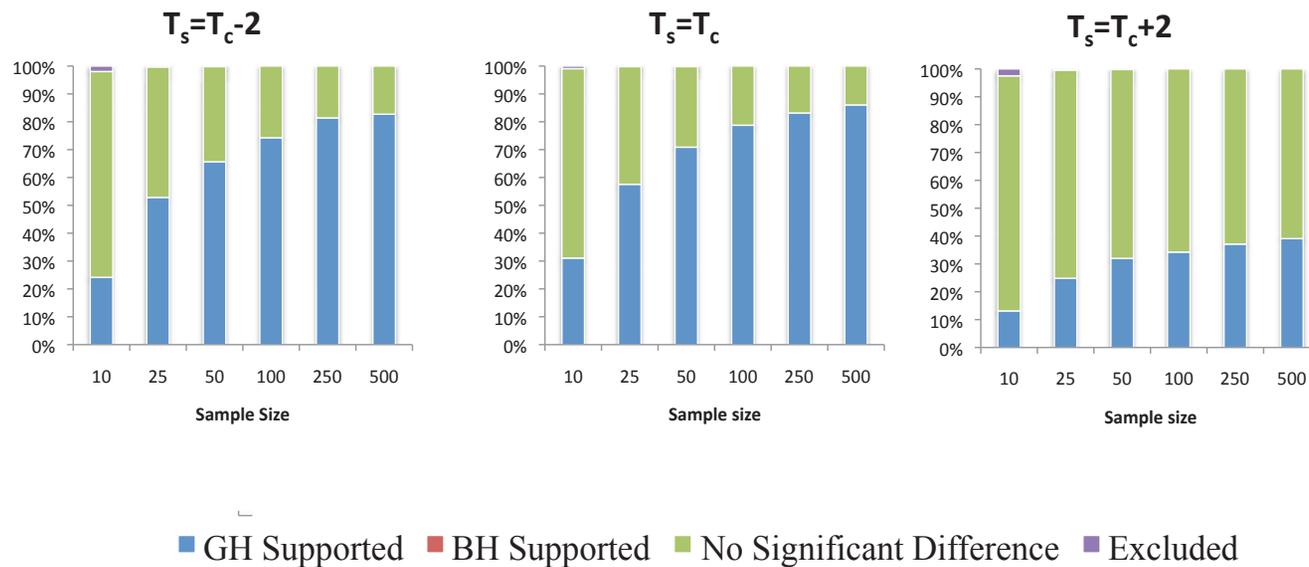


Figure 2.10 Tukey box plots comparing Z and Z_2 estimates for the B-H and G-H models respectively for simulations not hitting a bound or producing an NaN in three scenarios: 1. All simulations regardless of AIC value. 2. Simulations where G-H had a strongly supported AIC value over the B-H model and 3. Simulations where the AIC values were not strongly different between the two models. Estimations were for yellowtail snapper, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$ and no variability for both growth and recruitment. The solid blue line represents the known value of Z_2 .

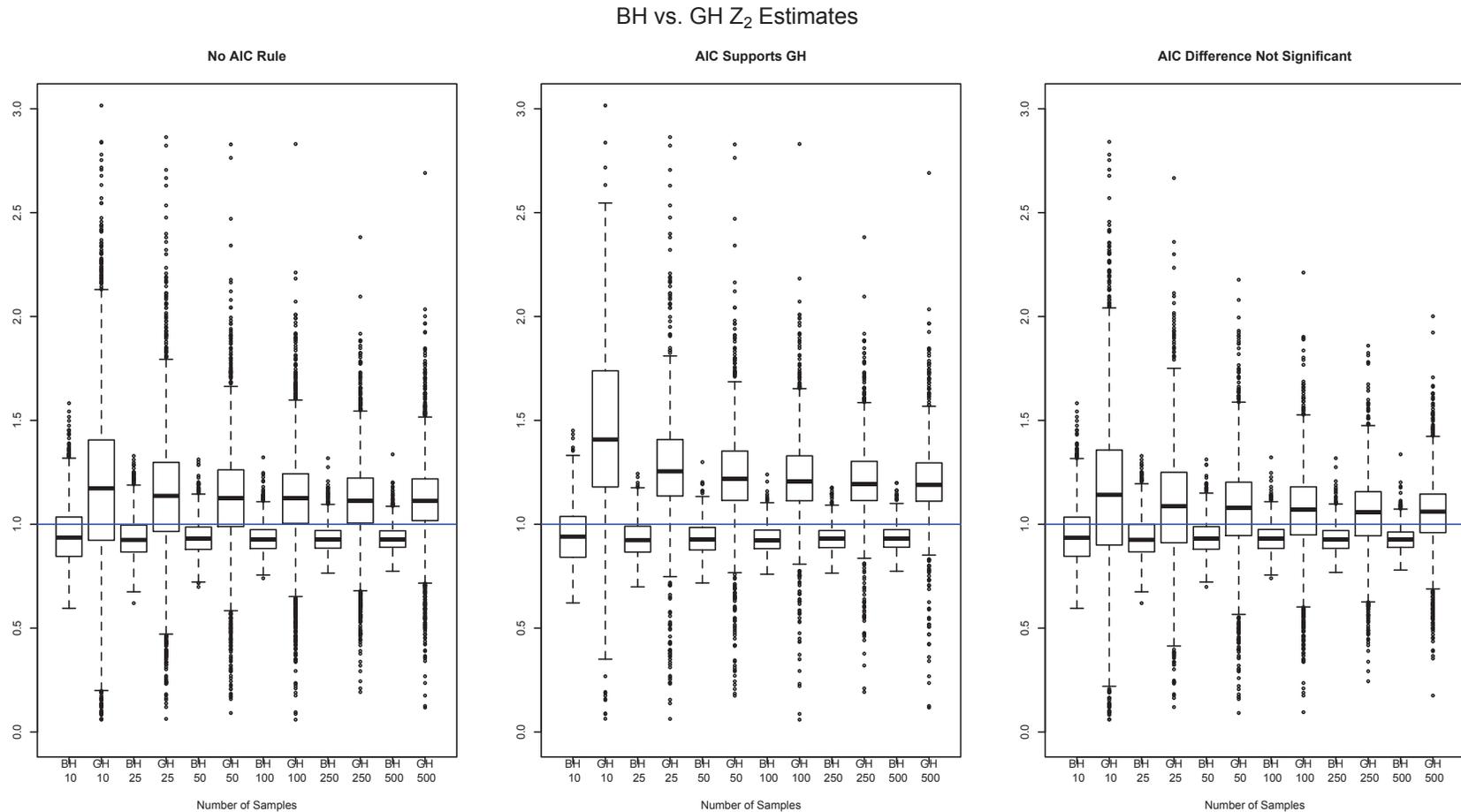


Figure 2.11 Tukey box plot comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound. Estimations were for yellowtail snapper, $Z_1=1.0$, $Z_2=0.5$, $Y_s=6$ and high variability for both growth and recruitment. The solid blue line represents the known value of Z_2 .

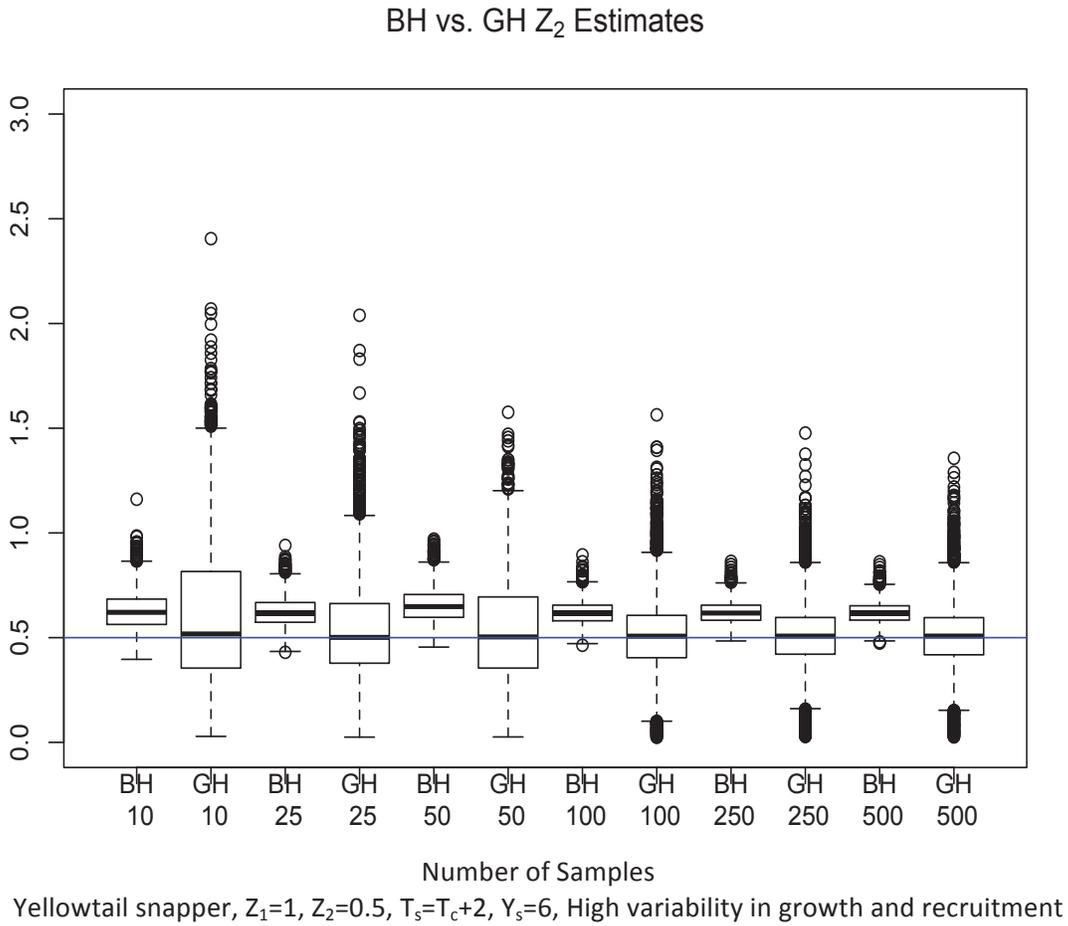


Figure 2.12 Tukey box plots comparing Z and Z_1 estimates for the B-H and G-H models respectively for all simulations not hitting a bound. Estimations were for yellowtail snapper, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$ and high variability for both growth and recruitment. The solid blue line represents the known value of Z_1 .

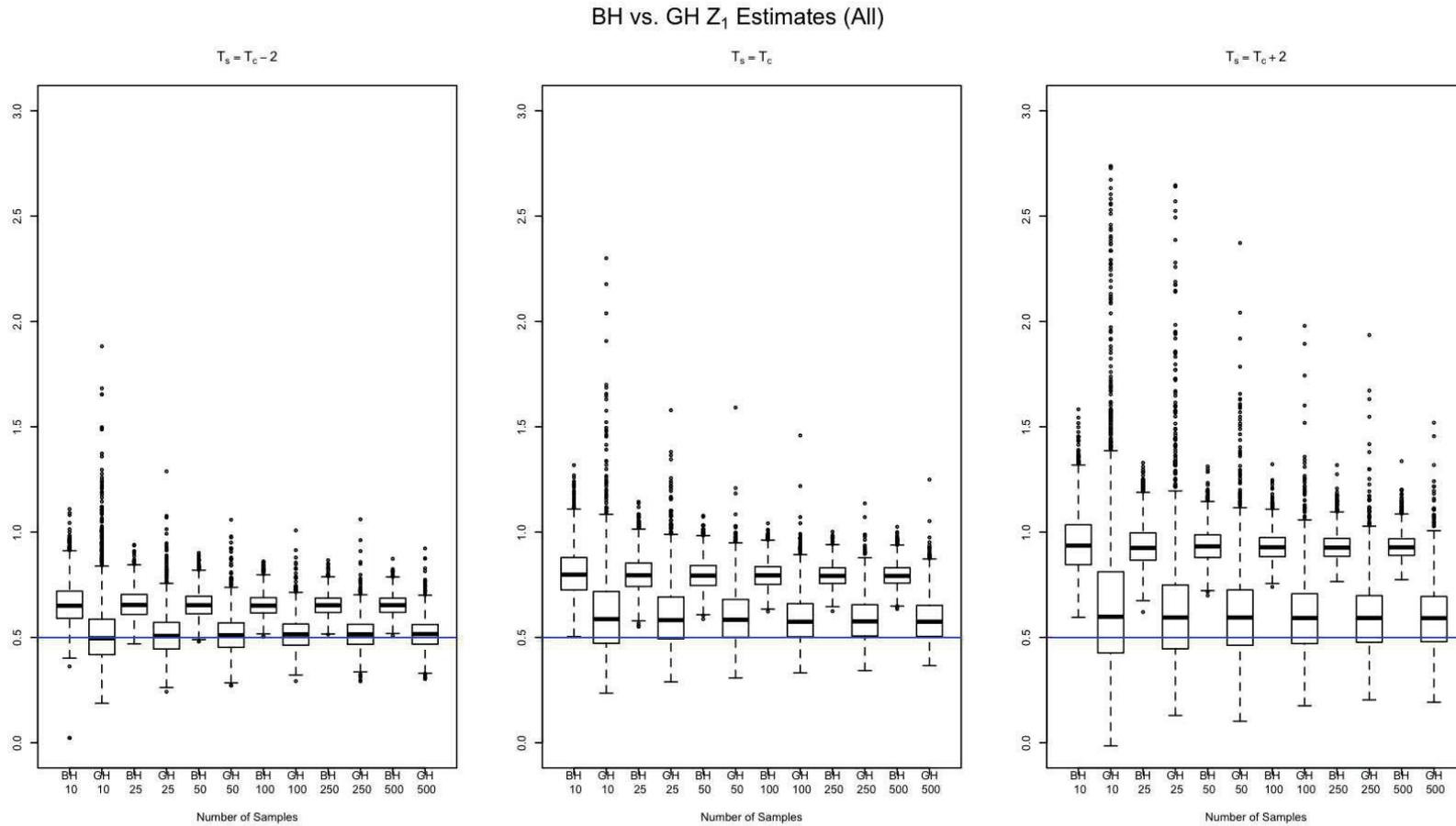


Figure 2.13 Tukey box plot comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound for four years, six years, and eight years of sampling. Estimations were for yellowtail snapper, $Z_1=0.5$, $Z_2=1.0$, and high variability for both growth and recruitment. The solid blue line represents the known value of Z_2 .

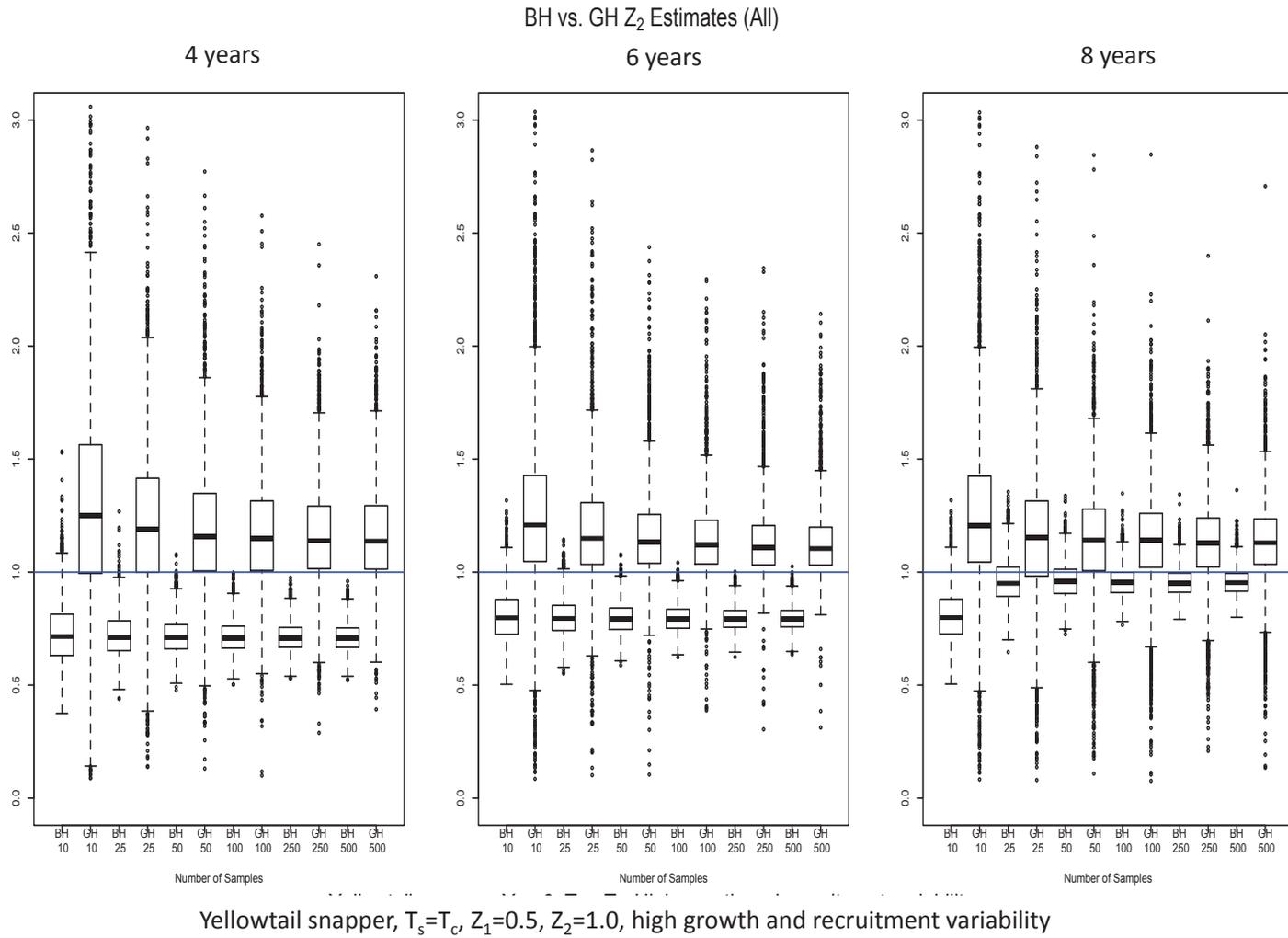
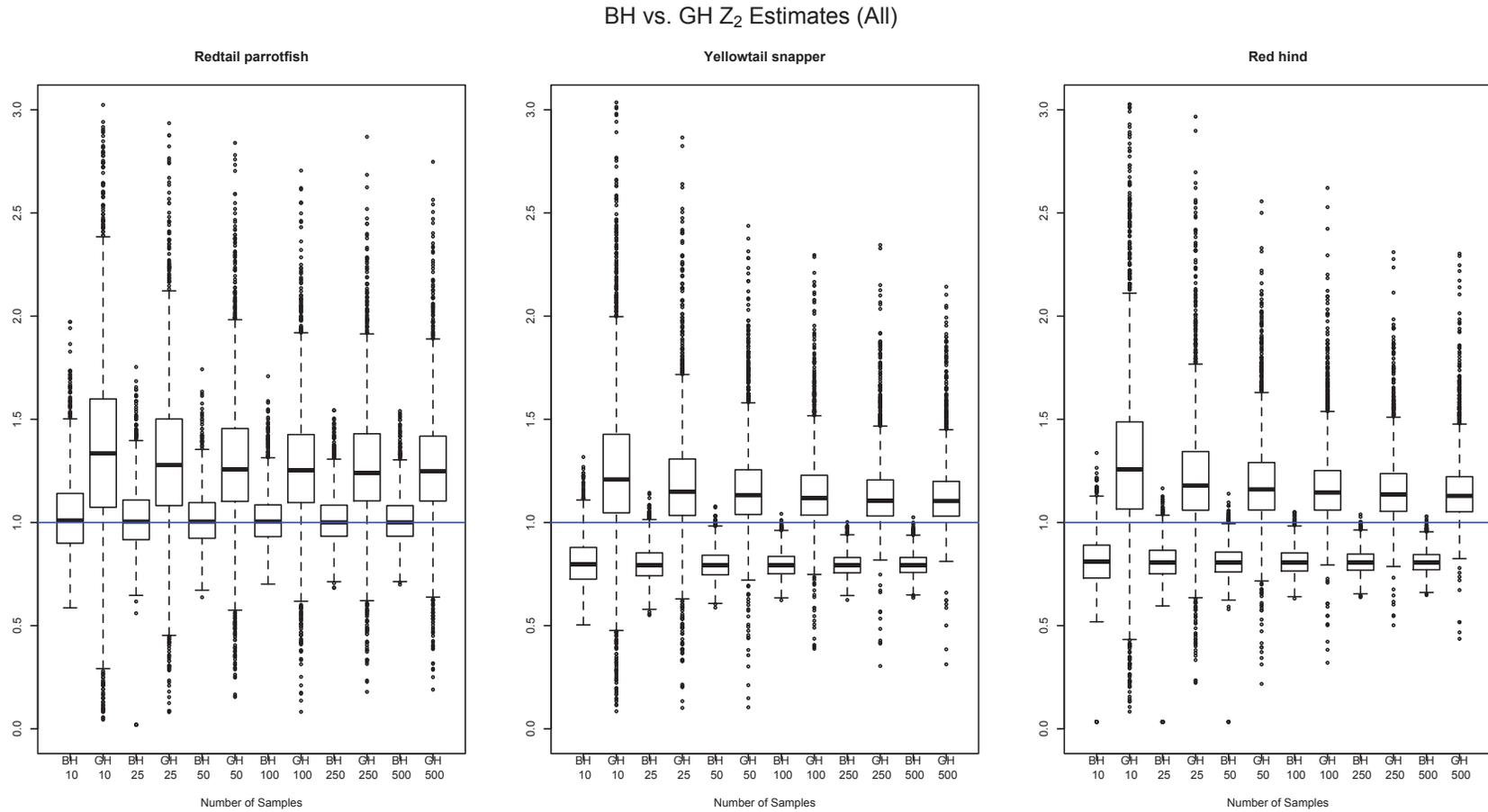


Figure 2.14 Tukey box plot comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound for redbtail parrotfish, yellowtail snapper, and red hind. Estimations were for $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$, $T_s=T_c$ and high variability for both growth and recruitment. The solid blue line represents the known value of Z_2 .



$Y_s = 6$, $T_s = T_c$, High growth and recruitment variability

Figure 2.15 Tukey box plot comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound for different sampling starting times relative to the time of change. Estimations were for redbtail parrotfish, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$, and no variability for growth or recruitment. The solid blue line represents the known value of Z_2 .

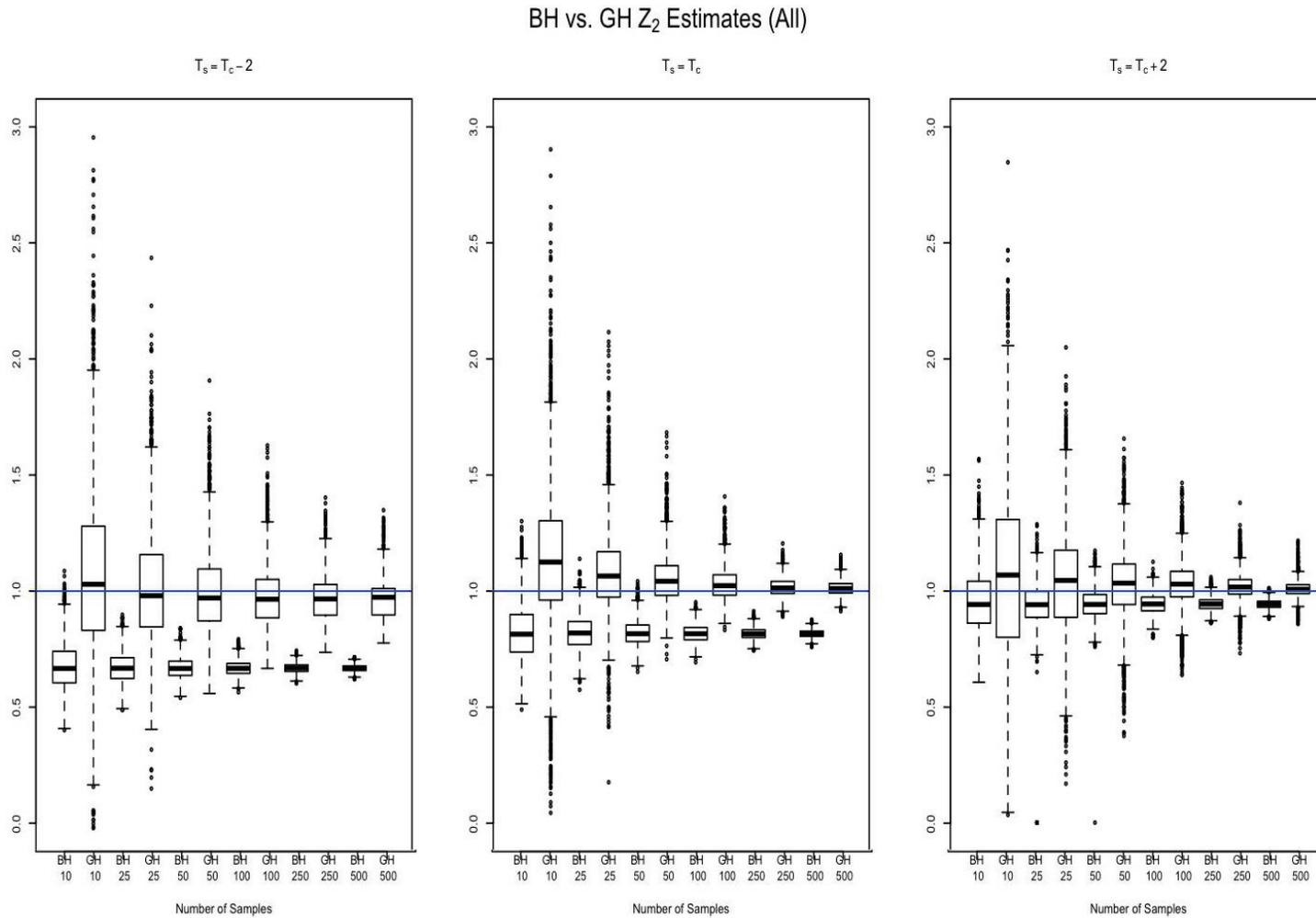
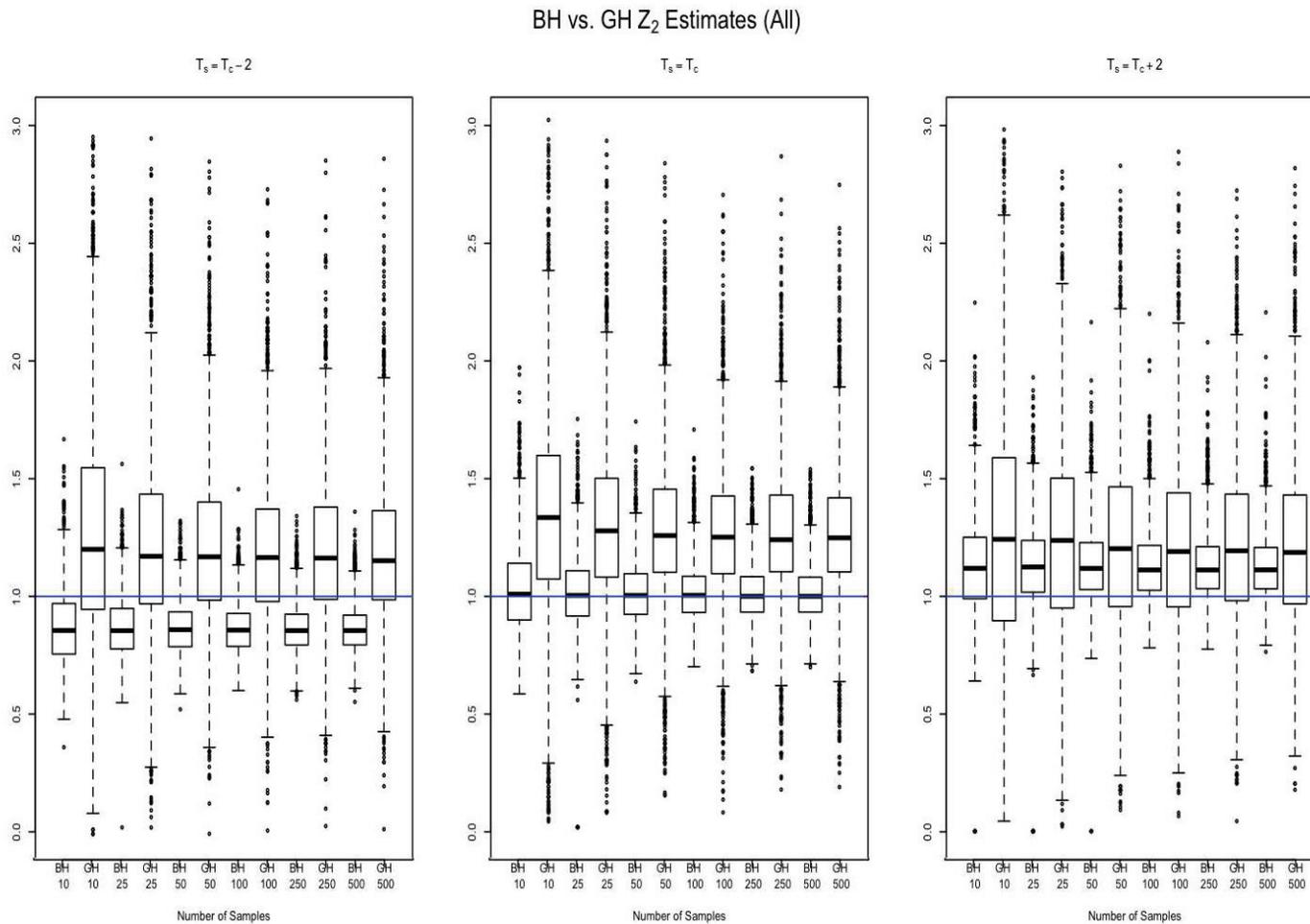


Figure 2.16 Tukey box plot comparing Z and Z_2 estimates for the B-H and G-H models respectively for all simulations not hitting a bound for different sampling starting times relative to the time of change. Estimations were for redbtail parrotfish, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$, and high variability levels for both growth and recruitment. The solid blue line represents the known value of Z_2 .



Redtail parrotfish, $Y_s = 6$, High growth and recruitment variability

CHAPTER 3—INFORMING MODIFIED DATA COLLECTION IN THE U.S. CARIBBEAN USING SIMULATION MODELING

Introduction

In many small-scale tropical fisheries (SSFs), detailed information and analyses of fish stocks are limited for many reasons. The fisheries are often artisanal in nature, spread out over many landing sites, catching multiple species with multiple gears (Salas et al. 2007). While those factors alone create a challenge, fishermen and managers also often do not have a relationship of trust and cooperation. This limits not only the quantity of data available, but also the quality of the data collected (Salas et al. 2007, Jentoft 1989). Further complicating the issue, lack of time and money are often listed as a limiting factor in making positive changes in data collection and analysis (Salas et al. 2007).

The U.S. Caribbean consists of the islands of Puerto Rico and the United States Virgin Islands (USVI). Like many other areas with SSFs, the U.S. Caribbean has had issues with data quantity and quality. As a result, the data collected in the past have been insufficient to complete an informative stock assessment (SEDAR 2009).

Stock assessments are not just effective tools for examining the trends and status of the fishery and assessing the potential impacts of alternative management actions. They are also the main source of information for decisions regarding annual catch limits (ACLs), limits for all federal fish stocks, required by the latest reauthorization of the Magnuson-Stevens Fisheries Conservation and Management Act (MSRA) (U.S. Department of Commerce 2007). These requirements have created significant challenges for management in the U.S. Caribbean as they try to meet the MSRA requirements without pre-existing stock assessments for their fish species.

Because time, money, and trust limitations are such a concern, it is important that stakeholders within the U.S. Caribbean understand why certain amounts and types of data are required for stock assessment. In addition, it is important for them to understand the tradeoffs between collecting more data and getting more accurate or precise information from the data given a

particular method of stock assessment. Council members and fishers have varying levels of sophistication in their understanding of the underlying theory and mathematics of stock assessment models used in management decisions. As a result, some do not understand the quantity, quality, or types of data needed in the process. Even further complicating the issue is a lack of understanding of how experimental design and sample size influence that timeline. Some stock assessment models claim to work well at “small sample sizes.” Yet the definition of “small” will vary depending on the species type, stock assessment model of choice, and overall sample design. It is important that all involved in the fisheries management process understand not only how long sampling needs to occur, but also at what magnitude per year and the relationship between the two variables.

Certain types of analyses, such as simulation modeling, can provide such information and can play a significant role in designing data collection. They are particularly valuable tools when little real data is available. Simulation models can create populations of hypothetical fish (based on real data on fish populations) where everything about that population is known and then extract data from that population to test out theories, assumptions, model behaviors, or experimental designs. This method of testing can help scientists, managers, and other stakeholders understand population dynamics, stock assessment models, and the implications of possible management actions in ways that would otherwise be expensive or difficult, if not impossible. A completed simulation model based on U.S. Caribbean fisheries can be a powerful tool for guiding sample design, stock assessment choice, and influencing expectations for the region both now and in the future. The results from a simulation model can be used to explore the balance between sample size and the years of sampling needed to provide reliable estimations of important fisheries parameters, ensuring that extra time and money are not spent when unnecessary.

Improving data quality for stock assessment has been a priority in the region, especially with the new MSRA rules requiring the fisheries management councils to set ACLs for all fish stocks by 2011, but time and money resources are limited. The Caribbean Fishery Management Council (CFMC), its Scientific and Statistical Committee (SSC), and the 2009 Caribbean Data SEDAR group have all expressed a desire to use the Gedamke-Hoenig mean-length mortality estimator

(G-H model) to evaluate their fisheries, once enough quality data is available (SEDAR 2009). The G-H model is a stock assessment method evaluating the response of changing mean length values over time year and attributing those changes to changes in total mortality (Gedamke and Hoenig 2006). The method not only estimates whether a change in total mortality occurred, but the magnitude and direction of that change. Assuming the natural mortality rate does not change over time, the differences in total mortality are further attributed to changes in fishing mortality rates.

The G-H model has been applied to other data-poor situations, such as goosefish (Gedamke and Hoenig 2006). Initial testing indicated the model performed well, especially when it came to determining a pattern of exploitation (Gedamke and Hoenig 2006). The model has been put forward as ideal for data-poor fisheries, only requiring small sample sizes. However, it is unclear what the minimum sample size or number of years of a sampling program the model would need to get a realistic and informative estimations of the changes in total mortality rates.

Before a stock assessment is completed and used to inform management, it needs to be well understood whether or not the model is appropriate for the data available and what the caveats are for using that model. Choosing the best model for the data involves, among other things, understanding the assumptions, the inputs required, and the possible bias or uncertainty in estimations from that model. For some stock assessment methods, such as the G-H model, these things have yet to be thoroughly tested. Most of the cases used to test the G-H model utilized data directly from fisheries with limited samples available, where the actual total and fishing mortality rates are not known exactly. Simulations were utilized in the inaugural publication of the model, but the simulations presented there were limited in scale, only looking at the possible implications of miscalculating certain parameters over one set change in mortality ($Z_1=0.3$, $Z_2=0.6$) for one species of fish (Gedamke and Hoenig 2006). Simulations have yet to be published to determine the effects of sample sizes and the length of the sampling program on results and whether the life history of the species, the magnitude or direction of change in mortality, or the violation of the model's assumptions influence that effect.

Although groups involved in U.S. Caribbean fisheries have expressed an interest in using the Gedamke-Hoenig model, before doing so this understanding of the amount of data required and the possible outcomes if assumptions are violated needs to be understood in more detail. After further testing occurs, not only will there be a better understanding of the types and quantities of data needed to improve assessments, but there will also be further scientific justification for the use of the model for management.

In order to address the gap in knowledge about the behaviors and data requirements of the Gedamke-Hoenig model, as well as the misunderstandings in certain stakeholder groups about the quantity and quality of data needed for stock assessment, a combination of simulation modeling and stock assessment was completed to inform the region's fisheries scientists, management, fishermen, and other stakeholders as they redesigned the commercial sampling program. The goal was to develop a tool to determine the statistical tradeoffs of increasing the number of length samples taken per year and number of years of consistently sampling that would allow for the detection of a change in total mortality rates using the Gedamke-Hoenig mean-length mortality estimator across a range of possible life history parameters and model assumption violations.

Methods

To further examine the balance between sample size and sampling length of time, a simulation study was conducted with five major modules. The first was the population generation, used to develop a population of fish where all lengths of fish were known throughout the years. The second was the random sampling of fish from the generated population. Next, the samples were used to estimate total mortality rates using the G-H mean-length mortality estimator. For each simulation's estimations, results were calibrated to account for the programming language used for the model and differences between the population generation and estimation steps of the model. Finally, results for the calibrated model estimates were analyzed to evaluate performance in accuracy, precision, and overall variability. Each of these steps is outlined in detail below.

Population Generation

The simulation model was developed using the R statistical programming language (R Development Core Team 2010) with a simulated population of fish where life history parameters and fishing mortality histories were known exactly. Each population was initialized with 1000 individuals per each 1 cm length interval over the length distribution from the length of first catch (L_c) to the length at infinity (L_∞). The population was then projected forward by converting the lengths at time t (L_t) to ages (Equation 1a) and then increasing the age one time step (Equation 1b), before converting the ages back to lengths (Equation 1c). Any length bins remaining without individuals after each time step were filled with recruits. Recruits were either constant between each year, with 1000 individuals per empty length bin, or varied each year, depending on the scenario.

$$Age_t = \frac{-\log\left(1 - \left(\frac{L_t}{L_\infty}\right)\right)}{K} \quad (1a)$$

$$Age_{t+1} = Age_t + 1 \quad (1b)$$

$$L_{t+1} = L_\infty(1 - e^{-K(Age_{t+1})}) \quad (1c)$$

This was done for a seventy year time period to ensure the population had reached a stable length distribution. At year seventy ($T_c=70$), mortality rate of the simulated population changed (from Z_1 to Z_2 , where Z_1 designates the total mortality before the change and where Z_2 designates the total mortality after the change) with the direction and magnitude of that change varying by scenario. For each scenario, 2500 simulations were run.

Several different scenarios, with 2500 simulations each, were run where several parameters varied. The total mortality rate (Z_1 and Z_2), the direction and magnitude of the change in total mortality rate were two factors that varied: in half of the scenarios, total mortality rates increased (from 0.5 yr⁻¹ to 1.0 yr⁻¹) and in the rest total mortality decreased (from 1.0 yr⁻¹ to 0.5 yr⁻¹). Other factors included the year of the change in total mortality rate occurred in relation to the year in which sampling began (T_c) as well as the overall length of the time series (Y_s). Three commonly caught species in the U.S. Caribbean covering different von Bertalanffy growth parameter values (K , L_c , L_∞) were the basis for the simulated populations and included:

Yellowtail snapper (*Ocyurus chrysurus*), red hind (*Epinephelus guttatus*), and redtail parrotfish (*Sparisoma chrysopterus*). The growth parameter information came from Claro (2001) and analyses of existing U.S. Caribbean data by Todd Gedamke were used to calculate L_c (T. Gedamke, Southeast Fisheries Science Center, personal communication).

The consequences of violating the assumptions of constant mortality and growth have not been thoroughly studied for the G-H model, although we know some variation and uncertainty for these parameters are likely to occur in real data. To account for uncertainty and variability in the population, in some scenarios recruitment and growth rates (R and K; respectively) were randomly chosen from lognormal distributions, mimicking stochastic environmental changes on a year-to-year basis. The lognormal distribution was chosen because negative values of both growth and recruitment rates are impossible. For each rate, one of three levels of variability was chosen (none, low, or high) and all possible combinations were analyzed (Table 1). For the recruitment rate, the base number of recruits was 1000 and that was multiplied times a random number from a lognormal distribution centered around one with a standard deviation for the low level at 0.2 and while at the high level was 0.4 (Equation 2a; Equation 2b; Figure 3.1). The variability of the growth rate was centered at a multiplier of one, with the standard deviations at 0.25 and 0.5 for the low and high levels respectively (Equation 3a; Equation 3b; Figure 3.2).

$$\text{Recruitment} = f(x) = 1000 \left(\frac{e^{-((\ln x)^2 / 2(0.2^2))}}{x(0.2)\sqrt{2\pi}} \right) \quad (2a)$$

$$\text{Recruitment} = f(x) = 1000 \left(\frac{e^{-((\ln x)^2 / 2(0.4^2))}}{x(0.4)\sqrt{2\pi}} \right) \quad (2b)$$

$$\text{Growth rate} = f(x) = K \left(\frac{e^{-((\ln x)^2 / 2(0.25^2))}}{x(0.25)\sqrt{2\pi}} \right) \quad (3a)$$

$$\text{Growth rate} = f(x) = 1000 \left(\frac{e^{-((\ln x)^2 / 2(0.5^2))}}{x(0.5)\sqrt{2\pi}} \right) \quad (3b)$$

Little is known about the variability of growth and recruitment of the fish stocks in the U.S. Caribbean, so values were chosen so that at the low standard deviations there was approximately an equal probability of having a rate that was half of the mean as it was double the mean.

Standard deviations for the high levels of variability were chosen so that there was approximately an equal probability of having no recruitment or growth, as there was of the recruitment rate equaling four times the mean. For this study, the species chosen purposefully covered several possible life histories to determine the sensitivity of the model to differences in life history parameters. Given the uncertainty in the amount of annual in growth and recruitment rates, understanding some of the possible impacts of breaking the critical assumptions of constant growth and recruitment over the period of sampling on our results is more important at the present time than knowing impacts at specific magnitudes of the variation.

The selected growth rate value (K) was chosen as described above, but in addition, the von Bertalanffy equation was modified to account for this change (Equation 4). This determined the new length class for individuals by taking the old length the previous year and accounting for the change in K by calculating the new length with the new growth rate (K.var) and subtracting what the old length would have been with the new growth rate. By varying K this way, in certain scenarios the population went above L_{∞} .

$$L_{t+1} = L_{\infty}(1 - e^{(-K(Age_t))}) + L_{\infty}(1 - e^{(-K.var(Age_{t+1}))}) - L_{\infty}(1 - e^{(-K.var(Age_t))}) \quad (4)$$

Sampling

For each of the 2500 simulations, a set of length measurement samples was taken from the population in the last few years of the simulated population. These samples represented length samples that could be taken by port samplers at the dock. A range of samples sizes was analyzed (n=10, 25, 50, 100, 250, and 500 length measurements per year). Different number of years sampled were examined (Y_s), ranging from four consecutive years of sampling to ten years of sampling for each scenario.

In addition, when the year sampling started (T_s) relative to the year of change in mortality rate (T_c) also varied by scenario. Three different scenarios were examined. In the first scenario, sampling started the year the total mortality rate changed ($T_s=T_c$). In the second scenario,

sampling started two years before the change in Z occurred ($T_s=T_c-2$). In the third scenario, sampling began two years after the change in Z ($T_s=T_c+2$).

Looking at these possible T_s values is important because sampling does not always begin when a change in fishing mortality occurs and that can impact the model's ability to accurately and precisely estimate a change in mortality. In the case of the U.S. Caribbean, it is difficult to determine when these major changes occurred or will occur relative to when sampling will begin. Changes have likely occurred in the past due to changing regulations and have the possibility of occurring in the future. Given the relatively short sampling time frames examined in this study, it was important to understand the sensitivity of the model's estimates to all these possible scenarios.

Stock assessment model

For each set of length samples within a year, the mean length of the samples was calculated. This was done for each simulation, across all scenarios. These mean lengths were then used in Gedamke-Hoenig mean-length mortality estimator (G-H model; Gedamke and Hoenig 2006). The number of mean lengths used in each estimation was dependent on the length of Y_s (from four to ten).

Length-based stock assessment models, such as the G-H model are commonly suggested for use in data-poor situations, like those in the U.S. Caribbean (Pauly 1983, Jones 1984, Quinn and Deriso 1999). The G-H model evaluates changes in average length over time to estimate changes in total mortality rates. It requires initial guesses for the von Bertalanffy growth parameters, growth rate (K), maximum length (L_∞), and length at first capture into the fishery (L_c). These can be derived from an age-growth key from a data collection effort that does not have to occur annually. In addition, the model requires the mean length of the samples for each years of sampling effort. Using these values, it estimates the mortality rate before change (Z_1), the mortality rate after the change (Z_2) and the years since the change occurred (d) which leads to an estimate of the year of change (T_c). With this information and equation (5), you can solve for the parameters of interest using a likelihood function (Gedamke and Hoenig 2006).

$$\bar{L} = L_{\infty} - \frac{Z_1 Z_2 (L_{\infty} - L_c) \{Z_1 + K + (Z_2 - Z_1)^{-(Z_2 + K)d}\}}{(Z_1 + K)(Z_2 + K)[Z_1 + (Z_2 - Z_1)^{-(Z_2 d)}]} \quad (5)$$

While having similar data requirements as the B-H model, the G-H model accounts for changes in the mortality of the population (Z_1 to Z_2) (Gedamke and Hoenig 2006). Obviously, this is a necessary development in stock assessment because fishing behavior does change over time and needs to be considered in the calculation of important biological reference points often used to evaluate the fishery and guide regulations. Assuming the natural mortality rate does not change over time, the differences in total mortality rates are attributed to changing fishing mortality rates. Since fishing behaviors in the U.S. Caribbean have been changing in recent years due to changing regulations on all islands and the banning of gill nets in the USVI, the G-H model appears to be a good choice for a length-based stock assessment model.

There are several assumptions for the model, including constant growth of individuals and constant recruitment over time (Gedamke and Hoenig 2006). In this simulation model recruitment and growth rates did vary over time in certain scenarios to test the implications of violating this assumption.

The G-H model estimated Z_1 , Z_2 , T_c and variance (σ). While the G-H model is capable of estimating multiple changes in mortality, for this particular simulation model only one change was simulated, to simplify and increase the speed of the simulations.

Adjustments

Several adjustments of the final estimation values were necessary given the programming language used and models chosen for this project. A concern has been raised about the reliability of the optimization function in R (M. Prager, Adjunct Faculty Member, Virginia Tech Department of Fisheries and Wildlife Sciences, personal communication). To mitigate the potential effect of poor optimization in R and standardize the simulations, an optimization study was completed with the simulation model. It compared the five main algorithms within the `optim()` function in R to determine which would be most appropriate for the model. For this

study, I chose the limited-memory Broyden-Fletcher-Goldfarb-Shanno algorithm (LBFGS) with parscale option of the `optim()` function because it consistently gave results closest to the known values in the simulated population, it has more flexibility than the regular Broyden-Fletcher-Goldfarb-Shanno (BFGS) algorithm if major problems should arise in the future, and differences between the top two performing algorithms were generally negligible (Chapter 2, Table 2.2).

The population simulation and estimation procedures had slightly different computational assumptions. The population simulation was developed using a discrete growth function, where the population distribution across lengths was not continuous. In contrast, the estimation method was developed based on a continuous population distribution. Knowing this, to further calibrate and verify the model was working correctly, parameters were estimated using mean length data from the entire simulated population (i.e. with no sampling and ‘perfect’ data). The difference between the parameters estimated using lengths from the entire simulated population and the known parameters was used as a correction factor that was applied to all results within a scenario to correct for this behavior. Separate correction factors were developed for each scenario.

Evaluation

After generating the population and estimating the parameters of interest, several filters were applied to the results. These filters took out estimations that were considered invalid because they produced values that were not numbers (e.g., NaN) or estimates were at the limit of a predetermined upper and lower bound within the optimization (lower bound=0.01 and upper bound=3).

With the remaining successful simulations, the accuracy of each estimation was calculated for each individual simulation. This was measured by a delta value, or the known value of the parameter of interest for each simulation ($Z_{2,i}$) minus the estimated value of the parameter of interest ($\hat{Z}_{2,i}$) (Equation 5).

$$\Delta_{Z_{2,i}} = Z_{2,i} - \hat{Z}_{2,i} \quad (5)$$

The precision of individual simulation estimations was also evaluated. For each estimate within the optimization, a standard error was calculated. These standard errors were averaged within a scenario and their distribution examined.

Results

By completing a simulation study, everything about the created population of fish could be known and the distance from reality based on our chosen model, the G-H model, could easily be measured. The results here focus on the precision (the standard error of an estimation within one simulation), accuracy (the difference between the known and estimated Z_2 values), and overall variability (spread of estimation results in a set of 2500 simulations) of the Z_2 estimates, although the estimates of Z_1 followed a similar pattern and together Z_1 and Z_2 can provide information on trends in the fishery. While it is important to know the magnitude and direction of change over time, in many cases managers of the fishery are focused on knowing the current fishing mortality and current total mortality of the fishery. By knowing what is currently going on in the fishery, they can adjust regulations or enforcement to try to get the fishing mortality rate to the desired level. For this study, the initial mortality rate was Z_1 and current mortality rate was Z_2 .

Across all scenarios, there was a clear point where as sample size increased, an asymptote in mean length was reached, and no gain was seen in both the mean accuracy (Δ) and the mean precision of results (SE) (Figure 3.3). These patterns of diminishing returns were seen for simulations that differed by species, changes in Z , and values of T_s . When considered individually, those factors (species, changes in Z , and values of T_s) did not appear to influence the values of accuracy or precision for scenarios.

Certain tradeoffs exist in the relationship between sample sizes (n) and the years spent sampling (Y_s). Equivalencies exist, where a combination of a smaller sample size and longer length of sampling program produced approximately the same mean ΔZ_2 and/or mean SE as a larger sample size in fewer years (Figure 3.4). The combinations where equivalent values were obtained varied by situation. Within a set of equal mean ΔZ_2 , sometimes a similar asymptote as

seen in the previous results was present, where increasing either sample size or Y_s did not significantly change the mean (Figure 3.4). This was seen mostly at larger sample sizes.

The distribution of simulations for each of the parameters of interest also provided important information about the behavior of the G-H model in a potential Caribbean sampling program. For example, there was little difference between the scenarios regarding the mean values of the Δ values for Z_2 and the SE of Z_2 . However, when looking at the distributions of simulation results within each scenario, there is a clear advantage to increasing the number of samples per year and the years spent sampling (Figure 3.5; Figure 3.6; Figure 3.7). As the number of samples per year increases, the possible spread of results for a given scenario, or overall variability, around the measures of accuracy and precision get much tighter, especially in scenarios without any variation in growth or recruitment (Figure 3.5). With increased variation in both growth and recruitment, this pattern is also seen, although the variances were considerably broader for the Δ values (Figure 3.6). Overall variances, once a median value approached an asymptote (Example: $n=250$), also decreased in width with an increasing number of years spent continuously sampling. This pattern can also be thought of in terms of a shrinking confidence interval around the means for both the Δ values and standard errors. Species life history and the change in Z , as in our measures of accuracy and precision, did not show any major differences in variance within scenarios.

The relative time between the year sampling began and the year the total mortality rate changed (T_s relative to T_c) occasionally increased values of the median values of ΔZ_2 and the SE of Z_2 once the median Δ values and SE had stabilized. This was mainly seen in red hind, which was the slowest growing species simulated. It makes sense that it would take longer to see a change in this situation when fishing pressure is decreasing. With only a few years of sampling, if sampling occurred before the change, you would not be seeing much of the change in mean length to begin with because you would have very few data points reflecting a change. Because red hind are slower growing, the changes in mean length would not be as extreme as the faster growing species and it would be more difficult to get accurate estimation of the magnitude of change with only a few data points (Figure 3.8).

While the G-H model has the assumption that recruitment is constant over time, the mean estimates for Z_2 were close to the actual values of Z_2 , even when the variance in the growth and recruitment rates were at a high level (Figure 3.9). The standard errors seemed to not be influenced by growth variability, although recruitment variability did increase the amount of imprecision (Figure 3.10). However, the overall variability adds another layer of complexity. The simulations with recruitment variability, especially when set to the high level appears to increase the size of the confidence interval dramatically (Figure 3.11) when looking at the results for Z_2 alone. However, when looking at the results in conjunction with other parameters being estimated, such as the time of change and Z_1 , the variability is closely tied to the estimated year of change in Z . When the year of change is estimated to be near the end of the time series, the Z_2 estimates are based on only a few data points and are highly variable. An analyst would be able to detect these changes on a case-by-case basis, but further work should be done to examine these patterns. Variability in growth still does play a role, but does not seem to be the driving factor in the ability to accurately and precisely estimate Z_2 .

The model rarely encountered simulations where the parameter estimations included a non-number or hit a bound. Across all of the scenarios, the lowest rate of success was 80.32%, which occurred when growth variability was at a low level and recruitment variability was at the high level for yellowtail snapper, only three years of sampling had occurred, sampling had occurred two years after the change, and $Z_1=1.0$, $Z_2=0.5$. It is unclear why the lowest rate would occur in this situation and not when both growth and recruitment variabilities were at high levels, but it could be an artifact of the optimization procedure and the starting σ value used in the optimization. The majority of scenarios had a success rate of 98% or higher. In a non-hypothetical analysis, only one set of parameter estimations would be produced, because you would only have one mean length value per sampled year. For this study, 2500 possible outcomes per scenario are presented. If an invalid estimation result were to occur in a single analysis, little adjustments in the optimization and initial starting guesses could eliminate the error. In this study no such adjustments were done so that all of the results would be standardized.

Discussion

Within the limited parameter space examined, there was an overall strong pattern of stabilizing results after an asymptote was present with increasing sample size (n) in terms of accuracy, precision, and variance of the estimates. The length of the sampling program (Y_s) also appeared to have a diminishing returns pattern when looking only at the average accuracy and precision. Tradeoffs exist between sample size and the length of the sampling program, with situations where a smaller sample size for a longer sampling program had approximately the same accuracy as larger sample sizes for fewer years. However, the variance of the mean accuracy and precision showed that increasing the number of samples and years spent sampling greatly improved the probability of getting an accurate and precise estimate once results had reached an asymptote.

An important aspect of the model was incorporating uncertainty in both growth and recruitment to see how the estimates responded. In the case of growth variability, even at a high level, an annually varying K seemed to have little impact on the average Δ values, average standard errors, or overall variances (Figure 3.8, Figure 3.9, Figure 3.10). This was unexpected, given that the model assumed K remained the same over time, but could be an artifact of the values chosen for growth variability. The G-H model seems relatively robust to such variation, at least in the particular way and values growth was varied in the simulations. The driving force behind the increased variance of the estimates with variability appears to be the level of recruitment variability in these scenarios (Figure 3.8).

The G-H model is trying to estimate parameters from a change in points from a mean-length time series, rather than the average of a straight line. When variability, in the form of changing growth or recruitment, are added to the data, outliers and increased variance are much more likely to occur in any model. This is particularly true in the G-H model if the variability occurs towards the end of the mean-length time series, which would shift the entire mean-length time series, not allowing mean lengths to begin to stabilize, further complicating the estimation of multiple parameters in an already complex system. This would make the model most sensitive to spikes and valleys in recruitment values towards the beginning and/or end of the time series.

Larger sample sizes and sampling for longer periods of time make more of the time series available for parameter estimation, decreasing the variance.

The results from the G-H model should be interpreted carefully at smaller sample sizes, particularly when the assumption of constant recruitment is believed to have been violated. The time series of length frequency data used to conduct a mean length analysis would give indications of whether highly variable recruitment is present, but additional information should be explored and more effort put into understanding recruitment patterns on an annual or seasonal basis (depending on the fishery). Several methods exist for obtaining information on recruitment variability: directly measuring recruitment through baseline assessments and monitoring, estimating recruitment through stock assessment models such as virtual population analysis or statistical catch at length models, or by utilizing recruitment data from similar species in other regions with more data.

One of the species simulated, yellowtail snapper, had some recruitment variation information available for a Florida Keys stock, with a variation level of $\sigma_R=0.15$ for 1-year old recruits (Muller et. al 2003). However, the independent peer review of that analysis found this number to be unusually low compared to other marine species and suggested that the numbers used to derive the variation level could be caused by ageing errors, a non-representative age-length key, or unrepresentative sampling (Francis 2003). The SEDAR report also noted that the number might be an underestimation because the same age-length key was used over several years (Muller et. al 2003). Had any additional sources of recruitment data been available at the time of these simulations, the simulated recruitment variability could have been defined to better reflect reality and recommendations on which model to use and ideal sample sizes could be more narrowly defined. Using information from areas with more data and species similar to those in the U.S. Caribbean is a viable solution and should be explored further. An additional option is that a recruitment index could be calculated using the samples collected to supplement the understanding of recruitment (Gedamke 2008).

Implications for Management

Collecting additional recruitment information should be a priority for research in the area. However, until baseline data or supplementary data from other species are identified, effort should be given to collect large sample sizes over as many continuous years of sampling as possible in order to increase the probability of getting an accurate estimation of mortality rates using mean length mortality estimates.

While trends in fishery mortality can give managers a general idea of how fishing mortality has changed, fishing mortality alone is not a good means of detecting or determining overfishing. Overfishing occurs in a population when the fishing mortality rate is above the rate that would achieve maximum sustainable yield. Deciding whether overfishing is occurring in a stock is critical: as of 2010, the Magnuson-Stevens Fisheries Conservation and Management Act (MSRA; U.S. Department of Commerce 2007) requires that annual catch limits (ACLs) be in place for all fisheries undergoing overfishing and for all stocks by 2011. These limits need to be set at a level to ensure that overfishing is not occurring in a population. With a reliable estimate of Z , scientists and managers can make approximations to help determine if overfishing is occurring.

Length-based methods, such as the B-H and G-H models, and the estimates of Z from these models, can help determine the level of overfishing. If the natural mortality rate (M) is calculated, then it can be used several ways in conjunction with the estimate of Z . The difference between Z and M is attributed to the fishing mortality rate (F). Additionally, the natural mortality value approximates the fishing mortality rate at maximum sustainable yield (F_{MSY}). F can then be compared to F_{MSY} (F/F_{MSY}). If $F/F_{MSY} > 1$, then overfishing is occurring. If an assessment can provide this type of information, then managers can adjust regulations, enforcement, and ACLs to ensure that F/F_{MSY} does not reach a level indicative of overfishing.

With the current course of management, it is critical for managers to understand how scientific uncertainty plays a role in required MSRA regulations and how model choice influences the level of scientific uncertainty that needs to be incorporated into setting ACLs. ACLs are based on several factors. The first factor is the overfishing limit (OFL), which is a level of catch above which $F/F_{MSY} > 1$ and overfishing is occurring. Anywhere at or below the OFL is the acceptable

biological catch (ABC). The ABC is a level of catch set by each region's SSC to account for scientific uncertainty. From that point, the council sets the ACL, which is not allowed to exceed the ABC set by the SSC. In addition, the councils can set an annual catch target (ACT) at or below ACL to account for management uncertainty. If the ACLs are exceeded, then accountability measures are enacted to correct or mitigate for the excessive catch.

Stock assessment is in many ways subjective. In any analysis, all aspects of the fishery can not be accounted for, so it is important to have someone with knowledge about the system to look at other sources of information, explore patterns, and adjust the analysis to account for unique situations that occur in every system. The exclusion rules presented to limit the estimations used in the final analyses for the models discussed in this thesis are just the beginning of what can be explored. Analysts determine these rules based on their knowledge, and the values chosen can have a significant impact on results. These exclusion rules, and choice of model when AIC does not strongly support one model over another can be, and need to be, adjusted by each analyst to account for unique aspects of the system on a case-by-case basis. Other facets of fisheries information such as trends in recruitment, growth, and professional judgment can be used to inform these decisions. For example, analysis of residual values accounting for the difference in observed and estimated values of interest can help identify unusual patterns or outliers in data that can have a major impact on parameter estimations. Adjustments can then be made to account for this information. However, it is important for managers to understand the implications of the choices of both the model used and the rules used to choose that model on levels of OFLs and ABCs. Furthermore, they should understand how scientific uncertainty affects SSC recommendations to buffer OFLs and ABCs, i.e., the greater the uncertainty, the larger the buffer must be. With some models, the buffer for scientific uncertainty will likely be larger than that of other models.

Specifically regarding the G-H model, these tradeoffs between the level of uncertainty and risk need to be considered by analysts and managers when organizing a sampling program. Within the limited parameter space presented here, the level of uncertainty (based on the standard error and overall variance) was dependent on the model used, the number of samples, and the number of years spent sampling. The level of risk was also dependent on these factors, but the measures

were slightly different: a combination of accuracy, or how close to reality an estimate was, and overall variance, which gave an idea of the chance of getting an accurate (or inaccurate) estimation. Another important aspect of risk to consider is the direction of accuracy—whether the model was typically overestimating or underestimating total mortality rates. In an extreme case, this could mean that the analysis using that model indicates that overfishing is not occurring, when in reality it is. Deciding on a sample size and sampling program length that consistently underestimates mortality rates when mortality is increasing without accounting for that underestimation is, of course, much more risky than choosing one that tends to overestimate fishing mortality rate when it is increasing.

Ultimately, the amount of risk and which type of risk in the form of the choice of how accurate and varied estimates of total mortality rates should be is a value judgment, with no right or wrong answer. Naturally, many aspects besides accuracy and variance of stock assessments play a role in management decisions (e.g, monitoring costs, stakeholder satisfaction, etc.). For example, it might be acceptable to choose a more risky combination of sampling size and time because the cost is prohibitive for a larger program. Instead, the buffer for uncertainty would have to be larger. By better understanding the levels of risk based on model choice, sample size, and sample time, managers can develop more informed management decisions.

Caveats

The analyses here were finely tuned to the model of choice and the realistic needs of U.S. Caribbean. Each stock assessment model has different data requirements, and to optimize sampling for a different model, another simulation model would need to be completed.

The simulation model here also presents a broad range of possibilities for fish populations and sampling. As the groups of stakeholders reworking the data collection in the U.S. Caribbean further define their needs, the model developed here can recreate simulations to adjust for new information such as updated age-growth keys, narrowed down magnitudes of change to examine, or recruitment patterns. Specific recommendations about what sample sizes to use from this point forward, and for how long, cannot be given without knowing limitations on things such as which species to look at by island. The limitations in place now are too general to determine the ideal number of samples per species per year for the entire U.S. Caribbean sampling program to

minimize cost and time while still achieving the end result of accurately and precisely estimating the total mortality rate across the many different commercial fisheries in the region. However, now that the tool has been developed and these initial analyses have highlighted more refined analyses for future work. The recommendations can become even more accurate as we learn more about the life history parameters and the variability of those parameters (particularly data on recruitment and recruitment variability) of the species of interest as well.

Additionally, the results here simulated a random sampling program across time and space. Such a sampling program is unlikely to occur in the U.S. Caribbean in the near future because of the history and culture of collecting fishery dependent data in the region and limitations in personnel and money. It is highly likely that the number of samples and the length of the sampling program would need to increase to account for sampling that is clustered in order to achieve similar accuracy, precision, and variance to the results from this model. A study has been completed by the Southeast Fisheries Science Center, developing a multiplier for several species in the region to account for cluster sampling (Chih 2010). It would be wise for anyone using the model developed here to do so in conjunction with the information from that study before settling on a desired number of samples.

For this particular study, full analyses were only done for the changes of $Z_1=0.5$ to $Z_2=1.0$ and $Z_1=1.0$ to $Z_2=0.5$. A much larger parameter space and further analyses on the impacts of recruitment and growth patterns needs to be explored before determining if the estimation patterns presented above would hold for many other fish stocks and changes in total mortality rates.

Another consideration should be the methods used to vary growth and recruitment. The exact levels of accuracy and variance and the differences between the different levels of stochastic growth and recruitment are artifacts on the values chosen. In some cases, the values randomly chosen would not reflect a realistic pattern over time, as the values were randomly chosen from year to year and include some extremes of the distributions which were not based on other studies. If available, an analyst examining trends in growth and recruitment would be able to use

these trends as auxiliary data. Some of these unrealistic patterns in growth and recruitment would account for some of the estimations presented here as outliers.

It is also critical to note that the G-H model has been attempted in the past using U.S. Caribbean data. The assessment was thrown out because of doubts as to whether spatial assumptions had been violated (Gedamke et al. 2009). Using the existing dataset, it was unclear as to whether or not fishermen had changed their behavior to fish in deeper water, and therefore a different population of fish. Unless the new data collection program addresses the issue, whether by outreach or by simply clarifying the questions on the data form, or fishery independent surveys are conducted, this issue will continue to exist and subsequent assessments will also be rejected.

Literature Cited

- Beverton, R. J. H., and S. J. Holt. 1956. A Review of Methods for Estimating Mortality Rates in Fish Populations, with Special Reference to Sources of Bias in Catch Sampling. *Rapports et Procès-verbaux des Réunions, Conseil International pour l'Exploration de la Mer*. 140: 67-83.
- Chih, Ching-Ping. 2010. Incorporating Effective Sample Sizes Into Sampling Designs for Reef Fish. *Fisheries Research*. 105: 102-110.
- Claro, R., K. C. Lindeman, and L. R. Parenti (eds). 2001. *Ecology of the Marine Fishes of Cuba*. Smithsonian Institution Press, Washington, London. 253 p.
- Jentoft, S. 1989. Fisheries co-management: delegating government responsibility to fishermen's organizations. *Marine Policy* (2): 137-154.
- Jones, R. 1984. Assessing the effects of changes in exploitation pattern using length composition data. *FAO Fish. Tech. Pap. No. 256*, Rome, 118 p.
- Francis, R. I. C. C. 2003. Report on the 2003 Assessment of Yellowtail Snapper in the Southeast United States. National Institute of Water and Atmospheric Research. Client Report: WLG2003-54.
- Gaertner, D. 2010. Estimates of historic changes in total mortality and selectivity for Eastern Atlantic skipjack (*Katsuwonus pelamis*) from length composition data. *Aquatic Living Resources*. 23: 3-11.
- Gedamke, T. 2007. Estimation of Mutton Snapper Total Mortality Rate From Length Observations. SEDAR 14 Caribbean Yellowfin Grouper, Mutton Snapper, Queen Conch. North Charleston, SC. SEDAR14-AW-05.
- Gedamke, T. 2008. Total mortality rates of the barndoor skate, *Dipturus laevis*, from the Gulf of Maine and Georges Bank, United States, 1963-2005. *Fisheries Research*. 89(1): 17-25.
- Gedamke, T. and J. M. Hoenig. 2006. Estimating Mortality from Mean Length Data in Nonequilibrium Situations, with Application to the Assessment of Goosefish. *Transactions of the American Fisheries Society*. 135: 476-487.
- Gedamke, T, S. Hudy and K. McCarthy. 2009. Preliminary Evaluation of Available U.S. Caribbean Fisheries Length-Frequency Data and Spatial Changes in the Fisheries. SFD-2009-001, 50 p.
- Pauly, D. 1983. Some simple methods for the assessment of tropical fish stocks. *FAO Fish. Tech. Papers No. 234*, Rome, 52 p.

Muller, R.G., M. D. J. de Silva, and L. R. Barbieri. 2003. A Stock Assessment of Yellowtail Snapper, *Ocyurus chrysurus*, in the Southeast United States. FWC-FMRI Report: IHR 2003-10. 217 p.

Quinn, T.J. and R. B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press. New York. 542 p.

R Development Core Team. 2010. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing. Vienna, Austria.

SEDAR. 2009. Caribbean Fisheries Data Evaluation. SEDAR Procedures Workshop 3. North Charleston, SC. 183 p.

Salas, S., R. Chuenpagdee, J. C. Seijo, A. Charles. 2007. Challenges in the assessment and management of small-scale fisheries in Latin America and the Caribbean. Fisheries Research 87: 5-16.

U.S. Department of Commerce. 2007. Magnuson-Stevens Fishery Conservation and Management Act. National Oceanic and Atmospheric Administration. National Marine Fisheries Service. Public Law 94-265. May. 170 p.

Table 3.1 A table of the combinations of levels of growth and recruitment variability scenarios. This set of scenarios was repeated for each species and change in Z.

	Recruitment Variation	Growth Variation
Scenario 1	None	None
Scenario 2	Low	None
Scenario 3	High	None
Scenario 4	None	Low
Scenario 5	None	High
Scenario 6	Low	Low
Scenario 7	Low	High
Scenario 8	High	Low
Scenario 9	High	High

Figure 3.1 Examples of 100 randomly derived distributions of recruitment variation at both “low” and “high” levels.

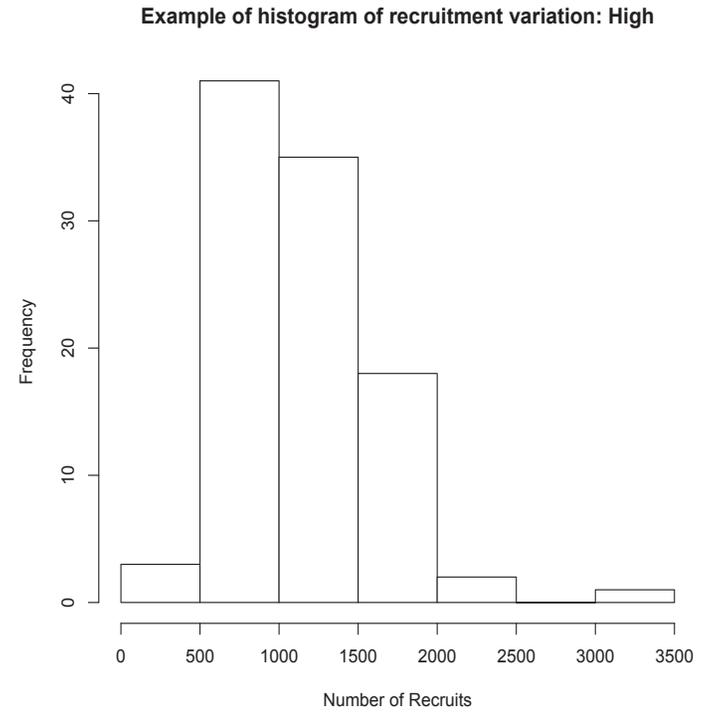
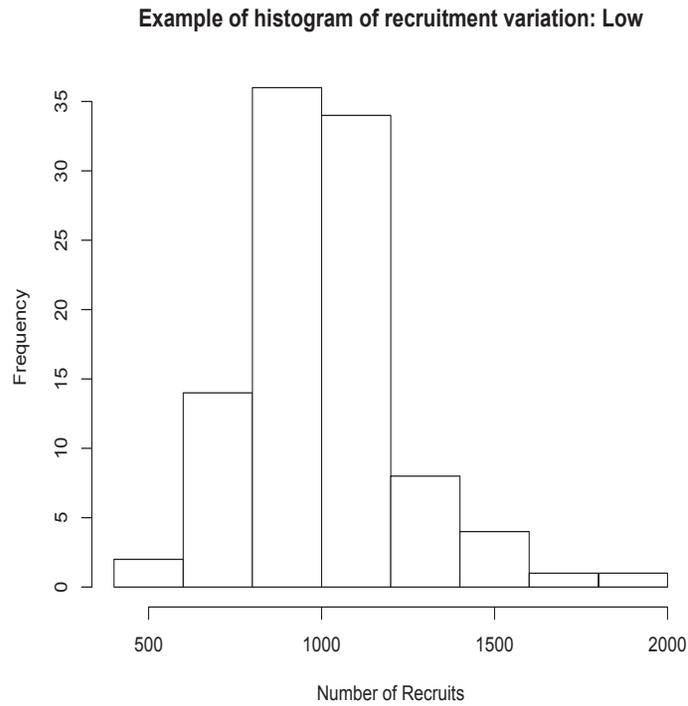


Figure 3.2 Examples of 100 randomly derived distributions of growth rate variation at “low” and “high” levels.

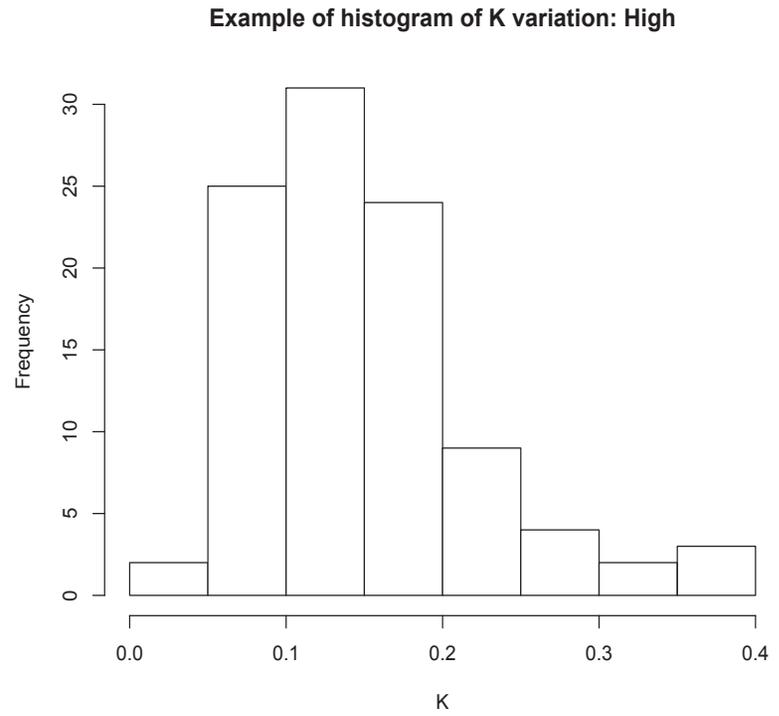
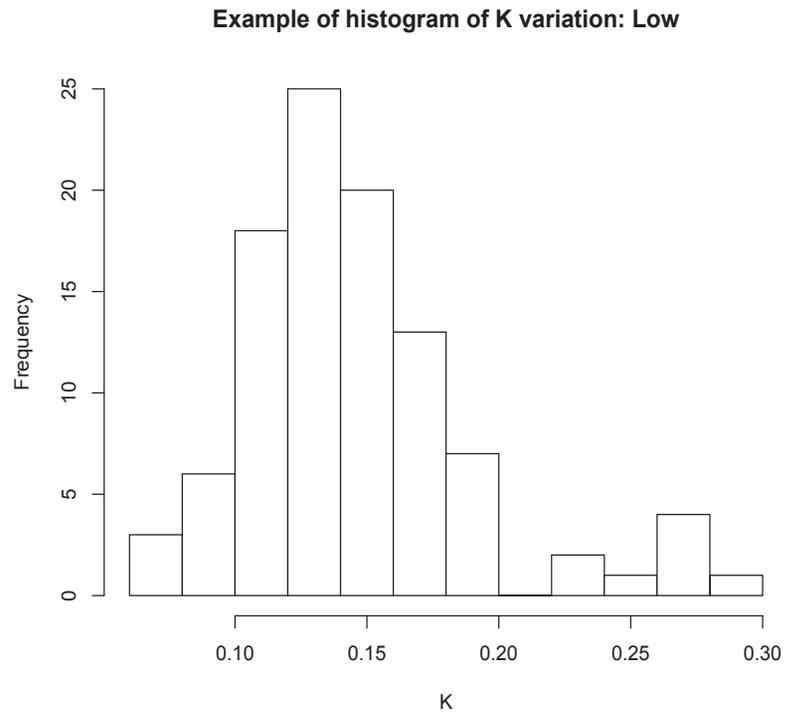


Figure 3.3 Example of stabilizing pattern in both accuracy and precision with increasing sample size. For this particular example, yellowtail were used, $Z_1=1.0$, $Z_2=0.5$, and growth and recruitment variabilities were at high levels.

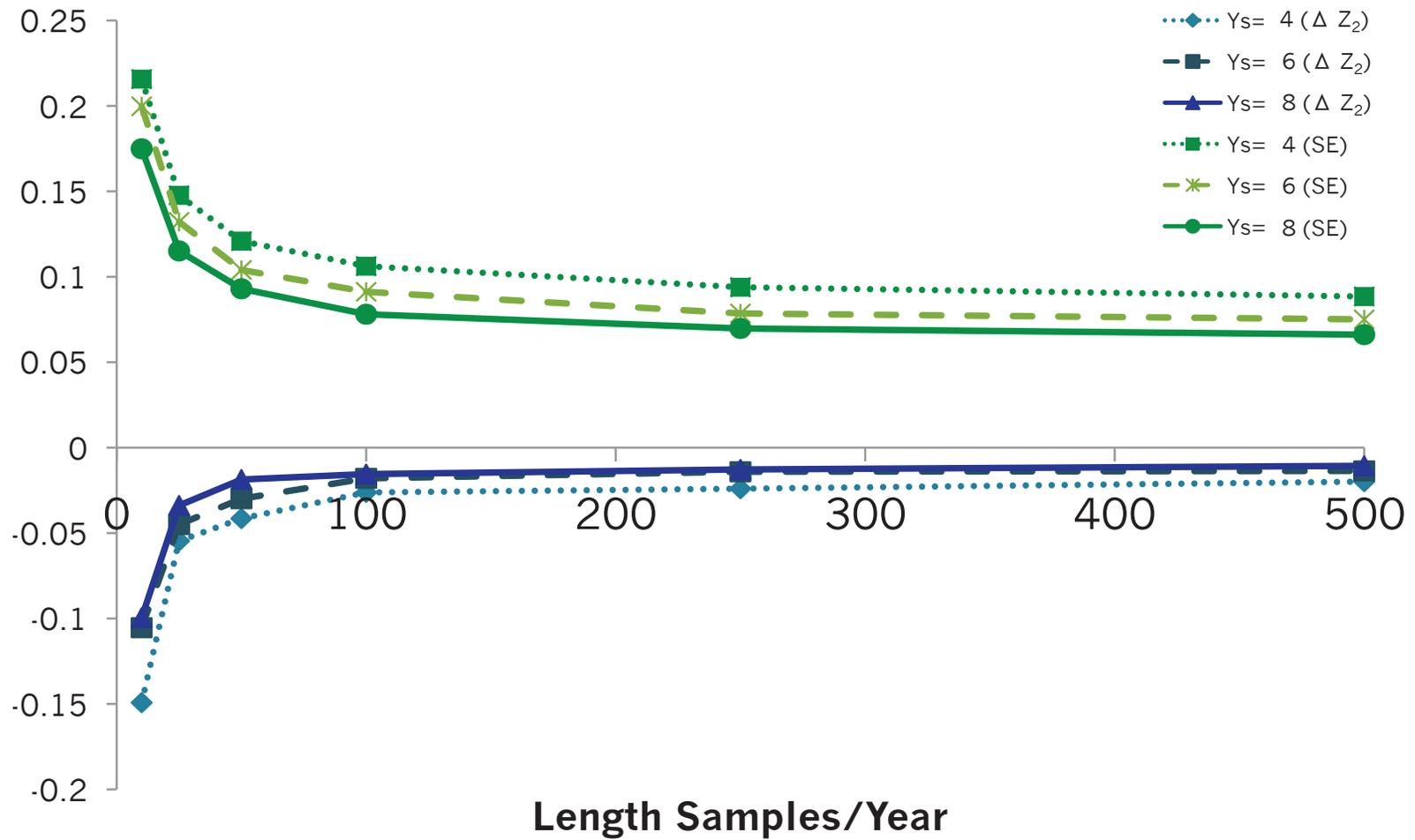


Figure 3.4 Contour plots showing the relationship between sample size and the length of the sampling program for both the mean ΔZ_2 and mean standard errors. Equal colors within an individual plot indicate a similar mean.

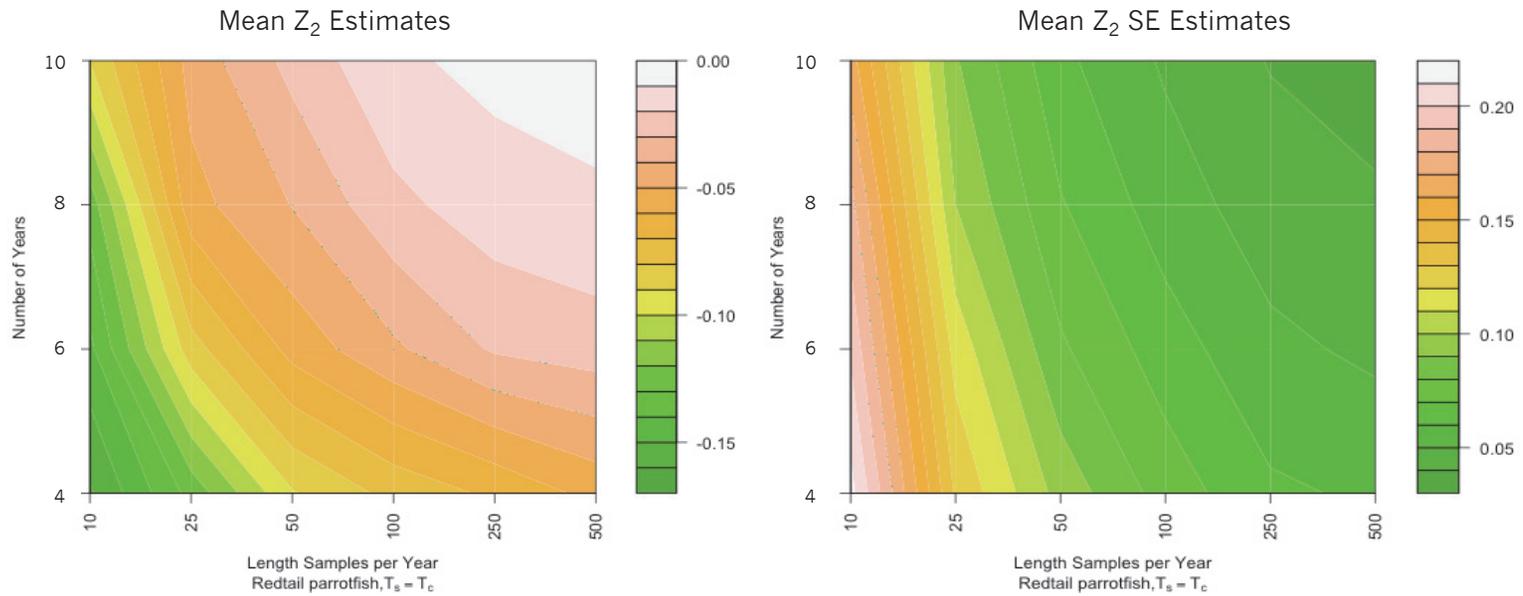
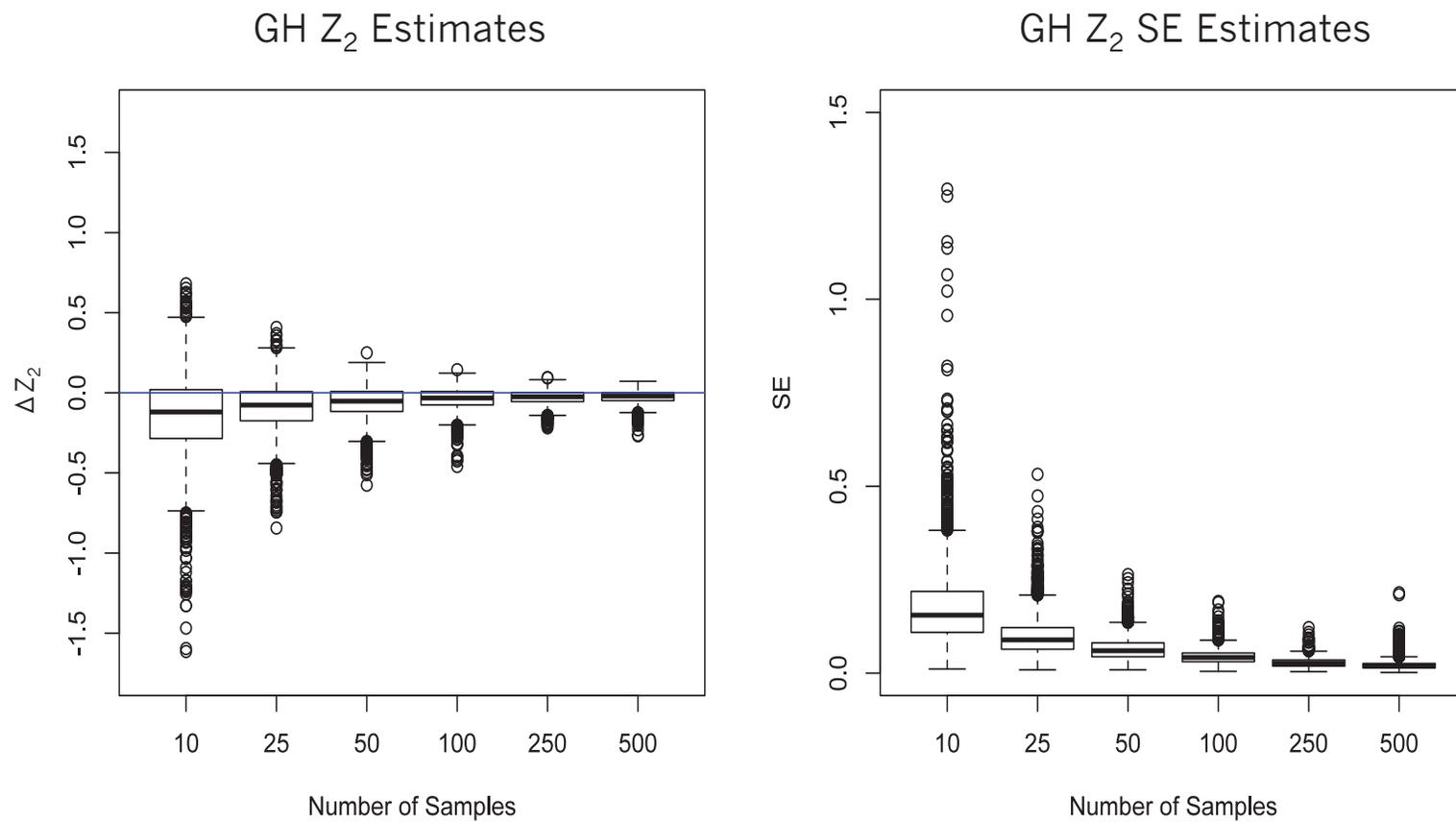
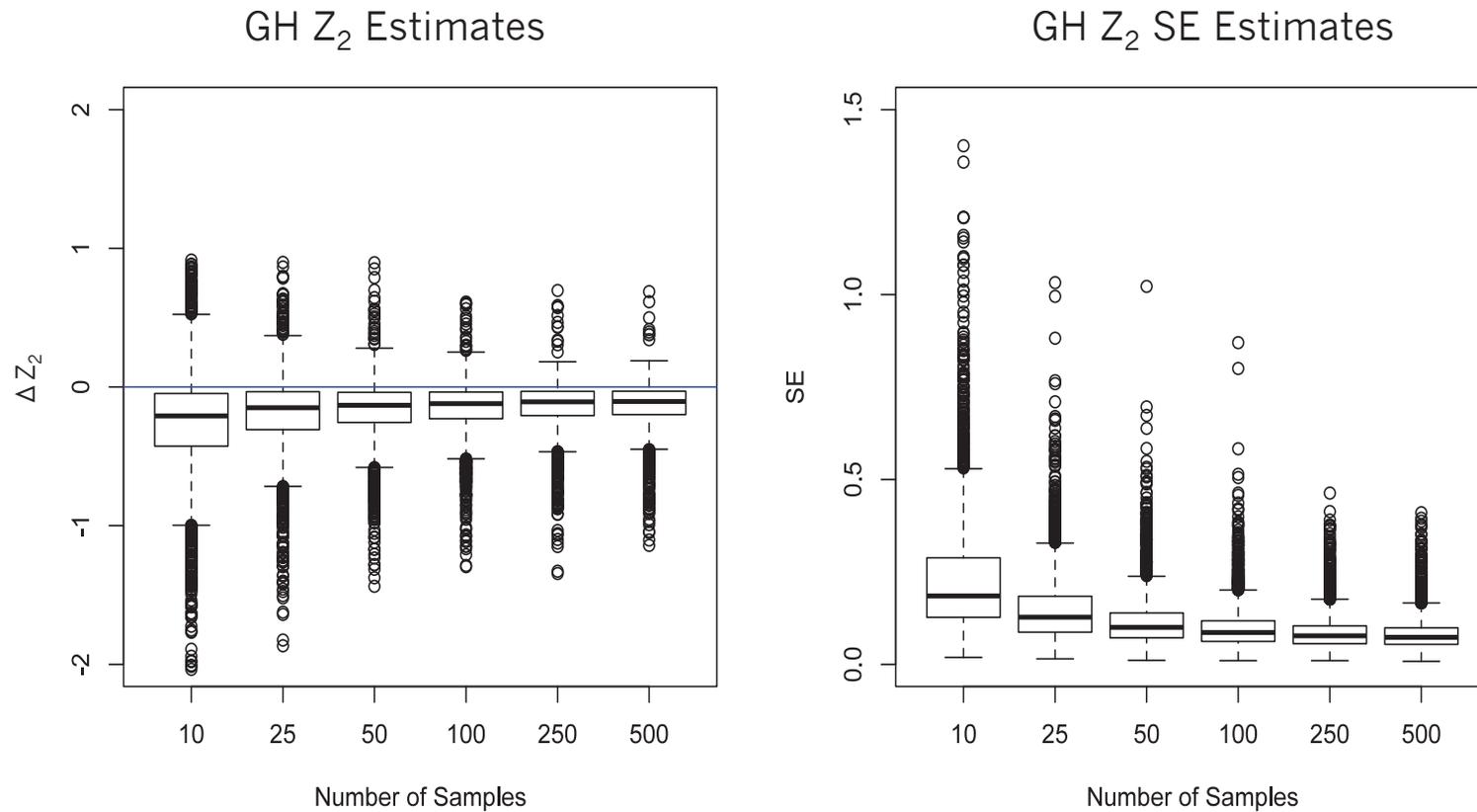


Figure 3.5 Example of decreasing variances in both accuracy and precision with increasing sample size. For this particular example, yellowtail snapper were used, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$, and no variability in growth or recruitment.



Yellowtail snapper, $Z_1=0.5$, $Z_2=1.0$, $T_s=T_c$, $Y_s=6$, no variability in growth or recruitment

Figure 3.6 Figure 3.4 Example of decreasing variances in both accuracy and precision with increasing sample size. For this particular example, yellowtail snapper were used, $Z_1=0.5$, $Z_2=1.0$, $Y_s=6$, and high levels of both growth and recruitment variability.



Yellowtail snapper, $Z_1=0.5$, $Z_2=1.0$, $T_s=T_c$, $Y_s=6$, high variability in growth or recruitment

Figure 3.7 Tukey boxplots of the ΔZ_2 values with increasing Y_s for redbtail parrotfish, with $Z_1=0.5$, $Z_2=1.0$, $T_s=T_c$, and $n=250$. Variability was low for recruitment only.

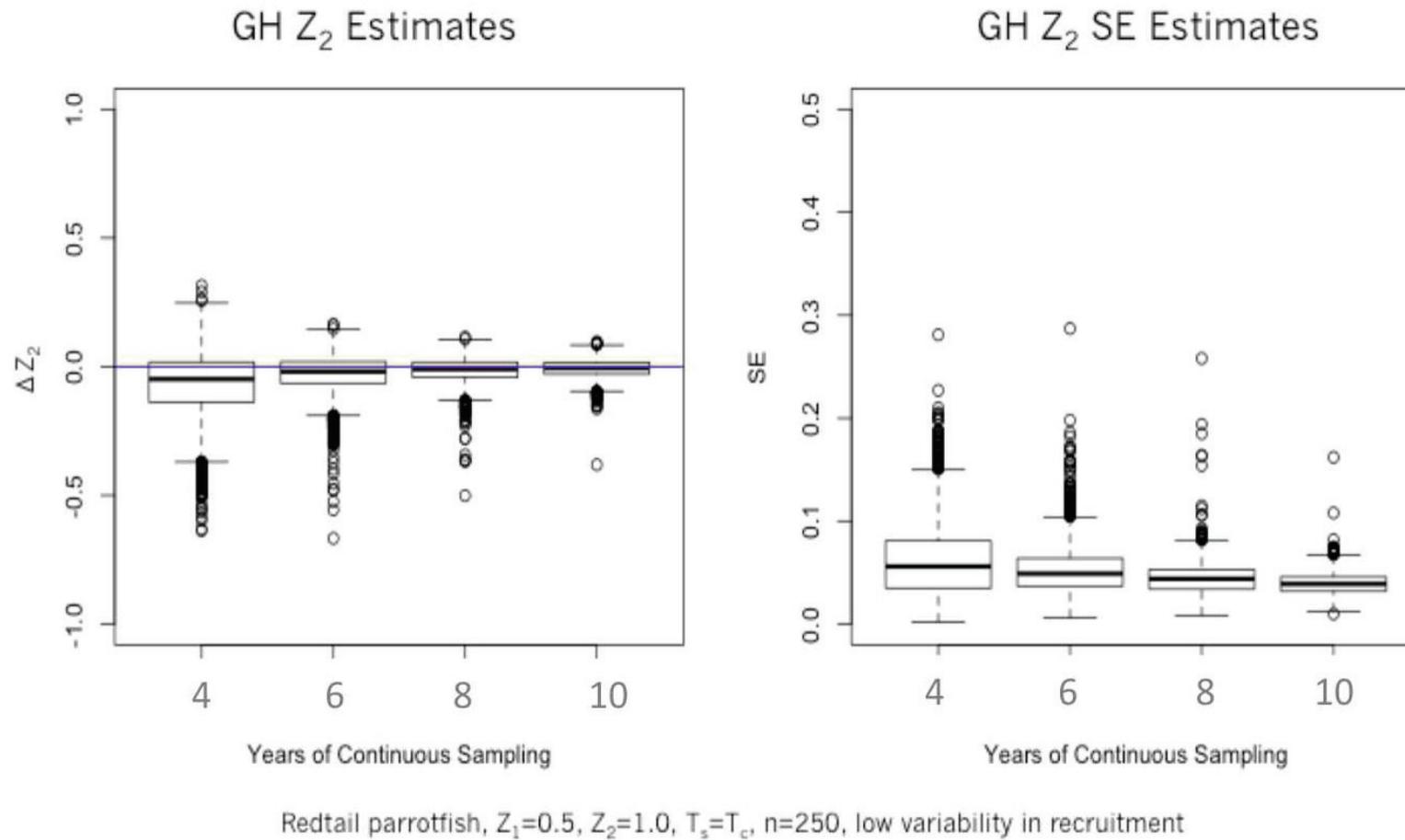
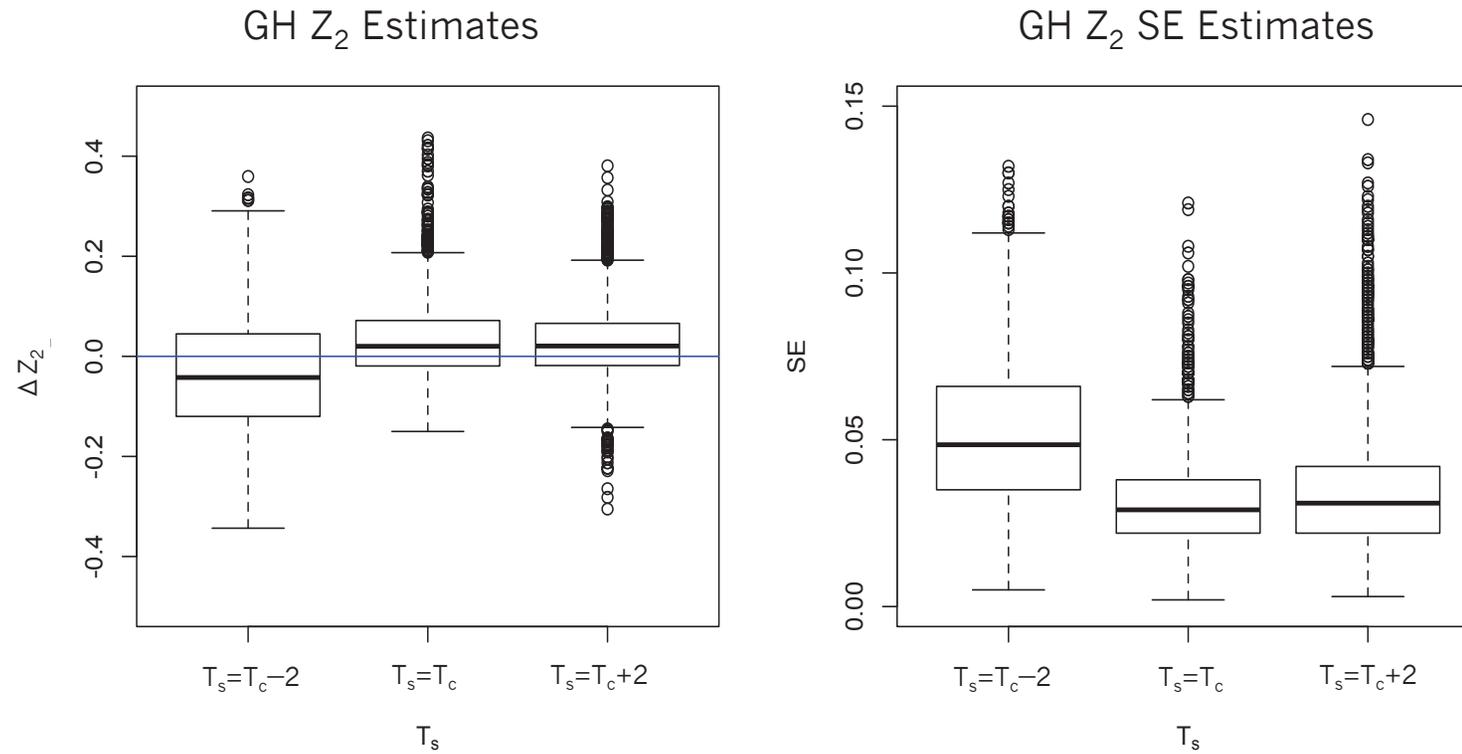


Figure 3.8 Tukey boxplots of the patterns in shifting T_s values for ΔZ_2 values for red hind with $Z_1=1.0$, $Z_2=0.5$, $Y_s=6$, and $n=250$. Variability was at a low level for recruitment only.



Red Hind, $Z_1=1.0$, $Z_2=0.5$, $T_s=T_c$, $Y_s=6$, $n=250$, low variability in recruitment

Figure 3.9 An example of the response to different growth and recruitment variability levels on the accuracy of Z_2 estimations. Yellowtail snapper were the species of interest, $Z_1=1.0$, $Z_2=0.5$, $T_s=T_c+2$, and $Y_s=4$.

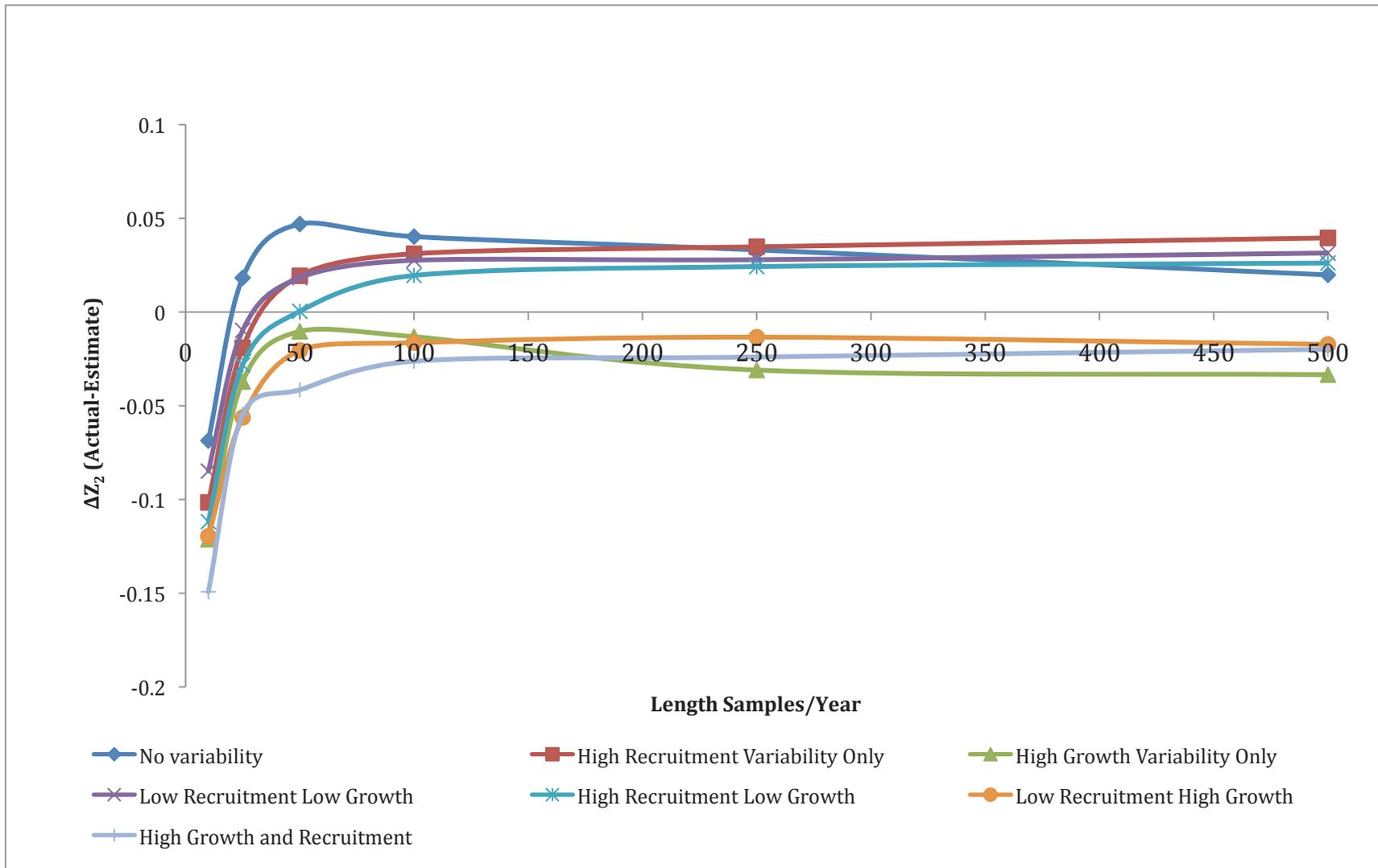


Figure 3.10 An example of the response to different growth and recruitment variability levels on the precision of Z_2 estimations. Yellowtail snapper were the species of interest, $Z_1=1.0$, $Z_2=0.5$, $T_s=T_c+2$, and $Y_s=6$.

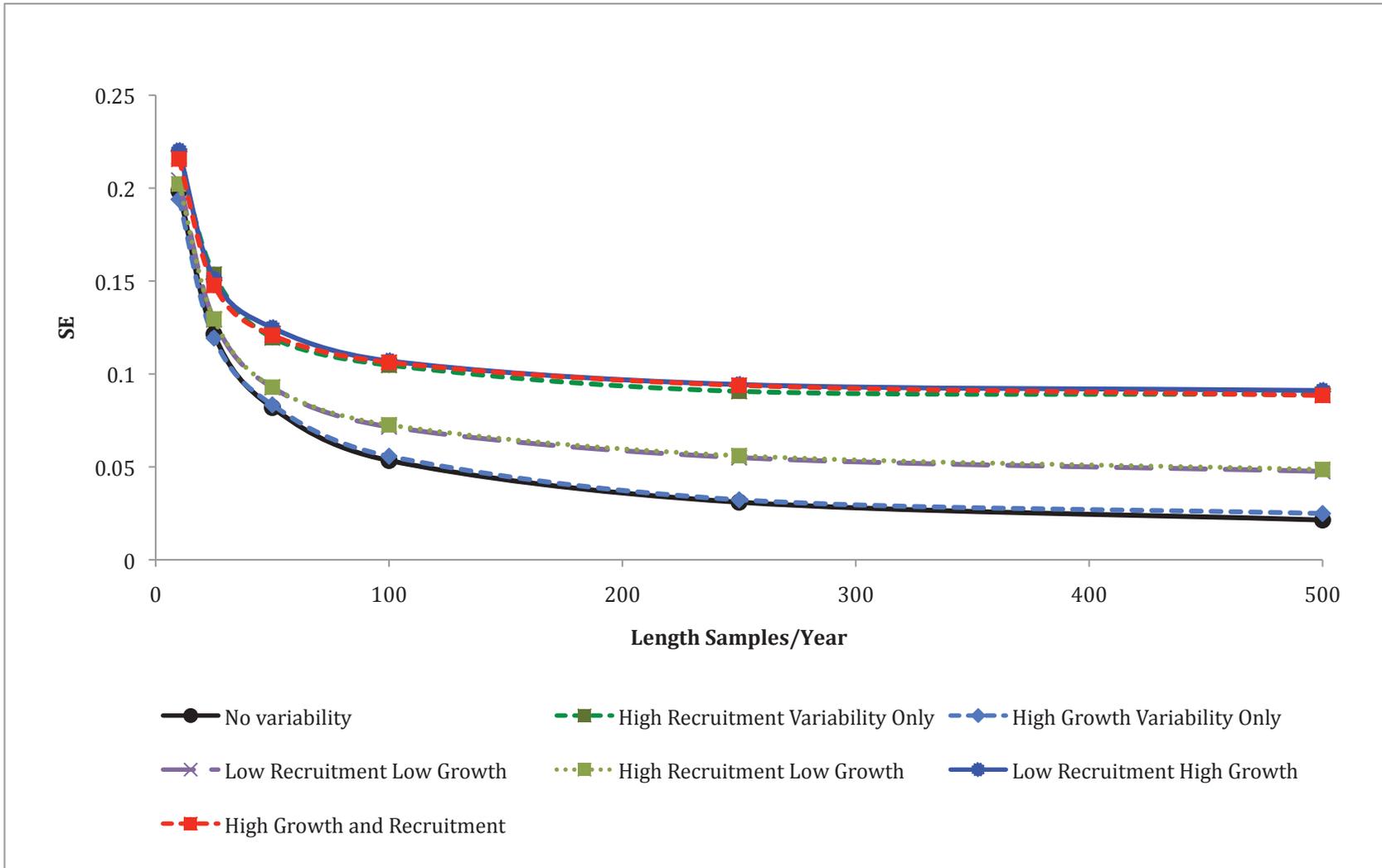
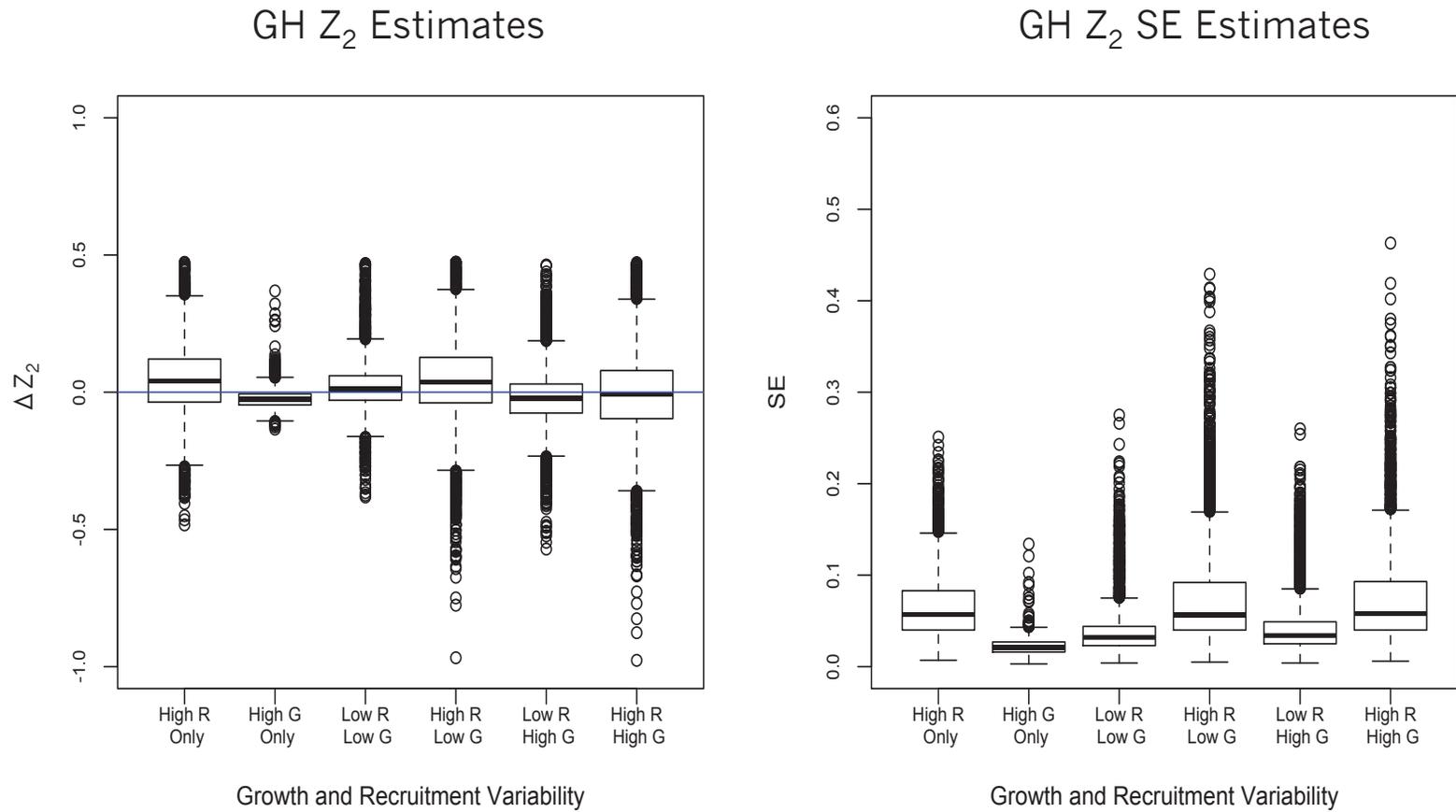


Figure 3.11 Tukey boxplots of the ΔZ_2 values for yellowtail snapper, with $Z_1=1.0$, $Z_2=0.5$, $T_s=T_c+2$, $Y_s=6$, and $n=250$.



Yellowtail snapper, $Z_1=1.0$, $Z_2=0.5$, $T_s=T_c+2$, $Y_s=6$, $n=250$

