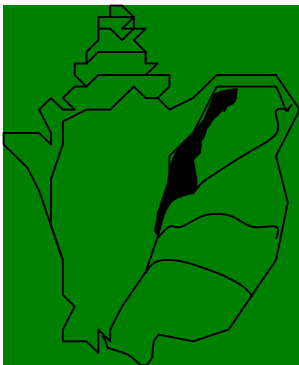
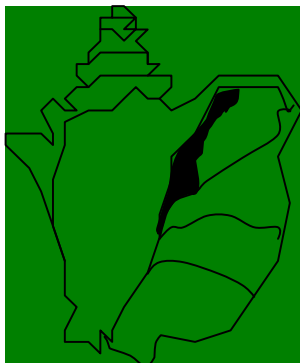


# CONCH (*Strombus gigas*) STOCK ASSESSMENT MANUAL



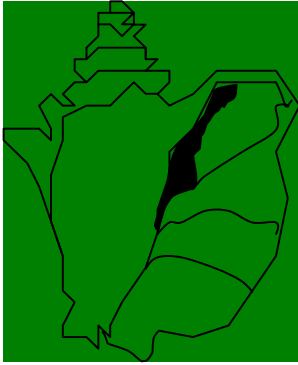
Nelson M. Ehrhardt and Monica Valle-Esquivel

CARIBBEAN FISHERY MANAGEMENT COUNCIL  
2008



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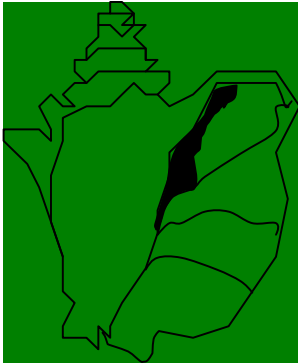
## PREFACE

This Manual constitutes an effort of the Caribbean Fishery Management Council to provide a framework for assessing the status of exploitation of the Caribbean Queen Conch, *Strombus gigas*, stocks. The aim is to facilitate the research work necessary to comply with the CITES requirements concerning the international trade of this protected large marine gastropod.

The original concept on the need to develop a conch stock assessment manual was proposed by Miguel Rolon, Executive Director, Caribbean Fishery Management Council, to a group of conch stock assessment scientists attending the Food and Agriculture Organization of the United Nations (FAO) Conch Workshop held in Kingston, Jamaica, 1-5 May 2006. The concept was to complement the FAO Manual for the Monitoring and Management of Queen Conch (*FAO Fisheries Circular*. No. 1012. Rome, 2005) regarding specific methodologies that could be best implemented in conch stock assessments.

This Manual was developed under contract for the Caribbean Fishery Management Council by the Rosenstiel School of Marine and Atmospheric Science of the University of Miami, Coral Gables, Florida.

Nelson M. Ehrhardt and Monica Valle-Equivel  
November 2008



## 1. INTRODUCTION

“Fishing is a relatively primitive form of production. It is essentially the age old hunting-gathering activity conducted with expensive and sophisticated modern technology” (R. Hanneson. Natural Resource Modeling, Volume 20, Number 2, Summer 2007). This simple and truthful definition of fishing over imposes the stringent need of fishery management, which requires stock assessment advice promoting sustainable long term yields. This is not only a statutory requirement in many countries but paramount to achieving the long-term potential harvests of the stocks. Very often, however, even sophisticated stock assessment methods do not lead to proper interpretations of fishing effects on marine animal populations. Our main problem is the use of model assumptions that, more often than not, limit the possibilities of a correct interpretation of exploitation effects on the dynamics of animal populations in the sea.

The conundrum of understanding exploited population dynamics from usually highly stratified biological, fisheries, and environmental data, many times precludes the opportunity of visualizing the real situation regarding the response of marine populations to exploitation. The Caribbean conch, *Strombus gigas*, variously known by local common names such as queen, jumbo or pink conch, botuto, caracol pala, caracol gigante, or lambi, is not an exception. It inhabits the Central Western Atlantic, but mostly in the western Caribbean Sea from Venezuela to Florida and The Bahamas to Bermuda. The species is the largest of the commercial marine gastropods in this region. Although consumed by local human populations since ancestral times, it is not but until very recently that the international markets for the species opened to prices never before imagined. Therefore, demand already grossly exceeds supply and control on fishing is badly required.

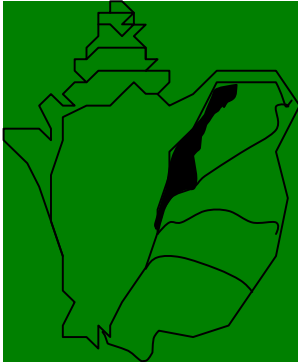
The species has a complex and highly sophisticated but plastic population dynamics. This is due to a distinct geographic identity, which frames growth, reproduction and recruitment of *S. gigas*. This characteristic imposes significant obstacles to model fishery exploitation in the highly heterogeneous physical features that predominate over the habitat range of the species. For the above reasons the species is protected under Appendix II of the Convention on the International Trade in Endangered Species of Wild Fauna and Flora (CITES).

In this work we attempt to bring together some fundamental conceptualizations regarding the complex task of assessing the status of exploitation of *S. gigas*. This is a required element by the CITES Scientific Authorities in the countries when reporting annual conch exports to the CITES. The CITES Scientific Authorities are prompted by the CITES to unambiguously demonstrate that exports and landings of the protected *S. gigas* are non detrimental to the sustainability of the populations on the long range and that they will not generate overexploitation conditions that may deplete local populations.

We present stock assessment models in a constructive approach with the understanding that three fundamental variables in *S. gigas* assessments and management are necessary under the CITES Appendix II:

- 1) population densities should be kept at a predetermined levels that will sustain the reproductive capacity of the species,
- 2) population abundance should be sufficient to maintain the required population density levels, and
- 3) fishing mortality should be regulated by management control of fishing capacity.

This manual is designed such that the fundamental requirements for annual landing definitions under the CITES frame are put in strict context, then that the critically important population dynamics features of the species are correctly identified and understood so that the status of stock recommendations by the CITES Scientific Authorities are unmistakably defined. Finally we provide stock assessment models that appear to provide robust answers to the many issues of *S. gigas* stock assessments.



## 2. CITES CONTROLS

Internal fertilization in *S. gigas* imposes biological demands on minimum population density levels such that males and females encounter and copulate. Due to this population density requirement and the low mobility of the queen conch, reproductive success may significantly be affected by fishery exploitation. Excessive landings and a perceived regional steady decline of *S. gigas* population abundance and densities resulted in conch being listed as commercially threatened by the CITES in 1985 (Wells et al., 1985). Declines in conch density persisted, causing CITES in 1992 to downgrade the status of queen conch to a listing in Appendix II, which requires signatory nations to manage conch stocks closely, and to monitor exports carefully to prevent moving the species to Appendix I, which indicates that the species is in danger of extinction.

The CITES is an international agreement (Convention) between governments established with the aim of ensuring that international trade in specimens of wild animals and plants does not threaten their survival. CITES requires each signatory country to nominate Scientific and Administrative Authorities. CITES Scientific Authorities of countries exporting *S. gigas* are continually challenged to determine whether a particular export will be detrimental to the survival of the species and to define which information and parameters are relevant to determine this. Therefore, it is important that the CITES signatory countries be provided with some general criteria and guidelines, as well as documented methodologies, in order to facilitate the formulation of Non-Detriment Findings (NDFs), and to make more complete and scientifically sound those evaluations required to improve the implementation of the Convention. The following information on CITES controls is taken from Wijnstekers (2005):

### **The Bern criteria**

With CITES Resolution Conf. 1.1 it was decided that in determining the appropriate Appendix in which a species or other taxon should be placed, the biological and trade status of the taxon should be evaluated together, as follows:

### **Appendix-II criteria with regard to the trade status**

Species meeting the biological criteria should be listed if they presently are subject to trade or are likely to become subject to trade. The latter situation can arise

where heavy trade in one species is extended to include similar species if demand grows or if supplies of the one species are depleted.

The amount of trade that a species can sustain without threat of extinction generally will be greater for species in Appendix II than for those in Appendix I, so there should be evidence of actual or expected trade in such a volume as to constitute a potential threat to the survival of the species. Appendix II serves in part as a monitoring tool (CITES Article IV(3)) to gather such trade data.

Article II contains the following fundamental principles with regard to the species to be included in Appendix II:

- (a) all species which although not necessarily now threatened with extinction may become so unless trade in specimens of such species is subject to strict regulation in order to avoid utilization incompatible with their survival; and
- (b) other species which must be subject to regulation in order that trade in specimens of certain species referred to in (a) may be brought under effective control.

### **Trade in specimens of Appendix-II species**

The conditions under which trade in specimens of species included in Appendix II must take place are laid down in Article IV, paragraph 1 of which provides that all trade in specimens of species included in Appendix II shall be in accordance with the provisions of this Article.

Article IV:

2. The export of any specimen of a species included in Appendix II shall require the prior grant and presentation of an export permit. An export permit shall only be granted when the following conditions have been met:

(a) a Scientific Authority of the State of export has advised that such export will not be detrimental to the survival of that species;

(b) a Management Authority of the State of export is satisfied that the specimen was not obtained in contravention of the laws of that State for the protection of fauna and flora.

3. A Scientific Authority in each Party (Signatory Country) shall monitor both the export permits granted by that State for specimens of species included in Appendix II and the actual exports of such specimens. Whenever a Scientific Authority determines that the export of specimens of any such species should be limited in order to maintain that species throughout its range at a level consistent with its role in the ecosystems in which it occurs and well above the level at which that species might become eligible for inclusion in Appendix I, the Scientific Authority shall advise the appropriate Management Authority of suitable measures to be taken to limit the grant of export permits for specimens of that species.

In addition to the non-detriment finding under paragraph 2(a), the provisions of Article IV.3 are essential for achieving the aims of the Convention with regard to the prevention of species becoming threatened with extinction as a result of utilization incompatible with their survival.

Every transfer of a species from Appendix II to Appendix I can therefore be considered as an example of the failure of the Parties to fulfill their obligations under the Convention.

The Scientific Authority should be able to assess the effects of trade on the populations of the species occurring in its country and must therefore be informed on any matter of relevance to that task. Unlike many other provisions, the text of paragraph 3 is rather detailed and adequately describes the obligation of the Scientific Authorities of exporting countries, i.e. countries of origin. This, however, does not make that task an easy one. Many countries of origin lack the necessary scientific data on the status of their animal and plant populations, which makes it impossible to calculate the effects thereon of different levels of exploitation.

### **Permits and certificates (Conf. 12.3 (Rev. CoP13))**

#### **VIII. Regarding permits and certificates for species subject to quotas**

RECOMMENDS that:

a) when a Party has voluntarily fixed national export quotas for specimens of species included in Appendix I, for non-commercial purposes, and/or in Appendices II and III, it inform the Secretariat of the quotas before issuing export permits and of any changes thereto as soon as they are made and it state on each export permit the total number of specimens already exported in the current year (including those covered by the permit in question) and the quota for the species concerned;

b) when a Party has export quotas allocated by the Conference of the Parties for specimens of species included in Appendices I and II, it state on each export permit the total number of specimens already exported in the current year (including those covered by the permit in question) and the quota for the species concerned; and

c) Parties send to the Secretariat copies of permits issued for species subject to quotas if so requested by the Conference of the Parties, the Standing Committee or the Secretariat

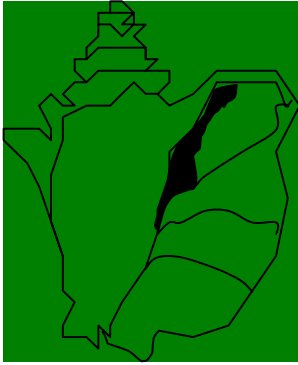
### **Conclusions**

The CITES clearly establishes protocols concerning the requirements of information on the effects of the exports (not landings) on the status of exploitation and survival of the species in Appendix II. This implies that the status of exploitation of queen conch stocks are to be evaluated considering the fishing mortality generated by those landings exported under the CITES export certificates as well as the landings that are locally consumed. In some countries local conch consumption is more significant than the export themselves, yet the CITES Scientific Authority has the mandate to assess the effect of all landings despite their final destinations and then report to the CITES Administrative Authority on the impact of the exports on the survival of the species. In fact, when local consumption in a given country is high and potentially detrimental to the survivorship of the species, exports under CITES certificates should not be extended.



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### 3. FEATURES OF STOCKS AND FISHERIES

Queen conch has a number of life history traits that make the use of assessment methodologies designed for finfish assessment problematic. In this section we briefly enumerate those biological and fishery aspects that are most significant to the stock assessment process.

Usually, conch form discrete aggregations limited in depth by the distribution of seagrass and algae cover. They are more often found at depths less than 25 meters (82 ft) but in heavily exploited areas greater abundances and densities are found in the 25-35 meters (82-115 ft) depth range (Figure 3.1). The species is easily detected and caught by commercial fishers using scuba gear or by free diving in shallower areas. This makes the species highly vulnerable to exploitation and generates opportunities for artisanal fishers to exploit the queen conch for their own consumption and for commercial purposes. The nature of the fisheries is diverse from small canoes carrying one diver and the diver helper (Figure 3.2) to commercial diving vessels that carry up to 40 divers and operate at

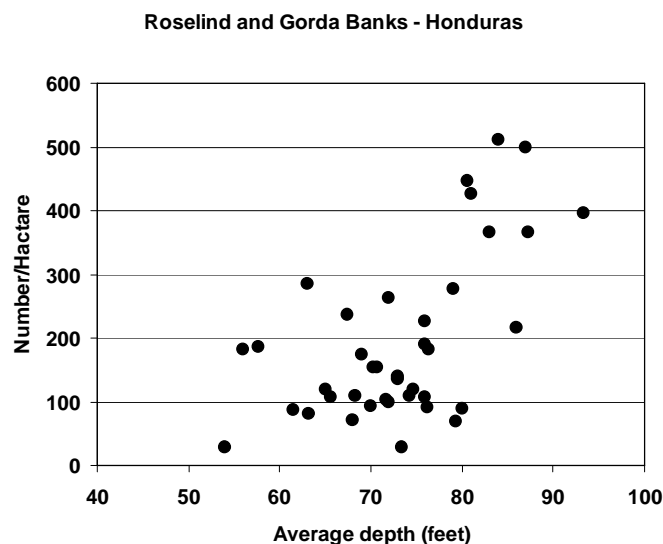


Figure 3.1. Depth distribution of queen conch densities in two fishing banks in Honduras (Ehrhardt and Galo 2005)

sea for 10 to 15 days and landing most of the product as 85 to 100% clean meat (Figure 3.3.). Hyperstability in conch catch per unit of effort is a common issue where effort targets with greater intensity those areas where high conch densities still remain. Due to the low mobility of conch there is no range contraction and local population density is not related to abundance but to the extent of localized habitat and how fishing intensity was temporarily deployed.



Figure 3.2. Small dingy with a conch diver and the diver helper.



Figure 3.3. Industrial vessels with accumulated daily 100% clean conch meat.

Diverse fishing conditions make difficult the implementation of formal statistical systems that could generate catch and fishing effort data for conch stock assessment purposes. Generally, there is lack of information on fishing effort and sometimes of catch. Most statistics are from exports that are registered for later reports to the CITES. However, the geographic identity of the conch and their limited migrations impose the need to separate landings according to the different fishing grounds visited by fishers. This may be easily accomplished in localized artisanal fisheries but it would be very difficult in the case of the industrial fleets that operate in several fishing grounds during a fishing trip.

The best fishery statistics are from those fisheries controlled by fishing cooperatives or fisher groups. The most problematic fisheries are those carried out with industrial vessels that accumulate catch from different fishing grounds. Very few countries have an accurate enumeration of the fishing capacities that are directed to conch fishing, and in some countries conch fishing is complementary to spiny lobster diving. The collection of biological data from landings from these fisheries is very restricted and formal protocols on how to collect these data are available in very few locations. With few exceptions, the lack of formal fishery statistical systems to collect queen conch data represent the most critical and challenging issue regarding conch stock assessment in the Caribbean region.

Queen conch fertilization is internal and successful mating requires minimum population densities of at least 56 individuals per hectare as defined by the CITES and demonstrated with data provided by Stoner and Ray-Culp (2000) (Figure 3.4). Successful mating observed in Florida conch stocks occurs when at least 200 conchs per hectare are present (Glazer, Pers. Comm). Therefore, monitoring conch population densities is paramount to the long term sustainability of the species. Population density estimates are estimated from diving surveys that are designed to follow standardized statistical procedures and are allocated to each fishing ground independently.

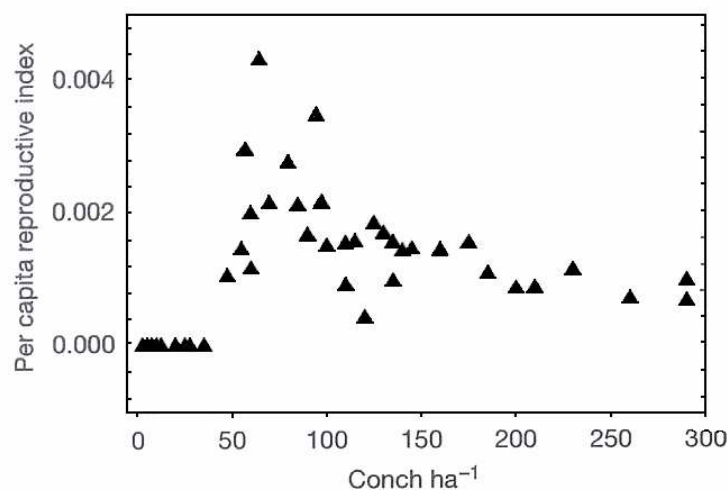


Figure 3.4. Queen conch density and reproductive index (From Figure 1 in Gascoigne and. Lipcius 2004, previously adapted from Stoner and Ray-Clup 2000).

Queen conch mate in summer and early fall in shallow, sandy areas. Mating generates large conch aggregations, which are highly visible and occur at a time coinciding with the seasonal closing of the spiny lobster fisheries in many of the conch exporting countries. This fortuitous event attracts idle spiny lobster fishing effort to conch fishing when conch catchability is at its maximum. Therefore, catchability changes seasonally as a function of population density. Spawning also occurs during this time of maximum exploitation with detrimental effects on the overall population fecundity.

Embryos emerge after 3 to 4 days as free swimming larval veligers, however, the effective duration of larval phase is not known precisely. Laboratory reared larvae lasted

from 12 to 75 days (D'Asaro, 1965; Ballantine and Appeldoorn, 1983; Davis and Hesse, 1983) and less than a month in the wild (Davis, 1994). Consequently, larvae of *S. gigas* have the potential to be transported over neighboring fishing grounds in the strong sea currents that prevail in the Caribbean Sea. Such potential colonization is consistent with the similarity of allelic frequencies found among conch stocks in the region. This condition significantly affects the assessment of the impact of fishing in each fishing ground as local recruitment may be influenced by exploitation on spawning stocks extra territorially.

Results from tagging studies show that queen conch has limited mobility (0.5 mile per month). Glazer et al. (2003) tracked adult conch with sonic tags for one year to estimate seasonal movement and home ranges in the Florida Keys. They report home ranges of <1 to approximately 60 hectares with most individuals moving over home ranges of less than eight hectares. This reduced mobility generates a geographic identity that mostly controls the character of growth. Therefore, *S. gigas* may exhibit small size shells among fully mature individuals in some places and large shelled but still immature conchs in some other neighboring areas (Figure 3.5). This condition mars the possibility of assessing conch stocks over an entire country jurisdiction and forces the assessments of localized fishing grounds. Geographic identity adds complexity to the stock assessment data collection requirements.



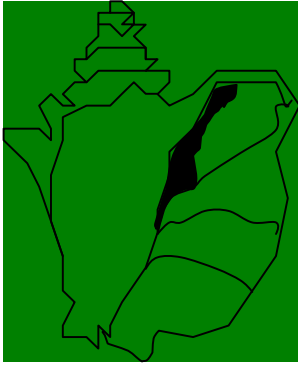
Figure 3.5. Immature (left) and mature (right) conch from two neighboring fishing grounds in The Bahamas.

Conch cannot be accurately aged as seasonal discontinuities of the growth are not deposited (registered) in the shell. On the other hand, conch shell morphology is highly plastic and may be quite variable among populations separated over short spatial scales (Figure 3.5). This geographic identity regarding growth limits the possibility of using indirect methods to age queen conch (e.g., modal progression analysis of siphonal length). Tagging studies show that queen conch reaches its full size at the onset of maturity at about an age of 3 years. It then changes the axis of growth by forming a “lip” that flares away from the shell and by thickening the shell throughout the conch’s life span. Therefore, siphonal length is a poor descriptor of growth after the age of first maturity. The normal queen conch life span is not known with any accuracy but is

estimated at between 20 and 30 years. This growth characterization mars most stock assessment techniques based on size or age frequencies observed in the landings. It also precludes accurate assessments of the yield generated by age under different fishing mortality regimes.

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## 4. POPULATION DENSITY AND STANDING STOCK ABUNDANCE ESTIMATION

### 4.1. Purpose of this section

The conditions of low mobility and minimum population density thresholds required to secure reproductive success in *S. gigas* are critical because exploitation may impair the ability in the species to maintain or recuperate such threshold densities in a reasonable time. The CITES basic decision criteria regarding critical queen conch population density levels is 56 conchs per hectare, which is used to draw judgments regarding the status of conservation of the species. The decision criteria, however, may be too liberal given new evidence showing that approximately 200 queen conchs per hectare are required for successful reproduction in Florida (Robert Glazer, Florida Fish and Wildlife Conservation Commission, Pers. Comm.). However, the mean densities in several of the important queen conch fished zones in the Caribbean region contained in the TRAFFIC (2003) report to the CITES queen conch 2003 revision are well below levels at which depensation has been shown to occur in conch populations (Stoner and Ray-Culp, 2000; Gascoigne and Lipcius, 2004). Despite these differences, the need to generate annual unbiased population density estimates is crucial to the queen conch management. Also, there is a need to express somehow, what fishing mortality or exploitation rates will allow the maintenance of stocks at the appropriate (target) density levels. However, surplus yield that could be potentially exported is a function of the fishing mortality and average population abundance (and not population density). This, then, is a complex problem to resolve, especially under the distinct geographic identity of the species which influences growth, reproduction and recruitment according to local habitat and environmental conditions. Consequently, queen conch form exploitable sub-stocks within given habitat configurations, resulting in different localized population densities and these densities need to be independently assessed. Therefore, a fundamental stock assessment task in support of queen conch management should be the periodic estimation of population density in each of the exploited fishing grounds. Plots of historic trends of such densities should provide guidance on the status of exploitation of the stocks as well as a benchmark for management purposes.

Also, standing stock abundance estimates (those abundances that are present at a given time in a given space) are important to the definition of potential annual landings (or quotas) that could be safely applied to queen conch. A simple comparison of realized

landings with the biologically acceptable annual landings under a given population density level should suffice to portray a queen conch stock condition under the CITES decision criteria. Geographic sub-stock identities suggest that there will be a need to estimate standing stock abundance, population density, and the corresponding biologically accepted landings separately by fishing ground. This process represents complexities regarding the sampling requirements and operational implementation of surveys designed to evaluate population density and standing stock abundance.

In the following section, a summarized set of statistical conditions pertaining queen conch populations are linked to discern the best statistical sampling design to respond to the above population estimation needs.

## **4. 2. Population density estimation**

### **4.2.1. Conceptual definitions.**

The first conceptual statistical consideration is that the primary variable (or sampling unit) of interest is not the individual conch but an area, quadrat or transect that will yield an estimate of the number of individual conch found (counted) in the area (the absolute density). The attribute of the primary variable is to allow expansion of certain knowledge obtained by sampling in it to the target statistical population. This allows estimation of the total abundance and average density of the conch stock in the target population. If the individual conch was the primary variable of interest, then individuals as sampling units will not generate an estimate of the total number of conch in the target population, unless all conchs in the target population are enumerated. Population density estimates (i.e., numbers per unit of area) must be estimated from the sampling units selected through some statistical procedure (discussed in the next section). Individuals, however, may be sampled within the sampling unit to generate other variables of interest such as size, sex composition, maturity, etc. In this manner, the primary variable or sampling unit will generate an absolute number of conchs, while the individual conch sampled within the primary variable will generate estimates such as average size (or maturity, sex composition, etc.) and variance. Note that in a sampling unit density is an absolute number while the attributes of the conch found in the sampling unit are average estimates with a variance. Several sampling designs can be applied to select the primary variable of interest to obtain unbiased estimates of population density. Randomness in the selection of the primary variable of interest is fundamental, although ultimately the individual conch is the focus of interest in the study. A random sample is one where all primary variables defined within a target population have the same probability (or opportunity) of being sampled (or selected).

The second conceptual statistical consideration is the definition of the target statistical population. Here, we are not referring to a biological population but to the statistical population of all possible sampling units that constitute the target statistical population. For example, if the target population is 100 m<sup>2</sup> and the primary variable of interest is 1m<sup>2</sup>, then a total of 100 possible primary variables are available and each has the same opportunity of being selected as a sample. The question that follows is how to define the target population if the spatial distribution of the conch is not known, and perhaps it is one of the objectives in a given survey designed to assess the characteristics



of a conch stock. In this regard there are two possible procedures: 1) establish a pilot study to delineate the possible spatial boundaries of a conch stock, or 2) collect information from knowledgeable fishers that have past experience on the distribution of the commercial concentrations of conch. The pilot study is usually too expensive and time consuming given that divers will have to search and define the conch stock boundaries. We recommend the second option with considerations for “tuning” (i.e., adjusting) future sampling experimental designs. In Figure 4.1 we show the second approach (the consulting approach) used in a large conch survey carried out in Honduras in 2006. In the process historic recollections of areas with high commercial conch densities (i.e., high catch per diving) either from memory, or better from fishing logbooks, are discussed among the experienced fishers and then plotted in charts such that a distinct set of fishing grounds is identified (Figure 4.2).



Figure 4.1. Honduran captains and boat owners describing their experiences to a scientist regarding the most likely conch fishing areas.

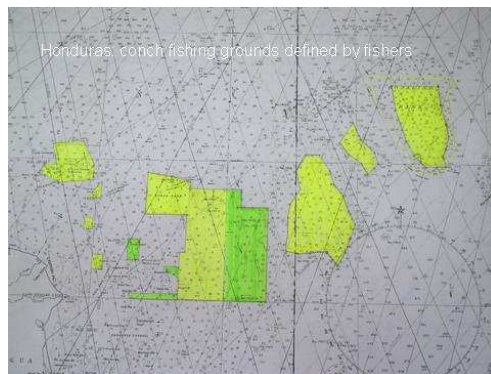


Figure 4.2. First hand definition of conch fishing grounds from experienced fishers.

Next, there is a need to define the standard size of the primary variable (or sampling unit) of interest. This will depend on several factors that affect diving, among which depth, bottom profile, habitat, currents, and visibility play major roles. Each of those factors has a different origin and here again it is important to have expert advice from those that have experience in the conch fisheries. The usual practice in conch dive surveys is to use a 100 m transect line with an observational width of 1 m on each side of

the transect line; hence, a 200 m<sup>2</sup> is covered by one diver and this area should represent the sampling unit. Our experience tells us that these surveys will be successful if professional commercial conch divers are used. Queen conchs are cryptic in that their presence is not always detected by a good diver that does not have experience with the species. Therefore, the density estimates will tend to be under estimated by an inexperienced diver.

The primary variables are very small given the relatively very large spatial distribution of the conch fishing grounds (or target population). As we shall explain in the following section, this condition will favor the adoption of more efficient statistical sampling designs.

#### **4.2.2. Sampling design models**

Several important statistical sampling designs are widely used to survey marine animal populations. Each has merits and also constraints that limit their uses. In this section we provide a view of the best known sampling methods from which the most applicable for conch surveys will be selected. Generally, sampling surveys could be designed in many different ways, however, for the purpose of this manual we distinguish four of those designs: 1) Simple Random, 2) Systematic Random, 3) Stratified Random, and 4) Stratified Systematic Random with Replication.

1) The Simple Random Sampling design, or unrestricted random sampling design, is the most general where the locations of the primary sampling variables (the sampling units where conchs will be counted) are selected at random among all possible primary sampling units in the target population (Figure 4.3). This method when applied to conch surveys is usually considered unreasonable because it has practical problems of applying (implementing) the random sampling sites in the field (i.e., accessibility, spatially unbalanced conch distributions, etc.). This emerges from the unknown heterogeneity of the conch habitat and consequently the unknown conch densities associated with preferred habitat. For this sampling design the simple arithmetic mean of the densities in the random sampling units obtained from the target population is an unbiased estimate of the population density. This is a result of the random selection of the samples. Therefore, the simple arithmetic mean in its formulation is an unbiased estimator but the estimate may have low precision (i.e., the samples are not optimally allocated and an excess of variance makes the estimates less efficient). This lower precision may significantly impact the analysis and conclusions on the status of conch populations in the different fishing grounds.

2) Simple Systematic (or Ordered) Random Sampling designs implement the primary variables (sampling units) systematically at predetermined intervals (i.e., sampling units are located at equidistant distances) (Figure 4.4). Randomization is introduced by selecting the first (start) site at random. The fundamental advantage in this design is the opportunity that the investigator has to spread out the samples over the target population following a simple protocol. It is assumed that the sampling units can be implemented in this fashion over the entire target population. This sometimes may result in sites where diving may not be possible due to bottom configurations (i.e., coral reefs, deep trenches, etc.). The requirement that the first (start) sampling unit site is allocated at random on the target population brings an added complication in that the

remaining ordered sampling sites have to be physically implemented on the target population once the first random site is selected. Therefore, there are more stringent requirements for a systematic sample when randomization is adopted.

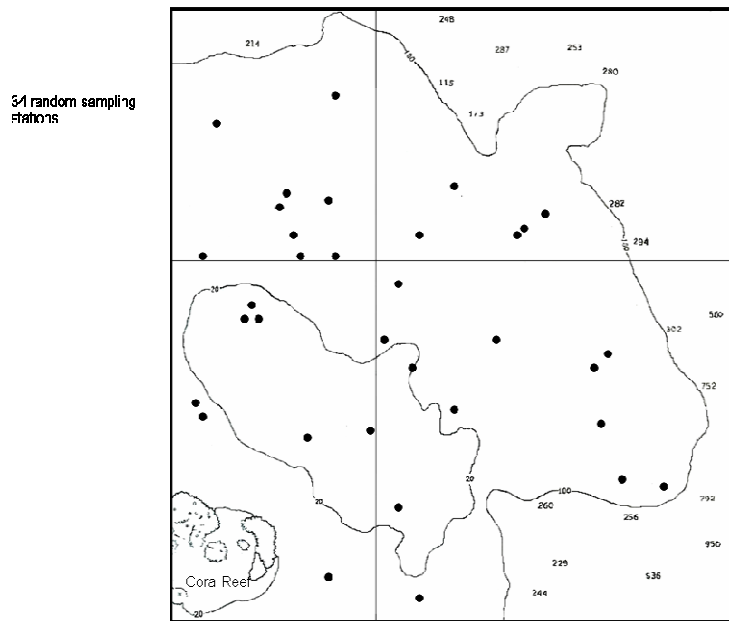


Figure 4.3. Fully randomized sampling design.

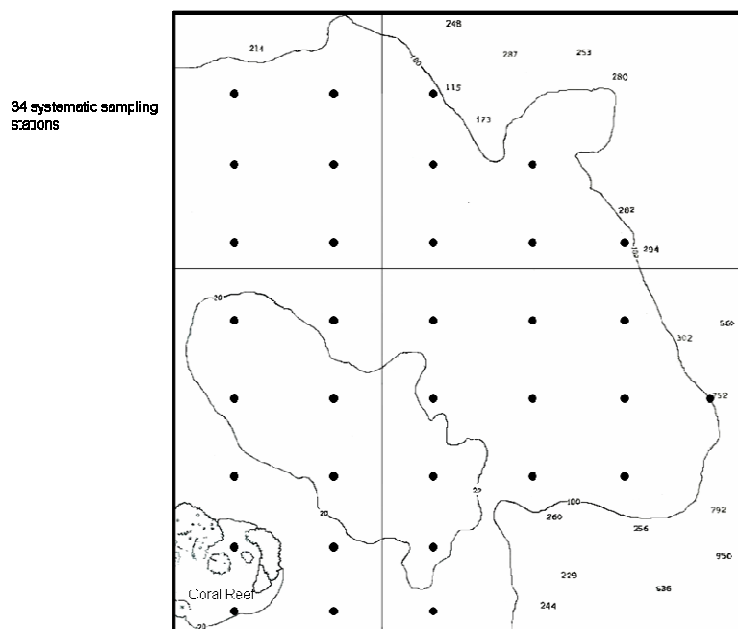


Figure 4.4. Systematic random sampling design

The standard formulations to estimate the arithmetic mean and variance of the population density under the systematic random sampling design are not the same as those in the simple random design. This is because an orderly selection of samples is executed while in the simple random sampling it corresponds to a random selection. The problem with taking observations in a systematic way, and not in a random manner, is that the same result does not hold. For the random systematic sampling, the rule is that the arithmetic mean will be biased; however, this bias may not have serious consequences when the target population is very large relative to the sampling unit. The latter appears to be the usual case in conch density population assessments when the primary variable of interest is an area within a range of 100 to 400 m<sup>2</sup> while the target population may be several thousand times this sampling area. More critical in the simple random systematic sampling is the fact that there is no systematic sampling formula to use to calculate an estimate of the variance. The lack of a reasonable variance estimate is the most serious disadvantage of taking just a single random systematic sample in one point from the target population. This problem is not associated with simple random sampling where all that is needed to know is the variance calculated from just one random sample. For this reason we do not recommend the use of simple systematic random sampling in conch surveys unless a replicate sampling is included. This sampling design is explained below.

3) Stratified Random Sampling designs. In a conch survey over a large area (large target population), homogeneity of population density should be rarely expected. This is especially true when density gradients as a function of optimal habitat of the conch are found. Also, queen conch exhibit distinct zonations with depth; therefore, a survey line beginning in a shallower point and moving toward deeper areas should typically encounter a population density gradient. Often at the start of a conch research survey the researchers will have only a preliminary idea (only from the information provided by the experienced fishers or from previous survey results) of what distributional differences may exist within the target population. In this situation a sampling scheme that defines sub-target populations within which density is more homogeneous than if no sub-target populations were selected is called a stratified random sampling design. Within the strata (sub-target populations) created by this procedure implementation of either a simple random sampling design (Figure 4.5) or a simple random systematic sampling design with replication (Figure 4.6) is possible. The advantage of this design is that the stratification procedure allows the grouping of biofacies or habitats specific to queen conch from those less appropriate to queen conch.

Stratified random sampling designs always result in a reduction of variance of the population density estimates because separate sampling is performed independently within each stratum; therefore, the total variance is partitioned among strata and within strata. The within strata source of variance will be the one associated to the precision of the population density estimate while the variance among strata is not. Of course the larger the variance among strata the stronger will be the evidence that the stratification process was successful (improved the precision of the estimate). Therefore, when using these designs care must be taken to define these strata as correctly as possible, otherwise the sampling modeling will not be successful.

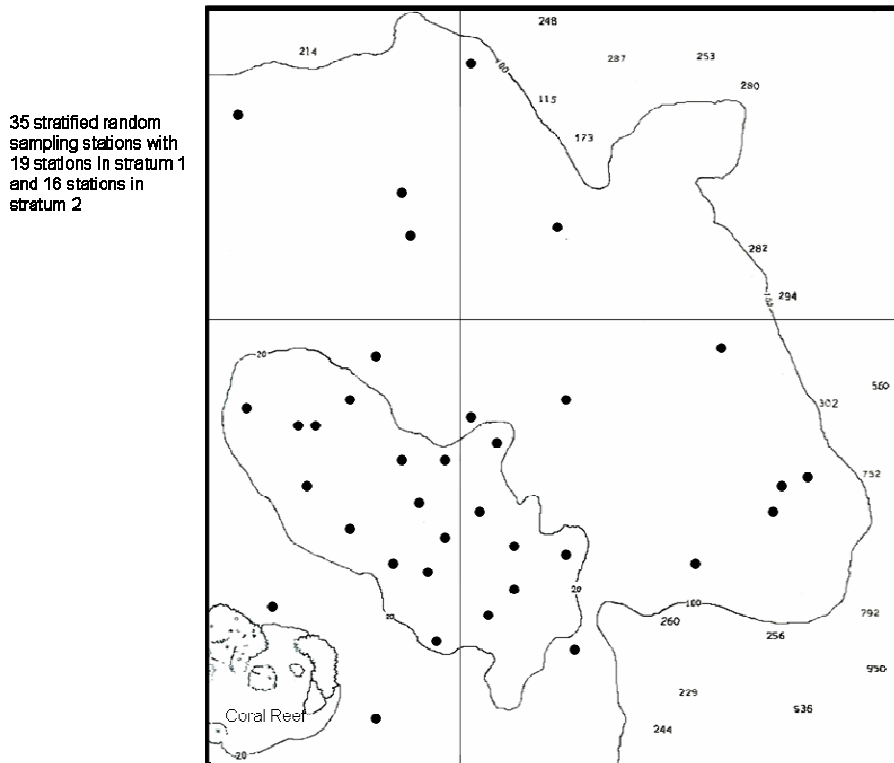


Figure 4.5. Stratified random sampling design with different sampling density.

4) Stratified Systematic Random Sampling Design with Replication allows more than one ordered set of observations, and as such, a consistent variance estimate of the population density estimate is obtained. This was the greatest drawback in the systematic random design with no replication explained previously. Replicates are additional sampling units randomly allocated about the systematic sampling site (or sampling station) (Figure 4.6). In the case of the less homogeneous population distribution usually observed with queen conch populations, this sampling design allows a wider and more even distribution of the sampling effort. Therefore, it provides with a greater chance to explore and estimate the true density under a randomized systematic sampling design.

Our advice is that queen conch survey designs should profit from careful analysis of the preliminary information available on the distribution of the species. This will facilitate the selection of the most appropriate sampling design. Our preference is always for stratified designs with either a fully randomized allocation of sampling units in each stratum or a systematic random sampling design with replication implemented in each stratum. By using either of these two sampling designs, one can expect to obtain information on the population density within distinctive habitats, as well as to calculate total estimates, with effective statistical properties, over the entire target population.

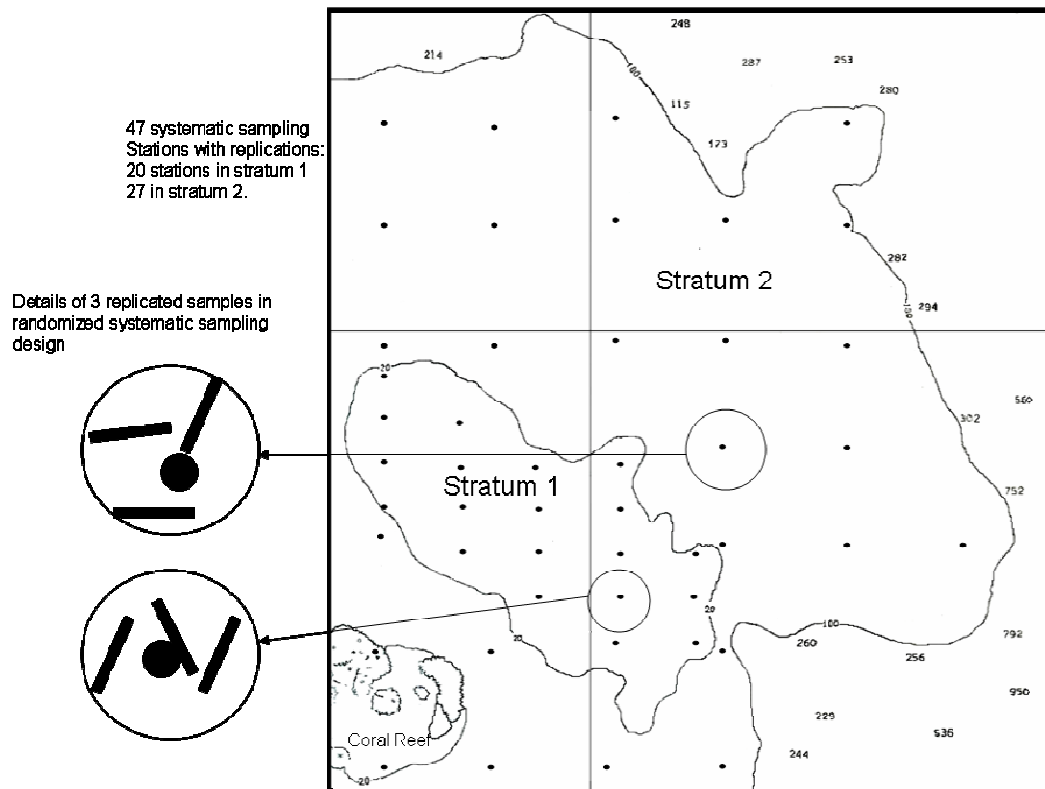


Figure 4.6. Systematic random sampling design with replications of transects (black rectangles within circles) within sampling points.

The conclusion on the two sampling designs selected is based on the following summary points:

1) Stratification creates more homogeneous sub-target populations; therefore systematic random sampling with replication is suitable. Likewise, the simple random sampling approach is favored by the more homogeneous distribution within the sub-target populations.

2) Large target populations relative to the size of the sampling unit will always favor the use of systematic random sampling design with replication because lack of true randomization is not of concern and it will allow the researchers to obtain more accurate delineation of the conch population distribution and their respective attributes (i.e. density, spatial size structures, spatial sex ratios, etc.).

3) If queen conch is distributed along a gradient, systematic random sampling with replication along the gradient will be superior to the simple random stratified sampling design. That is, the precision of the density estimate will be greater.

4) Considering the lack of homogeneity of the queen conch population density but also considering the very large target population relative to the sampling unit, a systematic sampling method should never be used without replication if precision of the estimates is expected.

5) Systematic sampling with replication is particularly important at uncovering hidden discontinuities of the queen conch density distributions (strata) in the target population. If implicit strata are found, then there will be a variance decrease if subsequent samples are taken within each stratum (i.e., it facilitates the target population stratification process).

6) Differing population densities mapped from systematic sampling with replications will allow comparison of areas (strata) relative to spatial biological characteristics of the queen conch.

7) Stratification will always contribute to a more efficient sampling design. Stratification will contribute to allocate sampling effort more effectively in those strata where most of the information of interest is located, conversely, it will avoid or reduce the sampling effort in those strata where it is expected that little or no information of interest will be found. Stratification will allow proportional allocation of samples in those areas with greater density gradients.

8) With simple random sampling there is always the risk of getting unrepresentative samples. For a larger target population stratified sampling will always give a much more representative picture of the total population, and therefore, of its counts, than will simple random sampling.

#### **4.2.3. Formulations for population density estimation**

The formulations provided in this manual are for the two sampling designs that we consider the most promising regarding the assessment of queen conch population densities. We believe that either stratified random sampling or stratified systematic random sampling with replications is a potentially powerful design for this purpose. Therefore, each stratum is treated separately in the calculations for obtaining the mean density, the variance, and the precision before results are obtained for overall (target population) density estimates. We need to make certain, however, that density estimates from each stratum are unbiased because only in this manner we can make use of a theorem in mathematical statistics that states the sum of unbiased estimates is itself also unbiased; therefore, the target population density estimate is the average of the density estimates obtained in each stratum.

In practice, there are several situations that may be encountered with queen conch spatial distributions that may prompt the use of one of the two sampling designs defined here. If the survey area is narrow or around reef systems, the systematic random design with replicates may not be implemented correctly because of spatial considerations. In this case it is advisable to stratify the area with the best information available on queen conch habitat and potential queen conch distributions and establish a simple random sampling within each stratum. Conversely, if the target population is large (e.g. Pedro bank in Jamaica, banks in the Nicaraguan-Honduran raise, or banks in wider shelves like in The Bahamas, Turks and Caicos Islands, etc.) it will be more suitable to implement a systematic random sampling design with replications.

In general, if the target population contains queen conch stocks with stratification within which conch are homogeneously (or randomly) distributed, and/or when the sample units are very small relative to a very large target population, then the formulation for the density estimators to use are those for simple random sampling.

## Glossary of sampling design symbols

$h$	Stratum subscript
$i$	Sampling unit subscript
$j$	Replicated sampling unit subscript
$a_h$	Area surveyed in stratum $h$
$n_h$	Number of samples in stratum $h$
$n$	Number of samples collected in statistical population
$S_h^2$	Sample variance in stratum $h$
$w_k$	Stratum weighting factor
$A_h$	Stratum area
$A$	Area of statistical population
$D_{hij}$	Density in replicated sample $j$ in sampling unit $i$ in stratum $h$ for systematic sampling random designs with replication or
$D_{hi}$	Density in sampling unit $i$ in stratum $h$ for stratified sampling random designs
$\bar{D}_h$	Average density estimate in stratum $h$
$\bar{D}$	Average density estimate in the statistical population
$N_h$	Number of total possible sample units in stratum $h$
$N$	Number of total sample units in the entire statistical population
$P_h$	Population abundance in numbers in stratum $h$
$P$	Population abundance in numbers in the entire statistical population
$T$	Number of strata in entire sampling population
$\text{Var}()$	Variance of an estimate
$\text{SE}()$	Standard Error of an estimate

Formulations used in density estimation are those provided by Cochran (1977). The basic statistical observation of conch density is the number of individuals counted in the sampling unit (i.e., the transect). Mean density in stratum  $h$  ( $\bar{D}_h$ ) and its variance ( $S_h^2$ ) are computed by

$$\bar{D}_h = \frac{1}{n_h} \sum_{i=1}^{n_h} D_{hi}$$

and

$$S_h^2 = \frac{\sum (D_{hi} - \bar{D}_h)^2}{n_h - 1}$$

In the case of the systematic random design with replicates,  $D_{hi}$  in the above formulation is replaced by  $D_{hij}$ , which are the densities observed in each replicated transect  $j$  in all sampling units  $i$  in stratum  $h$ .

Mean weighted queen conch density in the entire statistical population is estimated by



$$\bar{D} = \sum_h^T w_h \bar{D}_h$$

Where the stratum weighting factor is estimated by

$$w_h = \frac{N_h}{N}$$

Number of total possible sample units in stratum h ( $N_h$ ) is estimated as the ratio of the area of the stratum divided by the area of the primary unit or sampling area, or transect. Then

$$N_h = \frac{A_h}{\text{Transect\_area}}$$

Number of total sample units in the entire statistical population ( $N$ ) is the sum of the number of total possible sample units in each stratum h ( $N_h$ )

The values of  $N$  and  $N_h$  may be very large and cumbersome to handle. For this reason, sometimes, the weighting factor is based on the number of primary sampling units or transects ( $n_h$ ) and the total number of primary units selected in the entire statistical population ( $n$ ).

Variance of the average population density ( $\bar{D}$ ) is estimated by

$$\text{Var}(\bar{D}) = \sum_{h=1}^T w_h^2 \left( 1 - \frac{n_h}{N_h} \right) \left( \frac{S_h^2}{n_h} \right)$$

The 95% confidence interval for the average density in the statistical population requires the standard error of the average density estimate ( $SE(\bar{D}) = \sqrt{\text{var}(\bar{D})}$ ) and estimated by

$$\bar{D} \pm t_{\alpha, n-1} SE(\bar{D})$$

where  $n$  is the number of samples collected in statistical population and  $t$  is the tabulated Student statistic with  $n-1$  degrees of freedom for an  $\alpha$  level of significance.

Estimates of average density obtained for each fishing ground of fishing bank should be accumulated through the seasons such that plots of these estimates and their 95% confidence intervals could show potential trends that should greatly help framing management of the queen conch stocks in each fishing bank.

#### 4.2.4. Formulations for population abundance estimation

Population abundance estimation follows a simple process of expansion of the stratum abundance estimates to total population abundance. The population abundance in numbers of queen conch ( $P_h$ ) in stratum h is given by

$$P_h = \bar{D}_h * A_h$$

Variance of  $P_h$  is estimated by

$$Var(P_h) = A_h^2 \left( 1 - \frac{n_h}{N_h} \right) \left( \frac{S_h^2}{n_h} \right)$$

Total queen conch population abundance in a given fishing ground will be

$$P = \sum_{h=1}^T P_h$$

And the variance of the total population abundance estimate is also equal to the sum of the variance of the strata estimates. That is,

$$Var(P) = \sum_{h=1}^T Var(P_h)$$

The standard error of the population abundance,  $P$ , is estimated by

$$SE(P) = \sqrt{Var(P)}$$

The 95% confidence interval of the population abundance estimate is calculated by

$$P \pm t_{\alpha, n-1} SE(P)$$

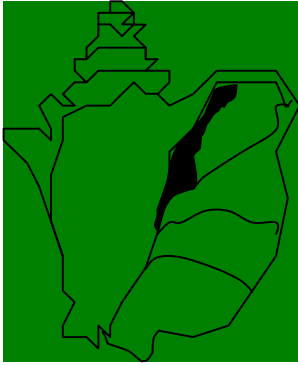
If annual surveys for density estimation are carried consistently and following the same statistical procedures, and covering the same area stratifications; then a trend in annual abundance can be plotted every year and used to check the fate of the queen conch population abundance in a given fishing ground or in all the grounds in a given country. Such abundance estimates are paramount for comparing abundance, densities and fishing mortalities after these data have been accumulated through several seasons.

As a reference or recommendation, once density estimates are accumulated through several seasons, fluctuations in density in given fishing grounds could be further analyzed using a doubly multivariate repeated measures analysis of variance (RMANOVA) with fishing grounds as a between-subjects factor. Also, Pillai's trace statistic could be used to detect differences in density among fishing grounds or among years, and Bonferroni tests could be used for post-hoc comparisons of factor levels. The error covariance matrix that is needed in some of these tests may be inspected using Mauchley's test of sphericity, and homogeneity of error variances can be checked using

Levene's test of equal variances. These are more advanced topics in statistical analysis that will need further explanations once the historic annual density and population abundance estimates are accumulated.

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## 5. ESTIMATING STATUS OF EXPLOITATION

### 5.1. Purpose of this Section

The CITES Scientific Authorities in each exporting country need to assess the status of exploitation resulting from the proposed queen conch landings and exports. Therefore, there is a need to estimate mortalities (natural and fishing), but growth is paramount to the estimation process. The unique geographic identity framing population dynamic characteristics of *S. gigas*, coupled to the highly stratified fisheries create insurmountable obstacles to statistically record biological and fishery information. Consequently, standard stock assessment procedures are difficult to implement and only approximate estimates of growth and mortality have been obtained throughout most of the extensive work pertaining to conservation of this species.

In the absence of exact methods, we recommend that queen conch stock assessments concentrate in the development of indices that could on the long range generate a signal that may suggest the status of exploitation. For example, a simple size based catch curve analysis could generate a seasonal slope (Figure 5.1, upper panel) that is a statistically robust estimator of average total mortality rate that may be affecting a given stock. Such estimate has a variance, which is simply the variance of the slope of the line. If such estimates are obtained for each season from well-designed sampling programs to collect information on the size structure of the landings, slopes will be robust estimators of total mortality even if total landings are not known. Therefore, total mortality estimation will serve the purpose of obtaining a seasonal point estimate and its variance such that they can be plotted for each consecutive season as shown in the lower panel of Figure 5.1.

In this section we propose methods to estimate seasonal total mortality (or survival) and exploitation rates based on models adapted to the general queen conch exploited population dynamics. We pay especial attention to the usual difficulty of measuring rates (e.g., growth, mortality, etc.) in queen conch. We begin by explaining some generic ways to express growth in a species that aging is not possible after reaching maturity and then use this knowledge in mortality estimation using meat weight frequencies, which are the most common conch parts landed. We include a discussion on natural mortality estimation and the use of two potential new approaches to assess conch mortality: 1) change-in-ratio estimators, and 2) tagging and fishing effort.

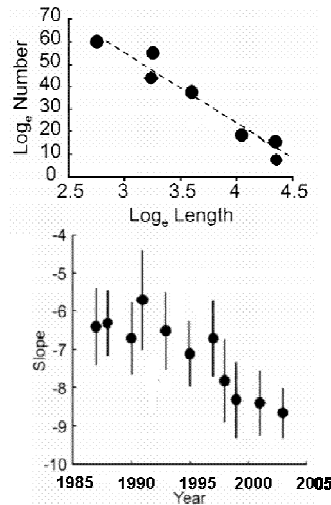


Figure 5.1. Simple linear regression plot of the relative (log scale) number of individuals at length (upper panel) and plot of the resulting slopes and variances corresponding to the seasons (lower panel).

## 5.2. Growth

Growth functions are an essential element in most stock assessment work. They provide useful information on life span, age structure of populations to estimate mortalities, biomass gains through age to estimate yields, etc. In the case of queen conch, growth cannot be easily modeled as the species do not deposit growth rings in hard parts that will express passage of time associated with size. Moreover, queen conch experience changes in their axis of growth as juveniles approach sexual maturity. Additionally, the species exhibits highly plastic shell morphology that depends on the local habitat characteristics giving individual queen conch a distinct geographic identity.

In the absence of hard parts to determine age of the individuals, the observed changes in the axes of growth and the distinct geographic identity preclude the use of indirect aging methods (e.g., modal progression). Therefore, development of simple growth functions for the species has proven difficult or impossible.

Tagging studies are very useful to measure and understand growth of juvenile queen conch while limited information on the direct observation of adult conch under controlled conditions have served the purpose of understanding aspects of the relatively slower adult growth. For the above reasons, we try here to establish a protocol that could provide a simpler frame to estimate growth parameters and functions useful to the aim of generating management advice.

### 5.2.1. Juvenile growth estimates

Juvenile queen conch growth has been extensively studied in the Caribbean as a consequence of their rapid growth in siphonal length and availability of juvenile siphonal length frequencies distributions. This characteristic has facilitated application of juvenile aging techniques based on modal progression. Because of the change in the axis of growth after the onset of maturity, similar aging analysis for older age groups is not

possible. Also tagging studies that measure growth over shorter time periods have been used to express growth during juvenile stages.

Results of these measures of growth have been used to fit von Bertalanffy growth functions in length ( $L_t = L_\infty(1 - \exp(-K(t - t_0)))$ ) mostly using indirect statistical methods for parameter estimation (i.e., Walford-type plots, etc.). In general, the growth parameters are for functions valid for ages 1 through 3; therefore, the asymptotic length may not have a realistic biological value but only one as a fitted parameter for the function within the specified age range. A list (not necessarily complete), of the principal works on aging and growth parameter estimation for juvenile queen conch compiled from the literature is given below, where  $L_\infty$  is the asymptotic length,  $K$  is the growth coefficient and  $t_0$  is the theoretical age when length is zero in the von Bertalanffy growth function.

Location	$L_\infty$	$K$	$t_0$	$\Phi'$	Source
San Andres & Providencia, Colombia	329.4	0.720		1.536	Garcia 1991
San Andres & Providencia, Colombia	350	0.270		1.127	Gallo et al. 1996
Providencia & Santa Catalina, Colombia	375	0.250		1.114	Marquez 1993
San Bernardo, Colombia	365	0.290		1.171	in Gallo et al. 1996
Boca Chica, Belize	268	0.223	-0.05	0.967	Strasidine 1988
Tres Cocos, Belize	332	0.207	-0.33	0.997	Strasidine 1988
Water Caye, Belize	269	0.209		0.94	Strasidine 1988
Quintana Roo, Mexico	360.77	0.456			Valle-Esquivel 2003
Quintana Roo, Mexico	341.7	0.580			Valle-Esquivel 1998
Pedro Bank, Jamaica	221	0.580	0.155		Tewfik 1996
Cabo Cruz, Zone A, Cuba	383.4	0.330	-0.05	1.241	Alcolado 1976
Cabo Cruz, Zone B, Cuba	380.6	0.287	-0.12	1.178	Alcolado 1976
Diego Perez, Zone A, Cuba	232.7	0.429	-0.09	1.21	Alcolado 1976
Diego Perez, Zone B, Cuba	207.6	0.442	-0.09	1.19	Alcolado 1976
Cayo Ancilitas, Cuba	259.8	0.571	0.09	1.366	Alcolado 1976
Rada Inst. Oceanol., Cuba	334	0.360	0.13	1.239	Alcolado 1976
Berry Islands, Bahamas	300	0.200	-0.65	0.952	Iversen et al. 1987
Six Hill Cay, Turks & Caicos	256	0.563	-0.16	1.356	in Appeldoorn et al. 1987
La Parguera, Puerto Rico, tagging	460	0.250	0.244	1.173	Appeldoorn 1990
La Parguera, Puerto Rico. LFA	340	0.437	0.462	1.328	Appeldoorn 1990
St. John, USVI	260.4	0.516		1.323	Berg 1976
St. Croix, USVI	241.7	0.420		1.212	Berg 1976
St. Kitts	331.9	0.347		1.221	Buckland 1989
Martinique, tagging	338.6	0.388			Rathier & Battagly 1994
Martinique, LFA	339	0.392			Rathier & Battagly 1994

We observe that parameter values may vary greatly within a given area, which may be expressing either true variability of the individual queen conch growth or a combination of growth characteristics as well as methods in data collection, aging techniques and/or growth function fitting algorithms. For this reason, we offer as reference average and variance of Von Bertalanffy growth in length parameters for juvenile queen conch grouped by general regions. In this manner, the user may have the opportunity to refer to these average values when researching queen conch growth. We found (Figure 5.2) a well known negative exponential distribution between the

asymptotic length and the growth coefficient. This distribution between the two parameters is expected from the nature of the von Bertalanffy growth function.

Location	Average $L_{\infty}$	Standard deviation $L_{\infty}$	Average K	Standard deviation K	Average $t_0$	Standard deviation $t_0$
Colombia	354.85	19.83	0.38	0.23	0.00	0
Belize-Quintana Roo	314.29	43.73	0.34	0.16	-0.19	0.20
Jamaica	221.00		0.58		0.00	0
Cuba	299.68	76.54	0.40	0.10	-0.02	0.11
Bahamas+T&C	278.00	31.11	0.38	0.35	-0.41	0.35
USVI	278.00	47.61	0.43	0.08	0.00	0
PR	400.00	84.85	0.34	0.13	0.35	0.15
Martinique	338.80	0.28	0.39	0.00	0.00	0

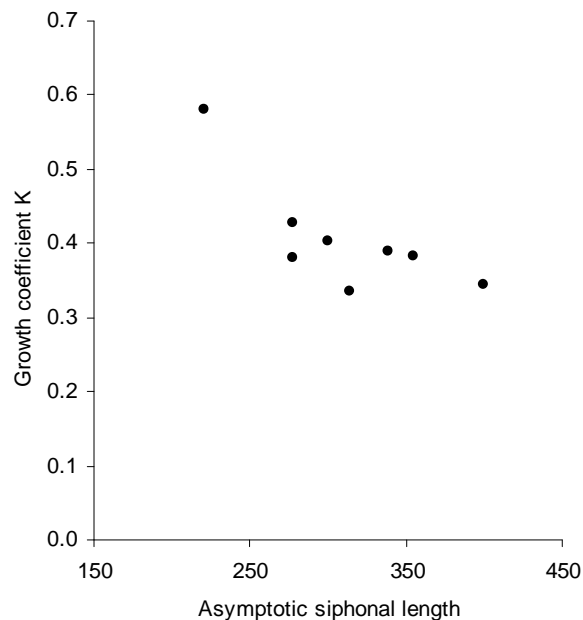


Figure 5.2. Trend between the growth coefficient, K, and the asymptotic length,  $L_{\infty}$ , of the average growth parameters for the von Bertalanffy growth function for juvenile queen conch in different regions of the Caribbean.

### 5.2.2. Length-weight relationships

Queen conch are often landed after removal from the shell, therefore length/meat weight relationships are particularly important. CFMC/CFRAMP (1999) provided a number of equations taken from Appeldoorn (1994) illustrating the relationship between weight (meat, tissue, and shell) and siphonal length for juvenile (J) and adult (A) queen

conch as well as lip thickness of adult conch, all from La Parguera, Puerto Rico. These functions are reproduced here:

Group Regression equation

LogY=a + b(LogX)	r <sup>2</sup>	N	Mean Log X	Mean Log Y
<b>Meat Weight</b>				
(J) Log(MW)= -2.535+3.486 Log(L)	0.926	94	1.838	1.254
(A) Log(MW)= -1.510+2.804 Log(L)	0.494	130	2.393	1.392
(A) Log(MW)= 2.212+0.163 Log(LP)	0.274	131	2.394	1.117
Log(MW)= -1.357+2.571 Log(L)+0.135 Log(LP)	0.684	130		
(A) Log(MW+100)= 1.797+0.232 Log(L)	0.354	130	2.101	1.117
<b>Tissue Weight</b>				
(J) Log(TW)= -2.286+3.459 Log(L)	0.925	94	2.053	1.254
(A) Log(TW)= -1.444+2.928 Log(L)	0.524	130	2.632	1.392
(A) Log(TW)= 2.469+0.147 Log(LP)	0.214	131	2.633	1.117
(A) Log(TW)= -1.294+2.726 Log(L)+0.118 Log(LP)	0.659	130		
(A) Log(TW+100)= 1.764+0.403 Log(LP)	0.321	130	2.121	1.117
<b>Shell Weight</b>				
(J) Log(SW)= -1.786+3.517 Log(L)	0.878	94	2.626	1.254
(A) Log(SW)= -0.286+2.530 Log(L)	0.347	130	3.237	1.392
(A) Log(SW)= 2.952+0.256 Log(LP)	0.579	131	3.237	1.117
(A) Log(SW)= 0.013+2.129 Log(L)+0.273 Log(LP)	0.822	130		
(A) Log(SW+100)= 2.793+0.293 Log(L)	0.633	130	3.720	1.117

All weights are in grams, siphonal length is in centimeters, and lip thickness is in millimeters. N is sample size. Logs are base 10. Meat weight=MW, wet-tissue weight=TW, shell weight=SW, juvenile=J, adult=A, siphonal length=L, lip thickness=LP. Mean X and Y values are provided to permit conversion to  $Y=u+vX$  where  $v=b/r$  and  $u=(\text{mean } Y)-v(\text{mean } X)$ . The functions are stratified by juveniles and adults and this makes difficult the use of such functions, especially due to the very narrow siphonal length range in the adults.

Data on % clean meat as a function of siphonal length for queen conch in Honduras (Ehrhardt and Galo, 2005) (Figure 5.3) and in The Bahamas (Ehrhardt and Deleveaux, 1995) (Figure 5.4) are indicative that growth in weight follows a power function with siphonal length. Sexual dimorphism in the above functional relationships was not significant.

An important issue is the various % clean weights reported in queen conch statistics. For this reason we provide results of clean weight conversions estimated by Ehrhardt and Galo (2005) (Figure 5.5.). In spite of the contentions that a large variance exists in the % clean meat weight relative to the initial weight, the results in figure 5.5 show the contrary. The functional relationships may be used to transform databases from different percentages of meat processing such that comparative results from assessments could be obtained.



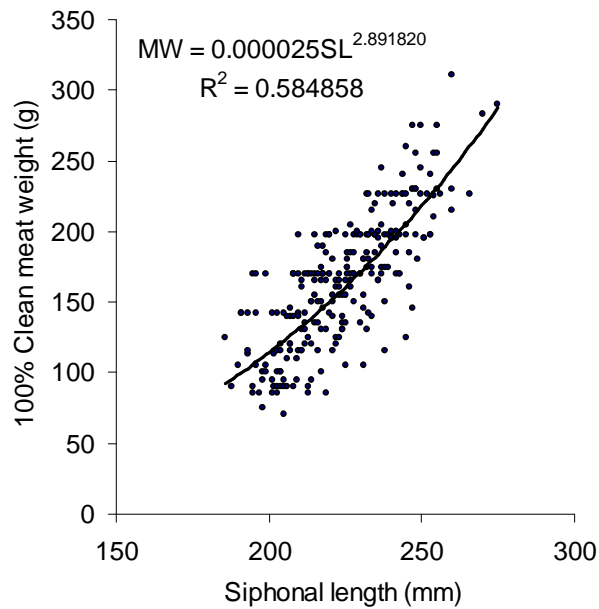


Figure 5.3. Meat weight in grams (100% clean) as function of siphonal length in millimeters for queen conch in Honduras.

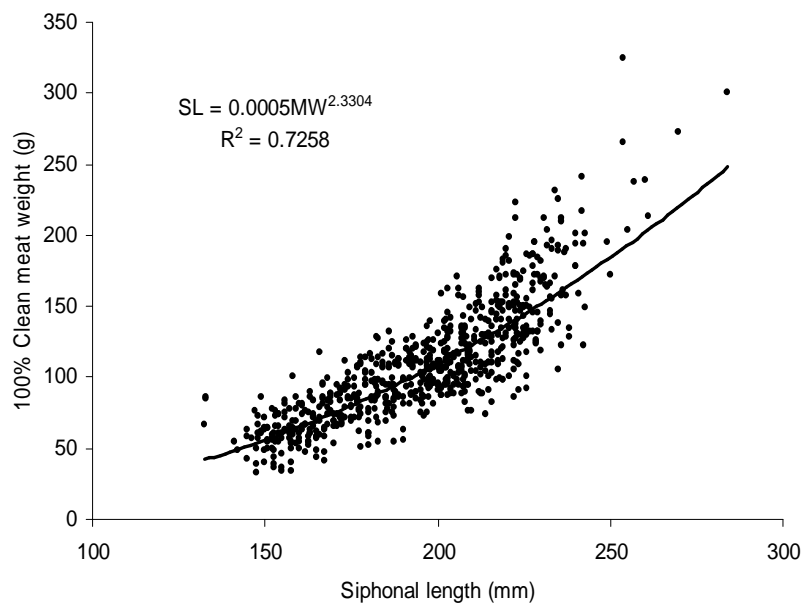


Figure 5.4 Meat weight in grams (100% clean) as function of siphonal length in millimeters for queen conch in The Bahamas.

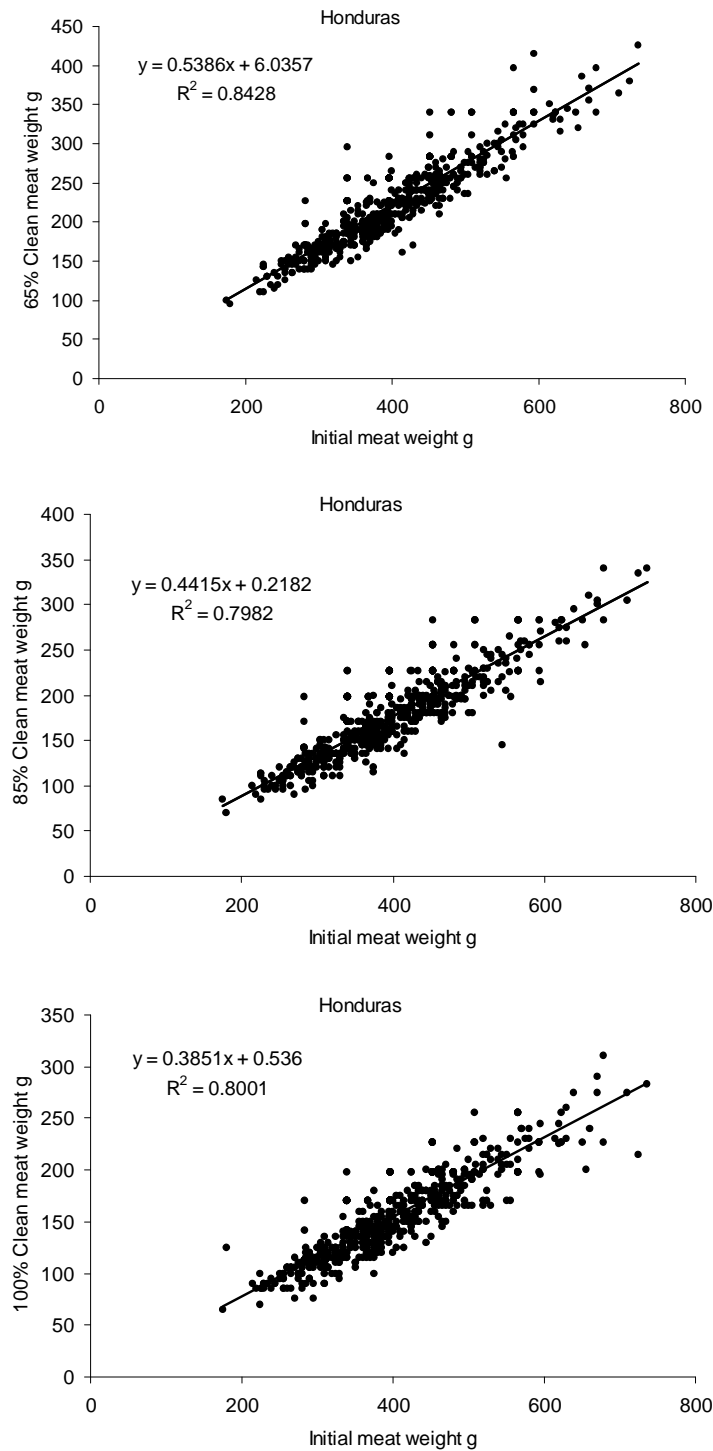


Figure 5.5. Meat weight reduction functions from initial meat weight.

### 5.2.3. Growth in weight modeling

#### 5.2.3.1. Apeldoorn's and Valle's Gompertz growth modeling

Appeldoorn (1988) developed an ingenious growth algorithm to express dynamic biomass growth of individual queen conch. The algorithm couples juvenile and adult growth in weight via a juvenile von Bertalanffy-type growth function of siphonal length at age converted to weight with the help of a length-weight relationship for juvenile conch. Then, he added to the juvenile growth process the weight-at-age in the adult stages. This was accomplished by modeling a function of lip-thickness at age and a lip-thickness-weight relationship for the adult conch. The resulting growth in weight at age data are subsequently modeled by fitting a Gompertz-type (double exponential) growth function in weight to the estimated juvenile-adult linked growth data. The Gompertz growth in weight at age function used by Appeldoorn (op cit) is expressed as

$$W_t = A1 * \text{Exp}(A2 * (1 - \text{Exp}(-A3 * t))) \quad (5.2.3.1)$$

where  $W_t$  is weight at age,  $t$  is age and  $A1$ ,  $A2$ , and  $A3$  are parameters that need to be estimated by non-linear statistical procedures.

Valle (2003) formulated growth in weight for conch following a similar Gompertz -type growth function but expressed the function as

$$W_t = W_\infty * \text{Exp}(\text{Log}(\frac{W_0}{W_t}) * \text{Exp}(-G * t))$$

where  $W_t$  is weight at age,  $t$  is age and  $W_\infty$ ,  $W_0$ , and  $G$  are parameters to be estimated by non-linear statistical procedures. Parameters for the above equation are given below:

Parameter	Mean	Variance (10% Coefficient Variation)	Covariance ( $W_\infty$ -G)
$W_\infty$	172.67	298.16	
$W_0$	0.19	0.05-0.35	
G	1.156	0.0134	-0.6

These parameters need to be used with caution because they are for specific stock simulations and the parameters estimated with specific data. Generally, however, these parameters should be estimated with appropriate data as indicated above for each queen conch fishing ground, given the distinct geographic identity of the queen conch that affects their growth.

The above formulations are data intensive because of the nature of the queen conch growth process. It depends on the availability of weight-at-age information for a wide range of ages with the given difficulty to age queen conch beyond the age of first maturity. Tagging studies with massive deployment of tagged conch that could survive at

least 6 or more years in the fishery will be needed to express these growth patterns (weight at age).

#### 5.2.3.2. Ehrhardt's approximation to growth in weight

Appeldoorn's multiple axis growth algorithm is rather data intensive, therefore an attempt was made by Ehrhardt (1999) to simplify the above algorithm such that a more readily available technique to express conch growth is available for stock assessment purposes. Simplification of equation 5.2.3.1 is possible when average weight of older (mature) animals is available, and a fairly good description of the juvenile growth is also available. This appears to be the case for the queen conch throughout the Caribbean region since there is an extensive literature with parameters on the growth of juvenile conch (see Section 5.2.1 above) as well as length-weight functions for these juvenile growth stanzas. On the other hand, extensive information on edible individual meat weight for the larger mature conch has been collected in most the regional fisheries. In the particular case of the Gompertz equation (equation 5.2.3.1), when age (t) is large, say equal to infinity, it reduces to

$$W_{\infty} = A1 * e^{A2}$$

Therefore, queen conch growth can now be expressed by an equation relative to the asymptotic weight ( $W_{\infty}$ ) at those old ages by

$$W_t = \frac{W_{\infty}}{W_{\infty}^{EXP(-A3*t)}} \quad (5.2.3.2)$$

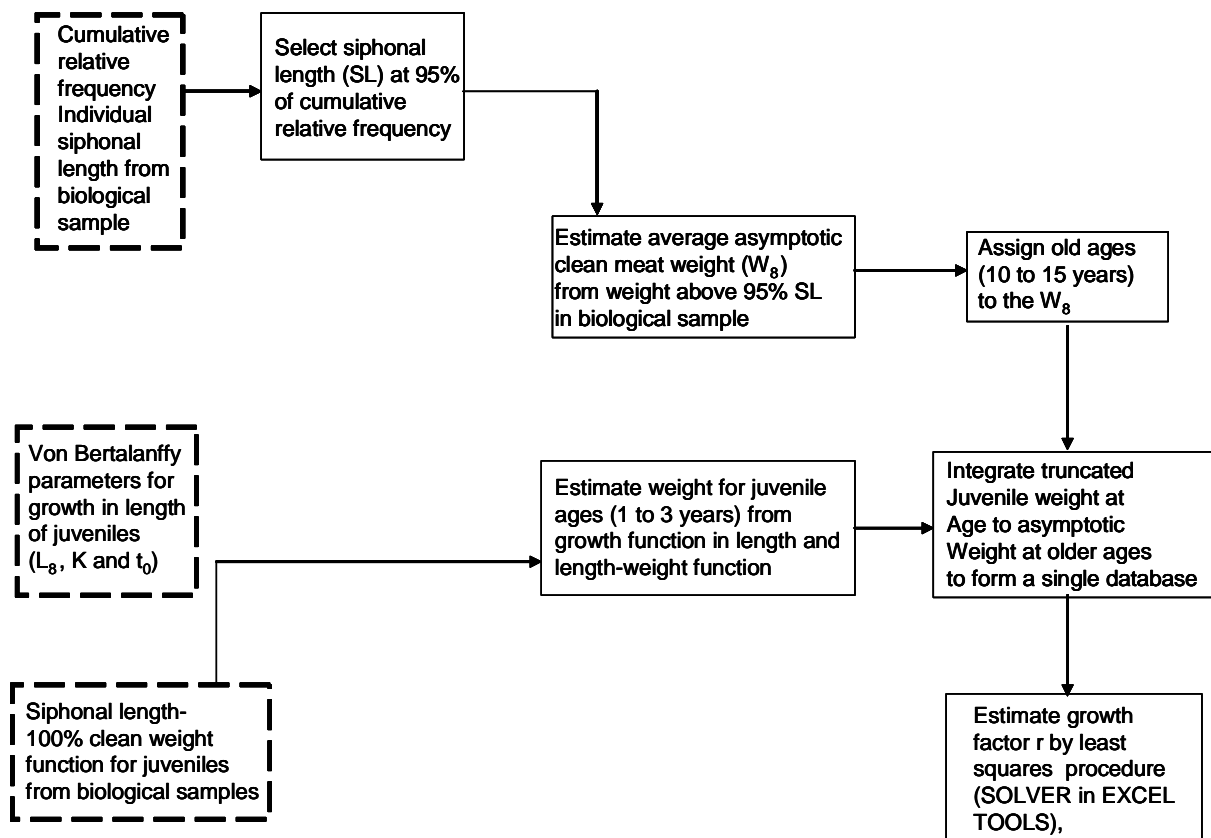
Since queen conch do not appear to grow in meat weight after the age of maturity; then the asymptotic meat weight,  $W_{\infty}$ , can be estimated directly as the average of the weight over a range of large size mature animals. Then the parameter A3 in the above equation is the only unknown parameter, which can be estimated by least squares procedures from a truncated growth in weight data series formed by the weight at age of juvenile stages and the average asymptotic weight assigned to larger, thus older ages. This may be easily accomplished with the SOLVER routine in TOOLS in EXCEL.

The merit of the equation 5.2.3.2 is that real data on meat weight of old animals and fairly well estimated growth in weight curves for juveniles are integrated to generate a growth curve that covers the whole life span of the species. This is done without the need of estimating growth in siphonal length and in lip thickness, and dubious lip thickness-meat weight relationships (usually with zero slope and very low correlation) corresponding to sizes when queen conch experience near zero meat growth.

#### Data and model fitting

The shortened version of the Gompertz growth model (equation 5.2.3.2) is highly sensitive to the selected asymptotic weight. A statistical protocol necessary to define this size is to first collect a siphonal length and corresponding 100% clean meat weight in a biological sample. It is recommended that such sample should be obtained by randomly

selecting a number of live queen conch and then collect the first 5 individuals in a siphonal length frequency to draw 100% clean meat weights. In this manner there will be a sample with good representation of larger and smaller individuals without the super numeric frequencies usually encountered in the intermediate siphonal lengths. Following the flowchart given below, the growth function estimation algorithm should start with estimating the cumulative relative frequency of the siphonal length measurements and then select the siphonal lengths corresponding to the 95% percentile (See figure 5.6).



FLOW CHART OF ALGORITHM FOR GROWTH PARAMETER ESTIMATION

The weights corresponding to siphonal lengths equal or larger than the siphonal length established by the 95% percentile (see Figure 5.7) are averaged and this average defined as  $W_{\infty}$ . In the case shown the  $SL_{95\%}$  corresponds to about 252 mm and the 100% clean weights correspond to those observations to the right of 252 mm  $SL_{95\%}$  in figure 5.7. An arbitrary old age (say 10 to 15 years) is assigned to the average 100% clean meat weight ( $W_{\infty}$ ) of 240.76 g estimated from the data in the figure.

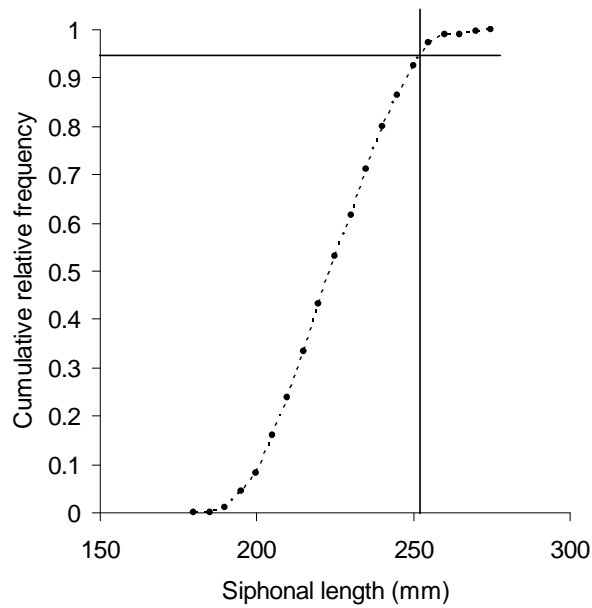


Figure 5.6. Cumulative relative frequency of siphonal length in a biological sample.

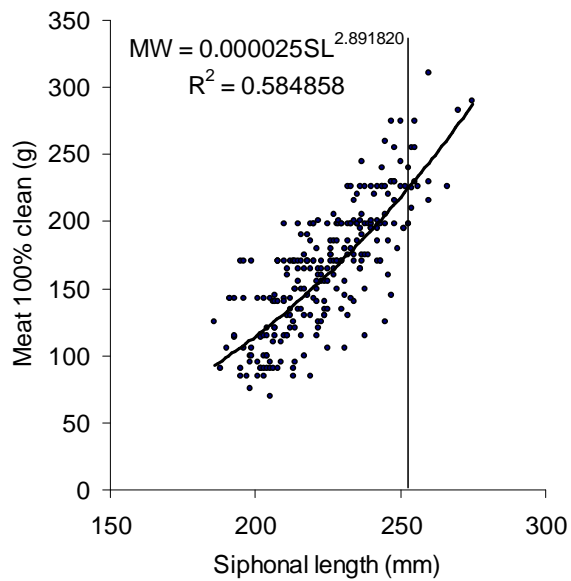


Figure 5.7. Clean (100%) weights corresponding to large individuals defined by a siphonal length equal or above to that length in the 95% percentile of their cumulative length frequency.

The next step in the algorithm is to estimate the weight at age of juveniles (i.e., ages 1, 2 and 3). This is accomplished from a von Bertalanffy growth in siphonal length expressed by the equation

$$L_t = L_{\infty}(1 - \exp(-K(t - t_0)))$$

with given parameters that can be from the tables presented in section 5.2.1 if the region is represented in that data, or from modal frequency analysis using 100% clean meat weight frequency data, or tagging data collected specifically for a given fishing ground. Then, using a length versus 100% clean meat weight relationship obtained from the biological data needed to construct figures 5.6 and 5.7, or from the literature, or from data in section 5.2.2, the siphonal length at age obtained from the von Bertalanffy growth function is transformed to weight at age.

The next step is to integrate the weight at age of juveniles obtained in previous steps with the asymptotic weight at an older age obtained from the average weight of individual with siphonal length above the size corresponding to the 95% percentile in the cumulative frequencies ( $SL_{95\%}$ ).

Example: Mean clean (100%) meat weight resulting from adopting  $SL_{95\%}$  in figure 5.7 is  $W_{\infty} = 240.76$  g (standard deviation = 32.71 g). Assuming juvenile von Bertalanffy growth parameters from the Caribbean Islands of Colombia and Belize (table in section 5.2.1)  $L_{\infty} = 326.91$  mm,  $K=0.31$  yr<sup>-1</sup>, and  $t_0 = -0.19$ , and siphonal length-100% clean meat weight function parameters from figure 5.7. The data integration for juveniles and adults are presented in Table 5.1.

Least squares fitting of the model in equation 5.2.3.2 using the SOLVER routine in TOOLS in EXCEL requires the formatting of a table of observed and expected values of weight at age (as shown in Table 5.1). The observed values are those estimated for juveniles via the von Bertalanffy growth equation and length weight relationship and the average asymptotic weight. The expected values are those estimated by the model in equation 5.2.3.2. Then the difference between observed and expected values (residuals) are squared and finally added up at the bottom of the column of the residuals squared ( $SSR=0.6$ ). This last quantity is the one that is minimized by the SOLVER routine by changing the value of the parameter  $r$  ( $r = 0.691$ ) given that the asymptotic weight was 240.76 g.

**Accessing SOLVER:** Open EXCEL and create a table exactly like the bottom part of Table 5.1 where the observed and expected values are estimated by entering the corresponding growth equation in the EXCEL template. For the residual squared enter the difference between the expected and observed values in between parenthesis and write the formulation for the square of a number. For the SSR block the column of the residuals squared plus two empty cells and click Epsilon ( $\Sigma$ ) from the Tool Bar. Once the table is correctly entered with all formulations click in TOOLS, then click in SOLVER. In the window that appears click in Set the Target Cell and click the cell where the estimate of the SSR (Sum of the Squared Residuals) should be (cell containing 0.62 in Table 5.1). In the SOLVER window where it says Equal to, fill in the spot indicating Min (for Minimization). Then click in the cell stating By Changing Cells and click the cell in the table that indicates the value of  $r$  that needs to be fitted (or where 0.691 is in Table 5.1). Finally, click in SOLVE and if SOLVER found a solution, click in Keep Solver Solution and then click OK.

Table 5.1. Integration of data on weight at age for a simulated condition in the South Caribbean region (Colombia-Belize).

Siphonal length-100% clean weight function				Average juvenile v. Bertalanffy parameters Colombia and Belize	
a	0.000025			$L_{\infty}$	326.91
b	2.8912			K	0.31
				$t_0$	-0.19
Residuals					Parameters
Age	Length	Weight	Expected	Squared	
0	18.7	0.1	1.0		r 0.691
1	100.8	15.5	15.4	0.01	
2	161.1	60.1	60.7	0.40	$W_{\infty}$ 240.76
3	205.3	121.1	120.7	0.17	
4			170.3		
5			202.4		
6			220.7		
7			230.5		
8			235.6		
9			238.1		
10			239.4		
11			240.1		
12			240.4		
13		240.8	240.6	0.03	
14		240.8	240.7	0.01	
15		240.8	240.7	0.00	
SSR				0.62	

The resulting fit is shown in figure 5.8 where observed values in Table 5.1 are shown as black dots while the expected growth curve is the line fitted. The estimated parameter  $r$  is 0.691.

Application of the growth model using data collected in The Bahamas by Ehrhardt and Deleveaux (1995) resulted in three different growth patterns for queen conch in three regions: Grand Bahama, New Providence, and Abaco. The resulting growth curves are presented in figure 5.9 as an example that growth may be quite variable among conch populations separated over short spatial scales.



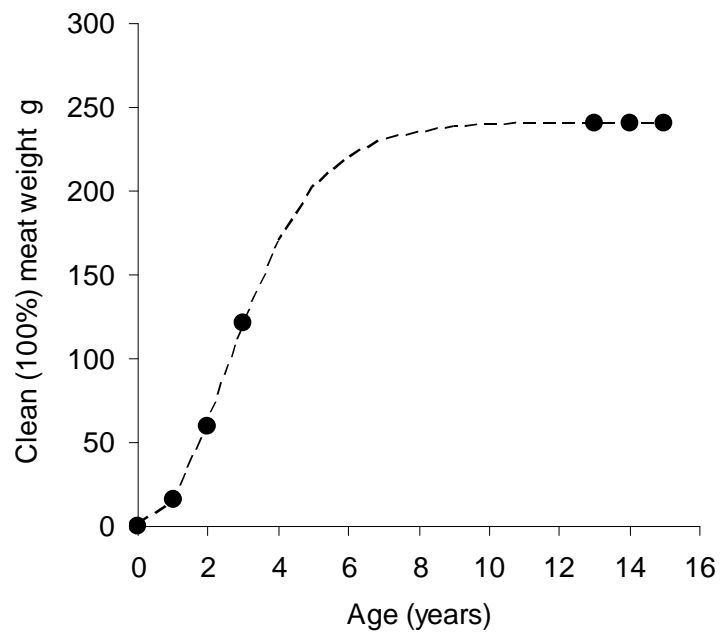


Figure 5.8. Observed and expected (fitted) values for equation 5.2.3.2

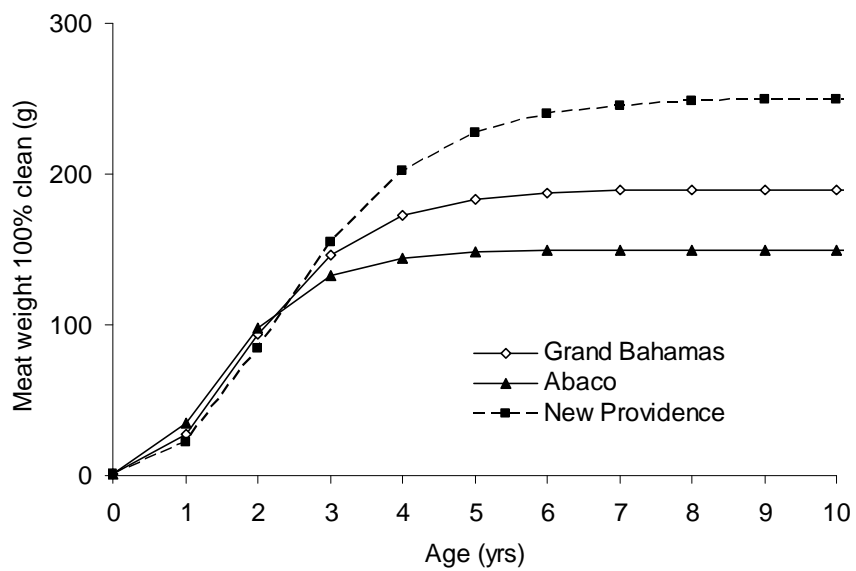


Figure 5.9. Growth in weight curves for queen conch in three areas of The Bahamas.

### 5.2.3.3. Comparison of Valle (2003) Gompertz growth function and Ehrhardt's simplified growth function.

The Gompertz growth function adopted by Valle (2003) was used in Monte Carlo simulations using the variance-covariance data matrix provided in the section 5.2.3.1 by Valle (this Manual section 7) to generate 1000 growth curves. From these curves the maximum, minimum and average weight at age were estimated. Using average juvenile growth parameters in length and average length weight functions for juvenile queen conch in Puerto Rico a growth in weight was estimated with the shortened growth function (equation 5.2.3.2). The resulting values are plotted in the figure 5.10 where a remarkable similarity is observed between the two very different procedures proposed to estimate growth of queen conch.

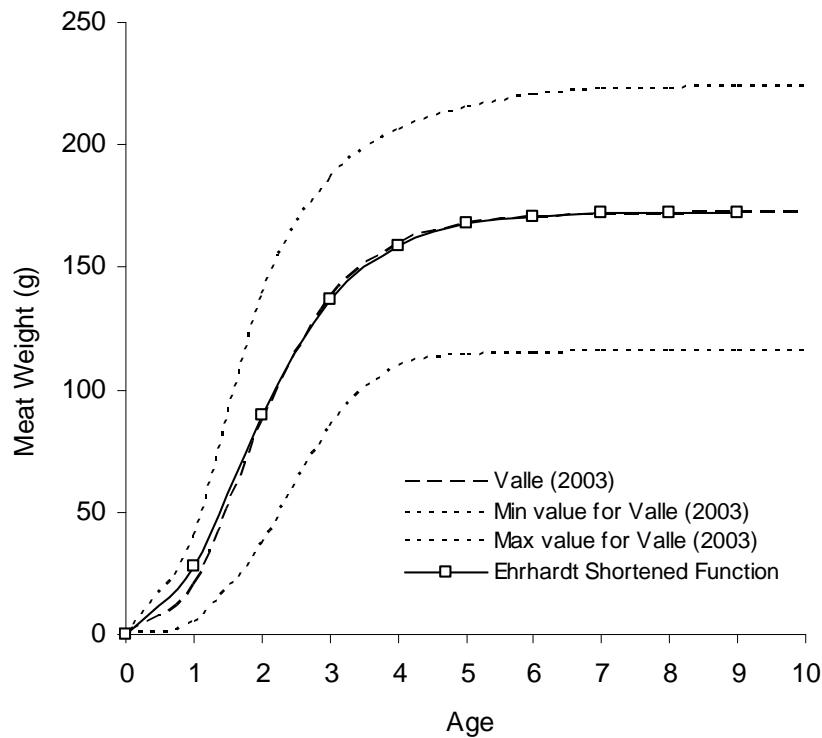


Figure 5.10. Comparison of the full deterministic Gompertz growth in weight model by Valle (2003) and the Ehrhardt shortened version of the Gompertz model. Minimum and maximum values for the full Gompertz model are also shown.

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### 5.3. Natural Mortality

The instantaneous natural mortality coefficient (M) is an important parameter in all analytical models that attempt to assess the status of exploitation of commercially exploitable marine fauna stock dynamics. Unfortunately, this population parameter is one of the most difficult to estimate due to the cryptic character of the natural mortality process. Queen conch may live for up to 30 years (Glazer, pers. comm.) – a likely indication that natural mortality should be at the lower end of the natural mortality estimated for animal populations in the sea. High predation induced mortality is likely for juvenile conch, but decreases significantly among larger juveniles (Appeldoorn, 1988; Ray-Culp et al., 1999). Adult conch are thought to have low rates of natural mortality, however few studies have examined this question. Appeldoorn (1988) examined the relationship between age and natural mortality in *S. gigas*. He derived a relationship between juvenile age and natural mortality and estimated natural mortality for adult conch aged at 4.25 years as  $M=0.52$ . Natural mortality of older conch have not been estimated, therefore natural mortality rates for the majority of the lifespan of queen conch are unknown. The age-mortality relationship was further developed (Appeldoorn 1988) by omitting mortality estimates of small juveniles that were not yet epibenthic and therefore not available to the fishery. The estimate of adult natural mortality was included in fitting the inverse Caddy age/mortality relationship. This model was believed to be the most appropriate because extrapolated adult survival rates were consistent with the estimated longevity of conch. The natural mortality-age equation provided by CFMC/CFRAMP (1999) based on Appeldoorn (1988) is

:

$$M_t = -0.242 + \frac{4.33}{t}$$

where t = age.

The above equation results in negative values for M with older ages (Figure 5.12) and CFMC/CFRAMP (1999) recommended restricting mortality to a minimum  $M=0.1$  and assumed to be constant with older conch.

Stoner and Glazer (1998) investigated natural mortality rates in juvenile queen conch in Florida and The Bahamas. They reported that M varied greatly among seasons, habitats, and conch aggregation density. Estimates of M ranged from 12.0 for small (45mm SL) conch to 1.0 for large juveniles (175-215mm SL). At one site, estimates of M varied from 1.0 to 4.0 over a seven year period; however, a second site located approximately 35 miles from the first had an average M of 4.71 over time for conch of similar size. The natural mortality estimates provided by these authors were compared with the model developed by Appeldoorn (1988) and their figure is reproduced here as figure 5.11. The very high estimates of M obtained by the later authors will necessarily imply that queen conch is an extremely short lived species. For example, annual shrimp species have M values between 2.2 to 3.2 per year. Therefore, values of M in the range between 1.0 and 14 (Figure 5.11) will imply that there will not be queen conch alive after one year of age.

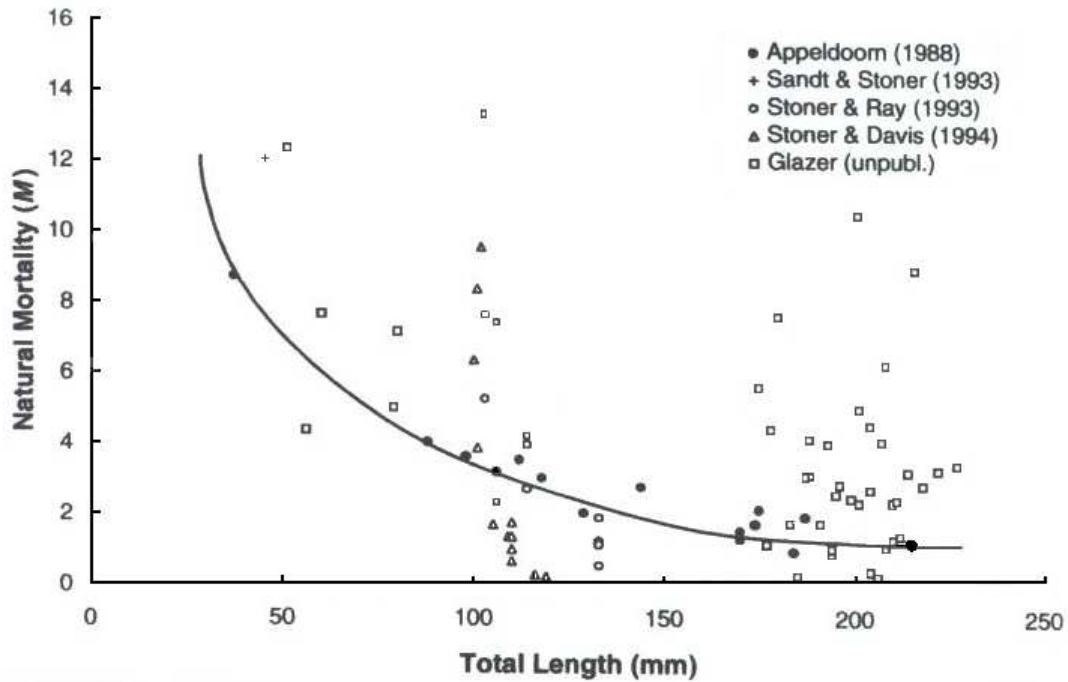


Figure 5.11. Natural mortality rates at length for queen conch. Figure reproduced from Stoner and Glazer 1998).

Valle (2003) modeled natural mortality of queen conch using tagging experiments in an inlet in Xel-ha, Quintana Roo, Mexico. The models were expressed as exponential function of siphonal age or siphonal length (SL):

$$M = 2.0482Age^{-1.1081}$$

or

$$M = 1988.8SL^{-1.4364}$$

These models appear to generate a more realistic natural mortality rate for a species that may live well over 20 years.

For reference purposes the estimated  $M$  at age with the equations given by Appeldoorn (1988) and Valle (2003) are presented in Table 5.2 and plotted in Figure 5.12.

Table 5.2. Estimated values of natural mortality at age by two models in the literature.

Age	Valle (2003)	Appeldoorn (1988)
1	2.05	4.09
2	0.95	1.92
3	0.61	1.20
4	0.44	0.84
5	0.34	0.62
6	0.28	0.48
7	0.24	0.38
8	0.20	0.30
9	0.18	0.24
10	0.16	0.19
11	0.14	0.15
12	0.13	0.12
13	0.12	0.09
14	0.11	0.07
15	0.10	0.05
16	0.09	0.03
17	0.09	0.01
18	0.08	0.00
19	0.08	-0.01
20	0.07	-0.03

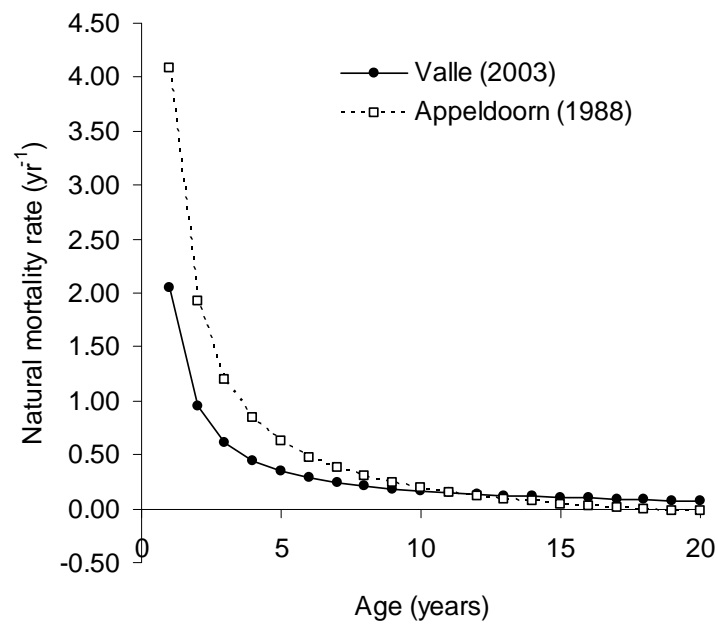


Figure 5.12. Natural mortality trends with age by two models in the literature.

The Appeldoorn (1988) natural mortality model as function of age was transformed by Ehrhardt (1999) into an equation as a function of meat-weight instead of age according to the shortened meat weight at age equation 5.2.3.2 presented in section 5.1. This simpler growth equation rearranged gives age  $t$  as a function of meat weight:

$$t = \frac{-\ln \left[ \frac{\ln \left( \frac{W_{\infty}}{W_t} \right)}{\ln(W_{\infty})} \right]}{r}$$

Hence, the natural mortality equation as a function of meat weight for the Appeldoorn (1988) model is

$$M_t = -0.242 - \frac{4.330 * r}{\ln \left[ \frac{\ln \left( \frac{W_{\infty}}{W_t} \right)}{\ln(W_{\infty})} \right]}$$

Similarly for the Valle (2003) model the natural mortality as a function of meat weight is

$$M_t = 2.0482 - \frac{\left[ \frac{\ln \left( \frac{W_{\infty}}{W_t} \right)}{\ln(W_{\infty})} \right]^{-1.1081}}{r}$$

For reference purposes the estimated values of  $M$  corresponding to 100% clean meat weight in grams for the above two equations are given in Table 5.3 and shown in figure 5.13.

Table 5.2. Estimated values of natural mortality at weight by two models presented in this manual.

100% Clean meat weight (g)	M Appeldoorn (1988)	M Valle (2003)
15	4.09	2.05
61	1.92	0.95
121	1.20	0.61
170	0.84	0.44
202	0.62	0.34
221	0.48	0.28
230	0.38	0.24
236	0.30	0.20
238	0.24	0.18
239	0.19	0.16
240	0.15	0.14
240	0.12	0.13
241	0.09	0.12
241	0.07	0.11
241	0.05	0.10

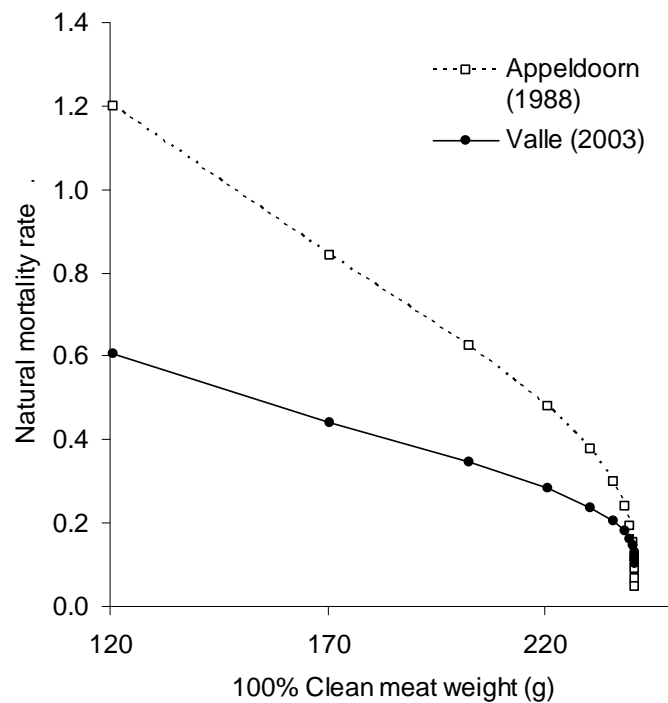


Figure 5.12. Natural mortality trends with 100% clean meat weight for the two models developed in this manual.



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## 5.4. Total Mortality

### 5.4.1. Weight converted catch curves (Ehrhardt, 1999)

A catch curve is defined as the frequency of animals in each age in a population. Catch curve analysis refers to the estimation of the total instantaneous mortality rate ( $Z$ ) by the slope of a regression line fitted to the natural logarithm of the abundance or catch in numbers of a given age  $t$ , on the age  $t$ . That is

$$\ln C_t = a + Zt$$

Since conch cannot be easily aged, or given that the siphonal length statistics are not usually available from landings, then  $C_t$  in the catch equation can be replaced by the number of animals in a given clean meat weight class. Thus, in the case when only weight frequency statistics are available; this is achieved by dividing  $C$  in the weight class by the time needed to grow through the weight class. This elapsed time is defined by the growth equation adopted for the species.

The simple growth equation 5.2.3.2 given in section 5.1, rearranged to give age as a function of meat weight is:

$$t = \frac{-\ln \left[ \frac{\ln \left( \frac{W_\infty}{W_t} \right)}{\ln(W_\infty)} \right]}{r} \quad (5.4.1.1)$$

Thus, if  $W_j$  and  $W_{j+1}$  are the lower and upper limits of a meat weight class interval  $j$ , respectively, then the time required to grow through size interval  $j$  can be expressed as

$$\Delta_{t_j} = t_{j+1} - t_j = \frac{1}{r} \ln \left[ \frac{\ln \left( \frac{W_\infty}{W_j} \right)}{\ln \left( \frac{W_\infty}{W_{j+1}} \right)} \right]$$

Therefore, a meat weight converted catch curve for queen conch is given by

$$\ln \left( \frac{C_t}{\Delta t_j} \right) = a + Zt'$$

where  $t'$  is the relative age of the conch at the mid-weight of the meat weight class interval  $j$ . This relative (median) age  $t'$  is computed from equation 5.4.1.1 derived from the simple growth in weight function where  $W_t$  is replaced by the average weight in the meat weight class interval.

Once  $Z$  is estimated as the slope of the linear regression fitted to the data, the fishing mortality rate ( $F$ ) may be estimated as the difference between the total mortality rate  $Z$  and the average natural mortality rate  $M$  for the meat weight class intervals used in the regresional range to estimate  $Z$ .

The variance of  $Z$  is the variance of the slope of the linear regression fitted to the data. This is given by

$$\text{var } Z = \frac{\sum_j^n (Y_t - \hat{Y}_t)^2}{\sum_j^n (t'_j - \bar{t}')^2} \cdot \frac{n-2}{1}$$

Where  $Y_t$  is the observed value  $\{\ln(\frac{C_t}{\Delta t_j})\}$  and  $\hat{Y}_t$  is the expected value estimated on the regression line. Also,  $t'_j$  is the median age for meat weight interval  $j$  estimated from equation 5.4.1.1, and  $\bar{t}'$  is the average of  $n$  median ages in the regression range. The regression range comprises the relative ages that are fully recruited to the fishery or fully represented in the biological samples from landings.

As an example, data for a fishing ground in the region Colombia-Belize with a 100% clean meat weight frequency distribution presented in Table 5.3, and the growth parameters  $W_\infty = 240.76$  g and  $r = 0.691$  for the simple growth equation given by equation 5.2.3.2, a weight converted catch curve analysis resulted in figure 5.13. The slope of the line resulted in an absolute value of 1.26 ( $= Z$  the total instantaneous mortality rate) or a survivor fraction ( $e^{-1.26}$ ) of  $S = 0.2837$ . The coefficient of determination is high, and equal to 0.97. The variance of the slope of the line is 0.005389 and the standard deviation is 0.07341. Therefore the 95% confidence interval for  $Z$  is given as

$$Z \pm 1.96 \frac{S \text{ standardDeviation}}{\sqrt{n}}$$

or 1.25 to 1.28.

The weighted natural mortality rate for the fully recruited meat weight range (140-240 g) resulted in a value of  $M = 0.86$  for the Appeldoorn base model and 0.45 for the Valle base model. These estimates are widely apart and a decision must be made on the best parameter to use. Because of the relatively greater stability of the  $M$  value provided by the Valle (2003) model (see Figure 5.12) we may be inclined to use the later parameter. In this particular case the fishing mortality rate ( $F$ ) is estimated by the difference between the total instantaneous mortality rate and the instantaneous natural mortality rate, that is 0.81 varying between 0.80 and 0.83 according with the confidence interval for the  $Z$  estimate..

Table 5.3. Frequency distribution of 100% clean meat weight for queen conch in the Colombia-Belize example and estimated values for the fishing mortality corresponding to each meat weight class interval and weighted average M for the regression range used in the fitting of the weight converted catch curve.

100% Clean meat weight (g)	Frequency	M Appeldoorn (1988)	M Valle (2003)
60	2607	1.94	0.96
70	3128	1.76	0.87
80	3650	1.62	0.80
90	19291	1.50	0.75
100	20855	1.39	0.70
110	44317	1.30	0.65
120	32846	1.21	0.61
130	29718	1.13	0.57
140	38581	1.05	0.54
150	25547	0.98	0.50
160	34932	0.91	0.47
170	19291	0.84	0.44
180	20855	0.78	0.41
190	8342	0.71	0.38
200	10427	0.64	0.35
210	3607	0.57	0.32
220	4085	0.49	0.28
230	3128	0.38	0.24
240	3128	0.16	0.15
Weighted average M		0.86	0.45

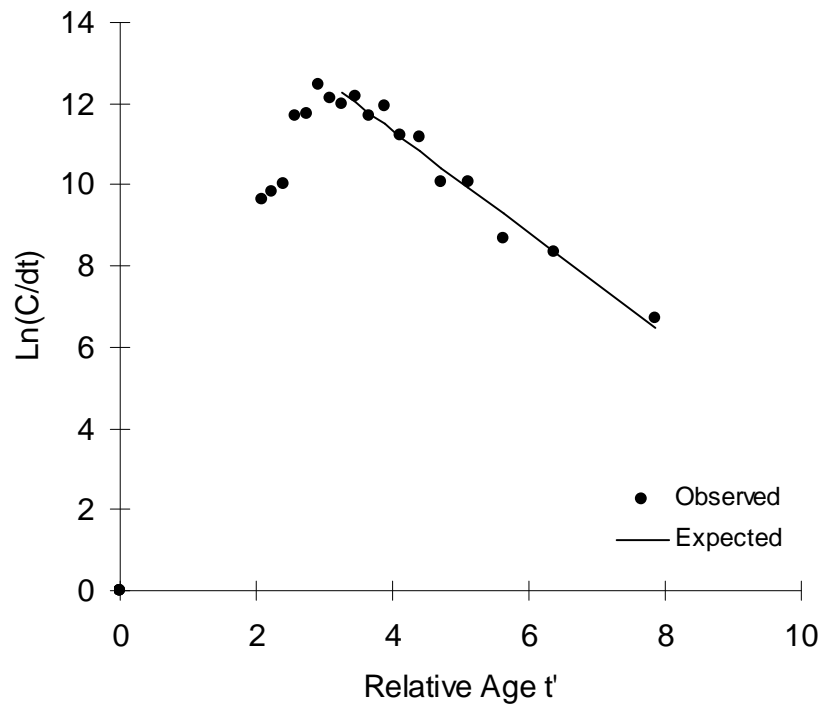


Figure 5.13. Converted catch curve for queen conch with data on growth given by equation 5.2.3.2. and parameters estimated for Colombia-Belize, and data on meat weight versus siphonal length given in Table 5.3.

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#### 5.4.2. Change-in-Ratio Estimators

Abundance and survival estimation techniques that use some sort of change in the relative abundance of two identifiable components of the population are known as change-in-ratio estimators (Paulik and Robson 1969). In the case of the queen conch, there are two definitely distinguishable components in their populations: 1) immature conch not presenting a developed lip, and 2) a mature component showing a well developed lip. These are two characteristics that are easily identifiable when whole individuals are landed, or in population density surveys.

The problem can be stated as follows: the fractions of mature and immature conch are measured at Time 1; then a measurable change in the numbers in both of the categories is obtained after a time, say at Time 2, that alter the initial fraction observed at Time 1. Measurements of individual conch in each category may be obtained from population density surveys (see section 4), or from well-designed biological sampling programs that check conch landings, at T1 and T2. We are interested in estimating an exploitation rate (u) that reflects the removals of conch from the two categories (i.e., mature and immature conch) between times T1 and T2.

We define exploitation rate as the fraction of individuals removed from the two categories (R) from the population (N1) at time T1. Since total removals and population abundance may not be easily obtained (i.e., estimated), then we circumvent this situation by using sample estimates of R that are defined as r, and sample sizes at T1 and T2 that we shall define as n1 and n2, respectively.

The general notation for this type of problems is:

x1 = number of mature conch in a sample n1 at time T1  
y1 = number of immature conch in a sample n1 at time T1  
n1 = total number of conch in the sample at time T1  
p1 = fraction of mature conch in sample n1 at time T1;  $p1 = x1/n1$   
x2 = number of mature conch in a sample n2 at time T2  
y2 = number of immature conch in a sample n2 at time T2  
n2 = total number of conch in the sample at time T2  
p2 = fraction of mature conch in sample n2 at time T2;  $p2 = x2/n2$   
 $rx = x2 - x1$ , net removal of mature conch between T1 and T2  
 $ry = y2 - y1$ , net removal of immature conch between T1 and T2  
 $r = rx + ry$ , total removals of conch between T1 and T2  
 $f = \text{fraction of mature conch in total removals} = rx/r$

In terms of formula development we have that the fraction of mature conch at time T2 can be expressed as

$$p2 = \frac{x2}{n2}$$

However,  $x2 = p1n1 + rx$ , or in words the number of mature conch in the initial sample (n1) at time T1 plus the number of mature conch removed (rx) during the time interval T2-T1. Also,  $n2 = n1 + r$ , that is the number of mature and immature conch in the sample at

time T1 plus the total net removal of mature and immature conch during the period T2-T1. Substituting these equations in the equation for p2 we have

$$p2 = \frac{p1n1 + rx}{n1 + r} \quad (5.4.2.1)$$

If the denominator and numerator in equation 5.4.2.1 are divided by the sample size at time T1 (i.e. n1), then

$$p2 = \frac{p1 + \frac{rx}{n1}}{1 + \frac{r}{n1}}$$

Given that  $f = \frac{rx}{r}$ , then it is replaced in the previous equation and after some algebraic manipulations we have

$$u = \frac{r}{n1} = \frac{p1 - p2}{p2 - f} \quad (5.4.2.2)$$

The last formulation is an expression for the exploitation rate, u, because it expresses the fraction of mature and immature conch removed from the population since T1 when the sample size was n1.

The formulation for the exploitation rate, u, has one very important data advantage, there is no need to estimate population abundance or to have a precise enumeration of the number of conch landed in each categories during the period T2-T1. Instead, it only needs a well-designed sampling protocol for estimating fractions of animals in each categories at times T1 and T2.

Example: In a seasonal queen conch fishery in The Bahamas, Ehrhardt and Deleveaux (1995) reported data on mature and immature conch from samples obtained in the Abaco Bight (Grand Bahama Island) in two sampling periods (T1 and T2). The first sample (n1) was obtained at the start of the season and the second sample (n2) at the time of the slack of the season. Seasonality of the fishery depends on the availability of fishing effort idle from the closing of the spiny lobster fishery in the period April-July of every year. The recorded data are:

Category	T1	T2	rx	ry	r
Mature (x)	2690	1720	970		
Immature (y)	380	240		140	
Total	3070	1960			1110

The above data are in numbers of individual queen conch with sexes combined. From these data

$$p1 = \frac{2690}{3070} = 0.876221; \quad p2 = \frac{1720}{1960} = 0.877551; \text{ and } f = \frac{970}{1110} = 0.873874$$

Therefore, the exploitation rate for the period between samplings is

$$u = \frac{0.876221 - 0.877551}{0.877551 - 0.873874} = -0.36156$$

The result obtained for  $u$  is that fishing mortality was 36.156 percent. The negative sign in the exploitation rate is indicative that animals were retrieved from the population. It is important to note here that if the rate would have been positive, then the indication would have been that animals were added to the population, which may be the case when intensive recruitment of new individuals takes place between T1 and T2. Therefore, it is advisable that a method such as this should be implemented for periods when fishing is intense and recruitment is the lowest or in fisheries when recruitment is stable throughout the season.

The ideal situation for application of this method will be for those queen conch fisheries where there is a 100% compliance of no catch of immature conch. The methods could also be used in situations when a diving survey to estimate conch population density at the start of a given period (say the fishing season), then another survey is carried out for the same purpose at the end of the fishing season, and records of conch landings are well established including biological sub-sampling of landings for estimating mature and immature categories in the landings.

A continuous change-in-ratio (CIR) method for estimating stock exploitation rate using data from monitoring stocks continuously during fishing is presented by Claytor and Allard (2003). The exploitation rate is estimated by fitting a nonlinear model to ratios of exploited catch over total catch (exploited plus an unexploited reference class that could be accommodated to mature and immature references classes in queen conch) as a function of the cumulative exploited catch. A method to predict the impact of season length restriction on exploitation rate is presented by the above authors. The continuous CIR method can provide daily, local, and length-specific estimates of exploitation rate. For similar sample sizes, continuous CIR estimates are better than CIR estimates based on pre- and post-season sampling as presented above; however, it is data demanding in the sense that a permanent monitoring of the landings from each queen conch fishing ground is needed. This later requirement is due to the geographic identity of the conch that may generate animals with different age or size at first maturity; hence, violating the class separation in the CIR protocol.

Finally, variance estimates of the exploitation rate in equation 5.4.2.2 may be analytically estimated following application of the Delta method for variances of functions as explained in Paulik and Robson (1969). However, the variance of  $p1$ ,  $p2$ , and  $f$  need to be estimated under assumptions that may not be possible to validate in the case of the queen conch. Therefore, the most practical way to resolve the variance estimation protocol will be through bootstrapping (re-sampling with replacement) the samples



expressing the composition of mature and immature queen conch collected at times T1 and T2. In this manner, an exploitation rate will be estimated for each bootstrapped sample and assuming that 250 re-sampled samples are obtained, then the variance of the exploitation rate will be estimated with the standard formulation for random samples using the average value of the 250 bootstrapped exploitation rates. Confidence interval for the mean of the exploitation rate thus estimated can be obtained by using the standard deviation of the estimate (=square root of the bootstrapped variance).

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- Ross Claytor, R., and J. Allard. 2003. Change-in-ratio estimates of lobster exploitation rate using sampling concurrent with fishing. *Can. J. Fish. Aquat. Sci.* 60(10): 1190–1203.

#### 5.4.3. Disappearance rate and catchability estimation from tagging experiments

Tagging queen conch has been widely applied in the Caribbean region with mixed results. Among the main obstacles with tagging techniques is the very slow rate of mixing of tagged and untagged conch in a given fishing ground. This is due to the reduced mobility of the conch, which does not allow the level of mixing that is required for tagged and untagged conch such that the two categories exhibit the same probability of capture. Secondly, the type of tags has been an issue because those that are adhered to the shell by using epoxy or glues are usually shed, not detected when caught, or lost. If tagging methods are going to be used in the assessment of mortality and exploitation we recommend the use of a simple plastic tag with a color mimicking the conch shell color to reduce predation or disturbance and that this tag be tied around the shell at a point where the tie will not slide off the coiling shell (figure 5.14). Thirdly, many tags are recovered by fishers but never reported. This is especially notorious in those fisheries where divers crack conch out of their shells while still under water and only the edible meat is brought back to the boat.

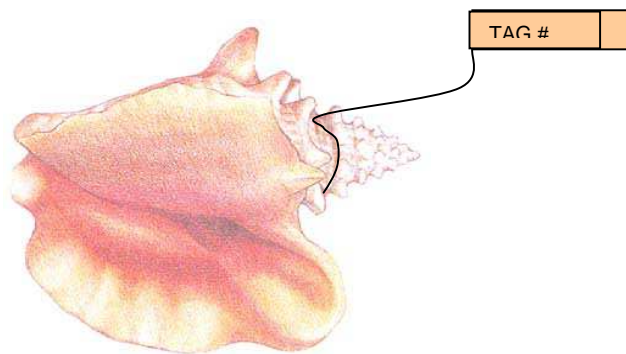


Figure 5.14. Diagram on how to attach a tag to queen conch

We include a method to estimate disappearance rates ( $D$ ) and catchability coefficient ( $q$ ) of queen conch. The disappearance rate ( $D$ ) includes the natural mortality rate, tag lost, burrowing behavior (i.e., divers do not see tagged conch when these are burrowed), etc. Emigration could be a factor in  $D$ ; however, due to the slow movements of queen conch we believe that emigration should not be a significant issue if tagging experiments are not carried out over long time periods. Catchability is the fraction of tagged stock captured per unit of fishing effort; therefore, the product of  $q$  times fishing effort is an estimator of the fishing mortality rate.

The model presented here was conceptually developed by Chapman (1965) and modified by Ehrhardt (1990) and adapted considering the characteristics of the queen conch fisheries and the biology of the species. Consider a tagging study implemented in a single fishing ground and consisting of a single tagging event. During this event  $T_0$  conch are captured, tagged, and released. It is recommended that the tagging protocol search for conch and tag-release them by spreading out the tagging effort over a wide area on the

fishing ground. Therefore, tag mixing is accomplished by spatially spreading out the tagging effort such that under the slow mobility of the conch accumulation of tags is avoided in a single release point. This initial tagged population ( $T_0$ ) will be available to the fishery in subsequent time periods (i). These time periods will need to be defined by the investigator(s) and the amount of fishing intensity will dictate the required time to accumulate tag returns (e.g., one or two months). Fishing effort ( $f_i$ ) will be exerted continuously during each i period and needs to be carefully recorded. Fishers should be fully aware of the tagging program and as far as possible they should be an integral part of the tagging program. It is expected that natural mortality continues to act with similar intensity upon tagged and untagged conch and that fishing will affect the tagged population in the same manner as the untagged population. Tagged conch retrieved by the fishing effort exerted during a period i will be classified as  $m_i$ . Consequently, abundance of tagged conch at the end of any time period i is given as

$$T_i = (T_{i-1}e^{-D} - m_i)$$

where D is the disappearance rate during time interval i. If the time intervals are short, say one month, average abundance of tagged conch during any time period i is approximated by the arithmetic average of  $T_{i-1}$  and  $T_i$ , thus given as

$$\bar{T}_i = \frac{T_{i-1}(1 + e^{-D}) - m_i}{2} \quad (5.4.3.1)$$

Also, the expected number of recoveries is expressed as

$$E(m_i) = qf_i\bar{T}_i$$

The maximum likelihood function modified from Chapman (1965) and assuming that the expected number of tag recoveries follows a Poisson distribution is given by

$$L = e^{-\sum_{i=1}^k qf_i\bar{T}_i} \prod_{i=1}^k (qf_i\bar{T}_i)^{m_i} / m_i$$

The maximum likelihood estimators for q and D are found by logarithmically transforming the previous equation and then differentiating natural logarithm of function L with respect to q and with respect to D. Setting the resulting equations to zero and solving for q gives

$$q = \frac{\sum_{i=1}^k m_i}{\sum_{i=1}^k f_i\bar{T}_i} \quad (5.4.3.2)$$

and solving for D gives

$$\sum_{i=1}^k q f_i \frac{d\bar{T}_i}{dD} = \sum_{i=1}^k \frac{m_i}{\bar{T}_i} \frac{d\bar{T}_i}{dD} \quad (5.4.3.3)$$

Replacing q from equation 5.4.3.2 in equation 5.4.3.3 gives

$$\frac{\sum_{i=1}^k m_i}{\sum_{i=1}^k f_i \bar{T}_i} \sum_{i=1}^k f_i \frac{d\bar{T}_i}{dD} = \sum_{i=1}^k \frac{m_i}{\bar{T}_i} \frac{d\bar{T}_i}{dD} \quad (5.4.3.4)$$

Partial derivatives in equation 5.4.3.4 are calculated for periods  $i = 1$  to  $k$  from functional forms developed from recursive equation 5.4.3.1 and given as

$$-\frac{d\bar{T}_1}{dD} = \frac{T_0}{2} e^{-D} \quad \text{for } i = 1$$

and

$$-\frac{d\bar{T}_i}{dD} = -\frac{d\bar{T}_{i-1}}{dD} - e^{-D} \left( \frac{d\bar{T}_{i-1}}{dD} - \frac{T_{i-1}}{2} \right) \quad \text{for } i=2 \text{ to } k$$

In the above equation  $D$  is the only unknown parameter and once the derivatives and  $T_i$ 's are estimated with an initial guessed value of  $D$  and introduced in equation 5.4.3.4, a numerical iterative solution can be achieved by using the GOAL SEEK function in TOOLS in EXCEL to solve for  $D$  in equation 5.4.3.3.

The following example will show the estimation procedure. Fishing effort statistics were collected from a conch fishing ground. These statistics were in diving hours measured as function of the number of divers, the average number of hours dived by diver in each fishing trip, and the number of fishing trips in period  $i$ . A total of 300 conch were tagged during a single tagging experiment; therefore  $T_0 = 300$ . The recaptures and fishing effort during two periods of 2 months each are given below,

Period $i=1$	Tagged conch recovered $m_1 = 30$ ; Fishing effort $f_1 = 1460$ dive-hrs
Period $i=2$	Tagged conch recovered $m_2 = 20$ ; Fishing effort $f_2 = 1200$ dive-hrs

Assuming  $D = 0.4$  as a starting value the following values for the derivatives and  $T_i$ 's are found

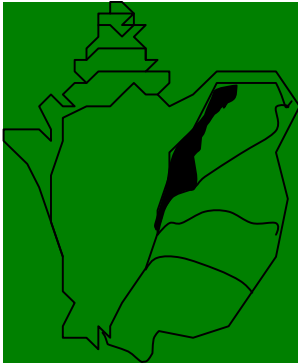
$$-\frac{d\bar{T}_1}{dD} = 132.7 \quad -\frac{d\bar{T}_2}{dD} = 359.5 \quad T_1 = 235.4 \quad T_2 = 188.3 \quad \bar{T}_1 = 267.7 \quad \bar{T}_2 = 211.8$$

With these quantities the sum of products and sums in equation 5.4.3.4 are estimated and the amount in the right of the equal sign in the equation is subtracted from the amount obtained in the left side of the same equation. The above calculations need to be implemented in a spread sheet in EXCEL. The cells with the value of the previous difference and with the initial value for D are used with GOAL SEEK function in TOOLS in EXCEL. When the GOAL SEEK windows appears in the screen in the “Set cell” command type the cell where the difference will be found. In the command “To value” in the GOAL SEEK window you should type the numeral zero. And in the command “By changing cell” in the GOAL SEEK window you should type the cell address where the initial value of D is found. Then press OK to get a solution for the value of D that satisfies both sides of equation 5.4.3.4.

The resulting value of D for the final iteration is 0.123, which is a disappearance rate every two months and for the length of the tagging experiment (i.e., 4 months). The value of q was found to be 0.0000768. Consequently, the fishing mortality rate for period 1 was  $F_1=0.11$  and for the second period  $F_2=0.09$ . If such tagging experiments are carried out in several occasions in the history of the fishery in a given fishing ground, then it will be possible to plot to trends in fishing mortality as well as disappearance rates. These estimates will be important sources of information to judge the impact of the catch on possible estimates of density and abundance that may also be obtained for such fishing ground.

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## 6. APPLICATION OF PRODUCTION MODELS TO QUEEN CONCH STOCK ASSESSMENTS

### 6.1 Introduction

The main purpose of a stock assessment is to provide indicators and reference points for the current state of the stock, the fishing mortality, and the reproductive capacity, which can be used to guide management decisions. Traditionally, queen conch stock assessments have been attempted by using methods developed for fish species. Due to fundamental differences in the population dynamics of gastropods such as queen conch relative to fish populations (as described in the biology section in Chapter 3) some of those methods have not proved suitable or applicable to conch. In some cases, the compliance with the basic assumptions required by the fish-based stock assessment methods cannot be adopted under the queen conch biological characteristics; in other cases, a careful review of the assumptions must be performed prior to the application to conch.

Data from queen conch fisheries around the Caribbean generally consists of bulk landings and of some measure of the effort exerted (i.e., number of boats, fishing trips, hours fishing, divers, scuba tanks) over a period of time. Information on the age or size composition of the catch is generally lacking, due to known difficulties in aging conch and to the diverse modality of the landings (i.e., whole with shell, semi-clean meat, clean meat). On occasion, there is also density and size frequency information from fishery independent surveys and tagging programs, which can be of extreme importance in the estimation of size/age composition and abundance indices. With these (limited) types of data, the options for assessment methodologies are restricted to production models and yield-per-recruit analyses.

There is consensus that the simplest and most appropriate models to set limit, precautionary, and target reference points for queen conch fisheries management would be biomass dynamics models (Medley, 2005). This section offers the option to use non-equilibrium production models as an assessment technique applicable to conch. A description of the main conceptual issues to be considered in conch assessment and management, an overview of biomass-dynamic models, a short description of the ASPIC software (Prager, 1994), the specific assumptions that need attention with conch fisheries,

the characteristics of the data required, the selection of modeling options, and the interpretation of results are discussed in this section. Worked examples are provided to demonstrate the use of ASPIC in conch stock assessments.

## 6.2 Conceptual issues in queen conch assessment and management

Essentially, there are four issues related to conch population dynamics and fisheries operations that need to be considered in production model assessments and in the definition and understanding of management benchmarks:

### 1) There is a need to develop and understand management benchmarks and reference points in the context of queen conch population dynamics.

Medley (2005) described the main data types, indicators of the state of conch fisheries (i.e., catch and effort, survey density, size frequency, tagging data), and useful reference points (i.e.,  $MSY$ ,  $F_{MSY}$ ,  $B_0$ ,  $F_{SPR}$ ,  $F_{opt}$ ). We know that recruitment success in conch depends on the copulation rate (or success of encounter of mates), which is greatly influenced by population abundance and density. When applied to conch, reference points based on spawner-per-recruit assumptions should consider functional aspects among population densities, copulation success, and recruitment throughput under different exploitation regimes. Thus, the fishing mortalities that generate target and limit densities should be used as an alternative to  $F_{SPR}$  benchmarks (Figure 6.1). In reality, the data to support the development of a spawner-recruit relationship for conch –and appropriate reference  $F_{density}$ – is still insufficient, but such benchmarks should be considered in the future.

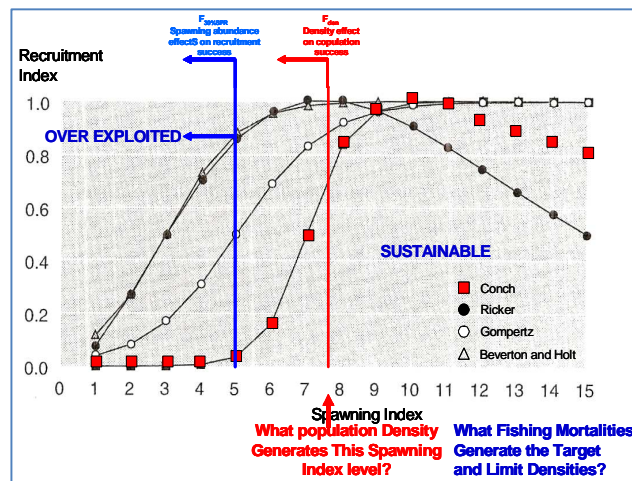


Figure 6.1. Comparative diagram of standard (fish) and conch spawner-recruit curves showing the positioning of target lines under a standard (fish) population reproduction scheme and a likely conch population internal reproduction.

Reference points from biomass-dynamic models, however, can have a wide application to conch fisheries management if the following issues are considered:

## 1) Population growth assumptions

Conch populations do not follow a logistic population growth as a consequence of the abundance and density factors affecting the reproductive potential. A steep Gompertz generation function is more likely to represent population growth in this species. The logistic model assumes that the maximum rate of production occurs at a biomass level corresponding to half the unfished biomass. In the Gompertz model the inflection point (of maximum production) occurs at lower biomass levels, under which the population tends to extinction (due to threshold abundance/density).

In consequence, reference points generated from biomass-dynamic models, such as the unexploited biomass,  $MSY$ ,  $f_{MSY}$ , and  $B_{MSY}$  differ under the logistic and Gompertz assumptions. Limits and targets should be set at lower values, corresponding to the  $MSY$  where optimum density and abundance (for optimum reproductive success) occur (Figure 6.2).

## 2) Hyperstability in conch CPUE

The spatial pattern of abundance and fishing effort and the relationship between abundance and capture success are combined into an aggregate catch-per-unit effort. CPUE is a crucial piece of information in biomass-dynamic models, and is commonly used as an index of abundance. The default assumption is that CPUE is directly proportional to abundance, which is the case when fishing effort is random with respect to the fished stock. In another pattern, known as hyperstability, CPUE drops slower than abundance at high abundance, which is expected at small spatial scales when handling times are large and the search is not random (Hilborn and Walters, 1992) (Figure 6.3).

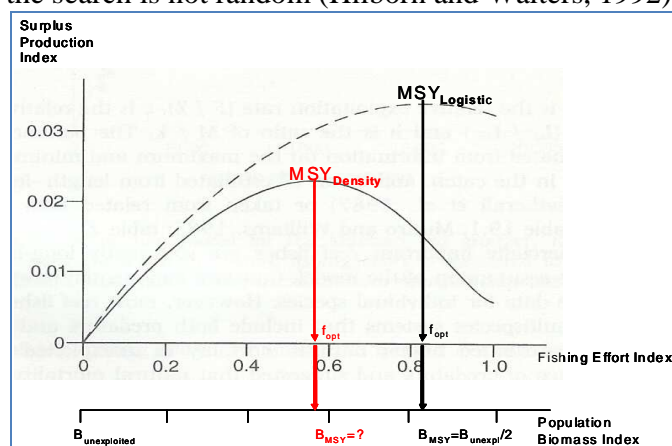


Figure 6.2. Comparative diagram of a fish and a conch surplus production curve showing the positioning of  $MSY$  under a standard logistic fish population growth and a likely conch population growth.



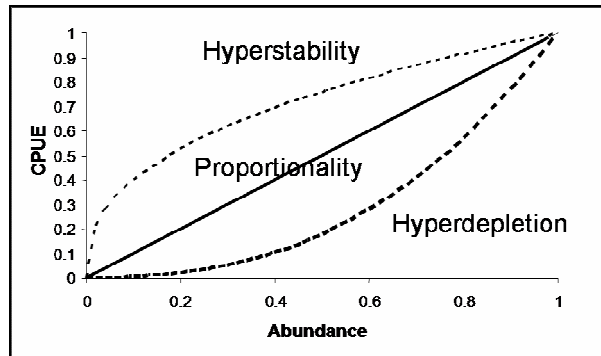


Figure 6.3. Hyperstability of catch per unit of effort and average population abundance when fishing on an aggregating conch population during reproduction.

In conch, hyperstability is more likely than proportionality because:

- Effort is targeted to areas of high density (i.e., sea-grass patches, spawning aggregations) due to slow individual movements. These areas are well-known by fishers, they start the search for new fishing grounds once an area has been depleted.
- Density is not related to abundance but to the extent of localized habitat.
- There are confounding biomass utilization and fishing capacity trends:
  - *Gear saturation effects at high abundances.* There are places where fishers can't handle more conch (due to gear limitations) or only catch the amount that they can sell.
  - *Effort sorting.* When abundance drops, only the best fishers keep fishing (i.e., those with greater technical efficiency such as newer/larger/ better vessels and diving gear, more operators, etc.). This would apparently reduce the fishing effort exerted (increasing CPUE), but the fishing power of fewer, selected fishers may overcompensate for the effort reduction.
  - *Covariation of effort with stock size in seasonal fisheries.* Some conch fisheries are seasonal, and increase the amount of effort during the warmer months, when easy to detect, high-density spawning aggregations are formed. Other fisheries increase effort when the lobster season is closed. In these cases, effort is not applied randomly, and is directly correlated with density or stock size.

### 3) Catch and effort data from different fishing grounds.

*Ecological fidelity.* Some adjacent conch fishing grounds display the characteristics of an individual stock (ecological fidelity), with marked differences in growth, size, natural mortality, and reproduction. However, catch and effort data generally pertain to a mixture of adjacent grounds, thus, the main assumption of a 'unit of stock' of production models is broken. Differences in population dynamic processes within each bank are ultimately reflected in the productivity of each stock. If catch comes from different stocks, then the basic production function ( $Biomass = Recruitment + Growth - Natural Mortality - Catch$ ) does not hold and production models may fail or give unreliable estimates.

*Morphological differences among adjacent fishing grounds.* One important difference among fishing grounds contributing to the same fishery is that there can be marked differences in the rate of individual growth, the maximum size, and the shape of the conch shell. Such differences have been reported even in contiguous banks, where climatic and oceanographic conditions are relatively similar (e.g., in islands and banks of the Bahamas, pers. obs.). This situation necessarily leads to the capture of individuals of a wide range of ages and stages of maturity, which is especially worrisome for the smallest individuals captured. Biomass-dynamic models treat all ages and sizes as undifferentiated biomass (already an oversimplification of age-structure), but the fact that the age/size structure of the catch is really so diverse, coming from different sub-stocks represents an additional problem. In fact, the individuals forming this undifferentiated biomass are not only of different ages, but may also have very different sizes of maturity, mortalities, and longevities.

### **6.3. Biomass Dynamics Models**

#### **6.3.1 An Overview**

Biomass dynamics or surplus production models are one of the simplest tools which can be used to characterize the status and productivity of a fish or shellfish population, as they require only a time series of catch and effort or relative abundance data. These models are particularly useful when the age-structure of the catch is unknown or limited. With key indicators of biomass change (e.g., CPUE, catch, effort, survey abundance), it is possible to derive estimates of variables that can be used as a reference for management advice: the current biomass ( $B_{cur}$ ), the pre-exploitation size ( $K$ ), the intrinsic growth rate ( $r$ ), the maximum sustainable yield (MSY), and the fishing effort at which MSY is achieved ( $f_{MSY}$ ). The key reference points are the biomass and the fishing mortality level at MSY. Management measures to rebuild a stock are implemented when biomass falls below  $B_{MSY}$  or fishing mortality exceeds  $F_{MSY}$ .

#### **6.3.2. Main assumptions and basic equations**

- 1) Unit of stock: the (fished) population is isolated, and closed to immigration and emigration.
- 2) All individuals in the stock are identical: growth, death, and birth rates are the same for all ages and sizes.
- 3) There are instantaneous responses to any changes in exploitation rates (i.e., no time lags).
- 4) The stock is in equilibrium state.
- 5) Changes in the biomass of a fish stock from one year to the next are caused by the interaction of four competing factors:

$$Biomass_{y+1} = Biomass_y + Recruitment + Growth - Natural Mortality - Catch \quad (1)$$

Recruitment of new individuals and tissue growth are sources of increase (production); natural and fishing mortality are sources of loss. The term 'surplus production' refers to the amount the population will increase in the absence of fishing, or

the amount of catch that can be taken while maintaining the biomass at a constant size (Hilborn and Walters,1992).

The effects of recruitment, growth, and natural mortality are combined into a single production function. Changes in stock size from one time period to the next are assumed to be the difference between this function and the catch by the fishery:

$$B_{t+1} = B_t + f(B_t) - C_t \quad (2)$$

with

$$\hat{I}_t = \frac{C_t}{E_t} = qB_t \quad (3)$$

where  $B_{t+1}$  is the exploitable biomass at the start of the following year,  $B_t$  the biomass at the start of year  $t$ ,  $f(B_t)$  is the biomass-dynamic as a function of current biomass,  $C_t$  is the catch (in biomass) during year  $t$ ;  $\hat{I}_t$  is the index of relative abundance estimated by the model,  $E_t$  is the fishing effort exerted, and  $q$  is the catchability coefficient. Equation (3) constitutes a very strong assumption: catch rates are linearly related to biomass.

### 6.3.3. Different production models

The main difference among biomass-dynamic models is the function describing the production of biomass  $f(B_t)$ , based on distinct population growth assumptions: logistic, exponential (Gompertz), and hyperbolic. The following biomass-dynamic forms are the most common:

$$f(B) = \begin{cases} rB \left(1 - \frac{B}{K}\right) & \text{Schaefer (1954) - Logistic} \\ rB \left(1 - \frac{\ln B}{\ln K}\right) & \text{Fox (1970) - Exponential (Gompertz)} \\ \frac{r}{p} B \left[1 - \left(\frac{B}{K}\right)^p\right] & \text{Modified Pella - Tomlinson (1969) - Hyperbolic} \end{cases} \quad (4)$$

where  $B$  is the current biomass,  $r$  is the intrinsic growth rate,  $K$  is the virgin biomass ( $B_0$ ) prior to exploitation, and  $p$  is the shape parameter of the Pella-Tomlinson (or Generalized) form, which permits asymmetry in the surplus-production curve and conveys the flexibility to represent the different biomass-dynamic models. If  $p=1$ , the function is equivalent to the symmetric Schaefer (or logistic) form; if  $p$  tends to 0, the function is equivalent to the Fox form; if  $p<1$  the function is skewed to the left, and if  $p>1$ , it is skewed to the right (Hilborn and Walters, 1995). These shapes are represented in Figure 6.4.

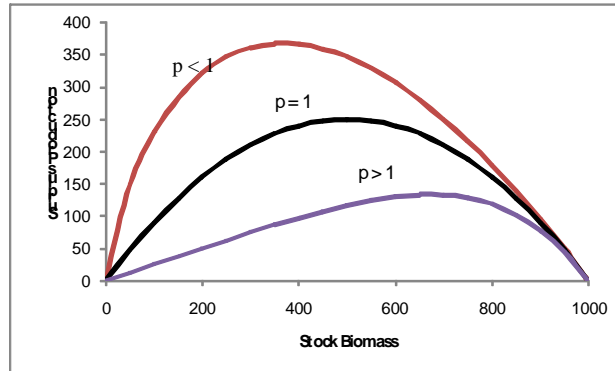


Figure 6.4. Shape of the Pella-Tomlinson biomass dynamic model with different values of parameter  $p$ .

#### 6.3.4. Selection of a population growth model for conch

Considering the characteristics of conch population dynamics and the reproductive issues associated to stock density and abundance, the Gompertz population generation function would best describe conch behavior. This function is useful to describe population growth in confined space situations. Conch habitat patches can be regarded as confined spaces with limited resources (including the availability of mates at low abundance/density). The curve has a sigmoidal, asymmetric shape that allows for slow initial growth, followed by an accelerated (exponential) period of growth, and then slow growth as resource limits are reached. The inflection point (of maximum growth) represents the critical biomass under which the population tends to extinction due to recruitment failure. The exponential (Fox) model assumes the Gompertz growth function, resulting in an exponential relationship between fishing effort and population size, and asymmetrical yield curves (Fox, 1970, 1975) (Figure 6.5). This model would be the most appropriate for production modeling of this species.

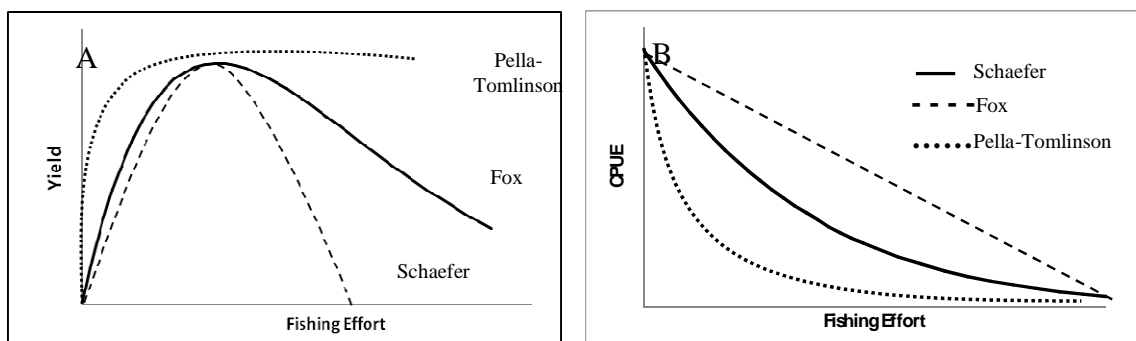


Figure 6.5. Hypothetical comparison between the Schaefer, Fox, and Pella-Tomlinson models of the relationships (A) fishing effort and equilibrium yield, and (b) fishing effort and CPUE.

### 6.3.5. Equilibrium vs non-equilibrium estimators

Equilibrium estimators assume that the population is in equilibrium. This means that the rate of change in biomass is zero so that  $B_{t+1}=B_t$  in equation (2) and the observation model is exact ( $I_t=qB_t$ ). In real populations, these assumptions do not hold. Equilibrium methods tend to produce optimistic assessments of stock status, with biased estimates of MSY and  $f_{MSY}$ . It is recommended that these estimators not be used, except for comparison with previous assessments (Hilborn and Walters, 1996).

Dynamic methods are those which do not make the equilibrium assumption. The three main types are process-error, observation-error, and total least squares estimators, that involve adding error to the population growth and the observation model functions – a more realistic assumption-. Observation error methods are considered to be the best estimators. A good description of all these estimators and the criteria for selection are provided in Hilborn and Walters (1996).

### 6.4. Data requirements and requirements of the data

The data needed to apply biomass-dynamic models to queen conch include: a time series of historic yield (catch in biomass) and a corresponding time series of relative abundance estimates (nominal or standardized CPUE and/or fishery-independent index). Recommendations for conch data collection programs as the basis for management are provided in Medley (2005). A description of the desirable characteristics of the data follows.

#### 6.4.1 Catch and effort data

The main problem with conch fisheries is the lack of formal statistical systems collecting appropriate catch and effort data. If one or more databases are available, the following recommendations are important to integrate and clean the information needed for production model assessments of queen conch.

- 1) Data from all available sources: commercial, recreational, and subsistence fisheries should be combined to estimate total catch and total fishing effort.
- 2) All the recorded catch and effort data should be converted to the same units (e.g., kilograms, metric tons, pounds, days, hours fishing, number of boats, etc.).
- 3) Verify if the landings represent conch landed whole, without the shell (unprocessed tissue), or clean meat. Catch data for the whole time series and from all sources should be converted to the same units, generally clean meat weight.
- 4) Conversion factors to transform tissue and total weight to meat weight should be developed for each fishery. Use conversion factors from neighboring stocks if no local morphometric relationships exist.
- 5) Consider other sources of error in the estimation of catch: underreporting and discarding. If there is clear evidence of underreporting (e.g., registered fishers vs fishers reporting), the catch can be raised in the corresponding proportion.
- 6) Select an appropriate unit of effort that is consistent across the time series. In conch fisheries, common effort units are: number of trips, boats, divers, diving tanks used,

days/hours fishing. With limited data, it is recommended that the number of boats or the number of trips be used.

7) Consider the significance of the effect of the geographical affinity of conch: fishery data can be accumulated over many fishing banks, with different productivities. Applying a production model to a mixture of data from truly different stocks creates a real problem regarding population generation rates in the production models. This issue is paramount in the application of these models to conch fisheries.

#### **6.4.2 Catch rate (CPUE) data**

Catch rate (CPUE) data are often the only information on the relative abundance of a conch population. The simplest way to estimate a time-series of nominal CPUE is to divide the landings taken by all boats targeting the stock by the effort exerted by those boats.

The use of CPUE as an index of relative abundance requires careful selection of the unit of effort, so that an increment in effort results in a proportional increase in catch. In conch fisheries, there are several issues with the estimation of effort and catch rates (Valle-Esquivel, 2002a, 2002b, 2003; McCarthy, 2007; Díaz, 2007):

- There may be considerable differences in the fishing power of the boats, related to size (*i.e.*, dingy boats *vs* large commercial vessels with 50-100 divers), the engine horse power, the gear used (scuba *vs* free diving), the depth fished, the time spent fishing.
- Fishing power may increase over time due to technological advances.
- Conch may not be the only target in multispecies trips: divers often spearfish and hunt lobster on the same trip and may change their behavior in response to local conch densities.
- Catch records may represent multiple trips.
- There are spatial patterns of abundance (*i.e.*, spawning aggregations) and fishing effort (fishers concentrate on high-density patches).
- Some boats may spend considerable time searching for aggregations, while others may spend most time fishing if the aggregation was located at an earlier expedition.
- Handling times may be significant, since conch are generally processed at sea.

To account for some of these sources of uncertainty and to homogenize effort when fishing power is variable, standardization of catch rates is recommended. When data sets are incomplete or lack the necessary level of detail regarding the fishery operation, nominal catch rates should be used.

#### **Standardization of catch rates**

Nominal catch rates obtained from catch and effort data can be standardized to calculate relative indices of abundance over time. The purpose of this standardization procedure is to investigate the influence of categorical variables on catch rates and to identify possible sources of extraneous variation that may be masking true trends in stock biomass or abundance.

Generalized linear mixed models (GLMM) are commonly used to estimate relative indices of abundance, and queen conch is no exception (Valle-Esquivel, 2002b;

McCarthy, 2007a,b). Two different methods have been tested in cases where conch is part of a multi-specific fishery: GLM and delta-lognormal models (Lo et al., 1992).

1) GLM models use only the positive CPUE observations of the target species (i.e., the trips where a certain amount of conch was caught) to standardize the catch rates.

2) Delta- lognormal models estimate separately: 1) the probability that a given trip is successful in catching the target species (proportion of positive trips), and 2) the mean catch rate of positive trips. CPUE is modeled as the product of these two components. Four main steps are involved in the standardization of catch rates (Valle-Esquivel, 2005):

1. *Identification of categorical variables.* Consists in conducting a thorough examination of the main factors present across a data set that may have an influence on CPUEs (positive observations) or on the probability of harvesting queen conch in any given trip (proportion of positive trips or success). Examples of factors to be considered in conch CPUE analysis include: year, season/month, island or shelf, area/region/coast, type of vessel, average depth of fishing, gear type, target species (i.e., conch trip vs. multi-species trip).
2. *Identification of levels within categorical variables.* Relevant “categories” or levels are created from continuous or nominal information within each factor to obtain a balanced statistical design (e.g., creating 4 seasons of the year from the 12 months available, or creating depth ranges rather than actual measurements). Other examples of levels include:

FACTORS	# LEVELS	LEVELS
YEAR	19	1983-2001
MONTH	12	1-12
SEASON	4	1-4
COAST	7	1-7
GEAR	3	1 (Spears), 2 (Skin diving), 3 (Scuba)
TARGET	2	0 (not conch trip), 1 (conch trip)

3. *Selection of categorical variables.* Stepwise regression procedures are used to determine the set of factors and interactions that significantly explain the observed variability. Factors are added sequentially to the model based on statistical criteria. The *year* factor should always be included because a time series is desired. Fixed factors and fixed and random interactions are evaluated under the same criteria and added to the model.
4. *Fitting Generalized Linear Models.* The final generalized linear model (GLM) under a Delta-Lognormal or Lognormal assumption is fit to the data with sophisticated computer algorithms (e.g., Legault and Ortiz., 1998; Ortiz et al. 2000, 2001) that can estimate standardized catch rates with confidence intervals.

Disadvantages of catch-rate standardization: 1) Requires detailed time-series of fishing effort. 2) Requires extensive data-base handling. 3) Requires an advanced level of expertise in the use of linear modeling techniques and statistical software packages. 4) Many (sometimes subjective) restrictions have to be imposed to the data to develop these indices such as: years included, gears included, upper and lower limits to CPUE values, definition of directed trips (targeting or not targeting conch) and successful trips (minimum amount of conch landed), fishing areas included, only records for single trips,

etc. (Valle-Esquivel, 2002). 5) Selection of factors and interactions is a laborious, cumbersome process. 6) Nominal and standardized catch rates may be very similar when data is limited. 7) Determining terms in the GLM models based purely on statistical criteria can lead to biased indices.

### **Contrast in the CPUE series**

The ability of any biomass-dynamic model to provide reliable results depends on the exploitation history of the fishery. There must be historical variation in stock size and fishing pressure to estimate reliable parameters of the biomass-dynamic models. Enough contrast in the CPUE data can provide information about the rate of growth ( $r$ ), the catchability coefficient ( $q$ ) and the unexploited biomass ( $K$ ). To be informative, the data should ideally include CPUEs at low stock sizes with low fishing effort (to estimate  $r$ ), CPUEs at high stock sizes with low fishing effort (to estimate  $Kq$ ), and CPUEs at high fishing effort (to estimate  $q$ ). It is very difficult to have data that represent all of these situations, but this ideal contrast should be sought after to construct reliable data-series. Common patterns observed in catch rate time series include (see Hilborn and Walters, 1992 for details):

- 1) One-way trip: effort increases gradually and catch rate declines continuously; not informative, provides uncertain to poor estimates.
- 2) Increasing effort followed by a period of decreasing effort: more informative, provides reasonably uncertain to good estimates.
- 3) Good contrast between CPUE and effort: high variation in CPUE and effort and rapid changes back and forth between high and low effort levels; provides best estimates, with some uncertainty.

Data from conch fisheries are likely to follow a one-way trip or increasing, then decreasing effort patterns. If a fishery has no time series, a short time series, or if the time series does not include both depletion and recovery periods, then a production model assessment cannot be applied (Medley, 2005). If a reasonable time-series exists, but there is a clear lack of contrast in the data to provide estimates of the three model parameters ( $r$ ,  $q$ , and  $K$ ), then it is possible to fix one of them to a value based on auxiliary information, such as knowledge of the biology of the species or similar species, abundance surveys, or tagging studies.

### **6.4.3 Fishery independent survey data**

Relative abundance indices from survey data are very useful for production model assessments because they can be used as alternative when CPUE proves unsuitable, in combination with CPUE, or as auxiliary information for the estimation of biomass. Recommendations to conduct conch surveys are provided in Medley (2005), and detailed methods to estimate population density and standing stock abundance are given in Section 4.



## 6.5. Recommended Software for Biomass-Dynamic Assessments: ASPIC

The ASPIC software<sup>1</sup> is a set of computer programs developed by Prager (1994) to estimate parameters of a non-equilibrium surplus-production model from fisheries data. It includes the option to fit the Schaefer, Fox and the generalized (Pella-Tomlinson) models. ASPIC incorporates various extensions to classical production models, including:

- Analysis of several simultaneous or sequential fisheries on the same stock.
- Partitioning fishing mortality by gear, time or area.
- “Tuning” the model to one or more biomass indices.
- Generalized estimation with more than one data series.
- Estimating missing values of fishing effort.
- Computing confidence intervals on reference points (e.g.,  $MSY$ ,  $f_{MSY}$ ,  $B_{MSY}$ ) via bootstrapping.
- Estimating projected trajectories of population biomass and fishing mortality rates.
- Constructing nonparametric tests of hypotheses about changes in catchability.

Input for this software includes a time series of yield (catch in biomass), one or more corresponding indices of abundance or effort series, and starting guesses for model parameters:  $K$ , the carrying capacity of the population;  $B_1/K$ , the starting biomass ratio;  $MSY$ , the maximum sustainable yield; and  $q$ , the catchability coefficient. Model outputs include maximum-likelihood estimates for these parameters, derived management benchmarks:  $B_{MSY}$ ,  $F_{MSY}$ ,  $f_{MSY}$ , and relative estimates of biomass and fishing mortality with respect to  $MSY$ :  $B/B_{MSY}$ ,  $F/F_{MSY}$ . A formal description of the theory behind ASPIC is given in Prager (1994).

## 6.6 Running ASPIC

Detailed instructions to operate the software, create input files, and handle and interpret the information from output files are given in the User’s Manual for ASPIC (Prager, 2004). This describes the key steps (based on the authors’ experience) needed to operate ASPIC and to run it with simple (conch) examples<sup>2</sup>.

- The ASPIC suite includes a main program to fit a non-equilibrium production model and several utility programs (ASPICP, FTEST, AGRAPH) to make projections, compare models, and make graphs, respectively (Prager, 2004). Only ASPIC and ASPICP are used in the examples that follow, but the other programs should also be explored for further analyses.
- ASPIC has three modes of operation. Only FIT and BOT are used here.
  - In FIT mode, ASPIC fits the model and computes point estimates of parameters and quantities of management interest, including time trajectories of fishing

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<sup>1</sup> The ASPIC software<sup>1</sup> (Prager, 2008) is freeware available online at <http://www.sefsc.noaa.gov/mprager/aspic.html>

<sup>2</sup> NOTE: This quick guide is not endorsed by the original author or NOAA-Fisheries and should not replace the official instructions provided in the User’s Manual for ASPIC (Prager, 2004).

- intensity and stock biomass. In BOT mode, ASPIC fits the model and computes bootstrapped confidence intervals on estimated quantities; execution time increases. In IRF mode, ASPIC conducts an iterative fit for analysis of 2 or more series.
- Analysis begins with FIT mode, including several runs to attain convergence and explore different model structures. After selecting model and data structure, BOT can be used to estimate uncertainty in assessment results.
  - The latest ASPIC version (ver. 5.x) has the option to fit the generalized model (Pella and Tomlinson, 1969) in addition to the logistic production model (Schaefer, 1954, 1957). The Fox (1970) model can also be defined in ASPIC as a special case of the generalized model (FOX option), by fixing the shape parameter to appropriate values.

Some recommendations (after Prager 2004) to operate the program are:

- Read the instructions on the user's manual (Prager, 2004) carefully.
- Plot the data to visualize trends.
- Modify existing input files rather than creating new ones and save with a different name. ASPIC inputs are very detailed, so it is recommended to follow the pre-established format to avoid errors. Follow the instructions to fill out each line of input precisely.
- **Starting guesses and bounds** – The model is very sensitive to initial parameter values, so they must be approximated the best possible way. If no prior information is available (e.g., values from previous assessments, absolute abundance estimates from surveys) use the options given in the manual to calculate starting guesses:
  - $B_1/K$ - Based on the belief about the stock's condition at the start of the data set with respect to the carrying capacity. Use a positive value  $0 < x < 1$ . A reasonable default is 0.5, but estimates are often imprecise, so the value can be fixed to 1 or to a range of fixed values.
  - $K$ - A real number 2-20 times the largest recorded yield.
  - $MSY$  – Use half the largest yield.
  - $q$  – Use  $q < 0.01$ . It is the catchability coefficient in catch-effort data series and in biomass index series it is the constant that relates the index data to biomass.
  - Start trials with wide enough bounds to encompass all possible values, then use more restrictive bounds.
  - If starting guesses are wrong, the model does not converge and the estimate may hit a bound. The ASPIC report (\*.fit) will indicate whether the starting guess was too low or too high.
  - If convergence is difficult, try a range of fixed values for one parameter and allow ASPIC to estimate the rest of the parameters. Once convergence is attained, narrow down the range for the fixed parameter, and run again.
  - After several runs with fixed values of one or more parameter combinations, the resulting biomass trajectories may provide consistent estimates of present stock status for management purposes.
  - Change starting guesses after using FIT mode, and before using the BOT mode. It is advisable to generate point estimates in FIT mode before using BOT mode.

- Repeat trials with several random number seeds.

- **Precision of parameter estimates:**

- Estimates of  $MSY$ , optimum effort ( $F_{MSY}$ ), and relative levels of stock biomass are more precise than absolute biomass,  $F$ , and  $q$ ,  $K$ , or quantities that depend upon them.
- Absolute estimates of  $B_t$ ,  $F_t$ , and  $B_t/K$  from ASPIC are not intended for use as management benchmarks.
- Trends in the relative abundance and fishing mortality trajectories, rather than point estimates of the parameters should be used as references for management.

- **Fitting criteria:**

- The model converges when the objective function is optimized. A message appears at the end of the screen output indicating that ASPIC ended normally. The ASPIC report includes the message ‘Normal convergence’.
- The model may also converge when it finds local minima, rather than the global minima. Check the output to find if the results are reasonable. Several trials with a range of initial guesses for each parameter must be performed to avoid local minima.
- The model may fail to converge when there is a poor agreement between the model and the data or when the starting guesses are out of range. Error messages appear indicating that a parameter is near the bounds or that results are trivial.
- If the objective function appears (from the screen output) to have been near convergence, try an ASPIC run using the previous run’s results as starting guesses.
- The last resource to attain convergence is to set one parameter (usually  $B_t/K$ ) to a range of fixed values and to analyze the different solutions.
- A quick examination of the fit to  $CPUE$  ( $r^2$  value) and of the  $B$  and  $F$  trajectories provided in the output files often helps to know whether the model converged or if the fit is good.

- **Determination of stock status:**

The goal of stock assessment is to determine whether the stock is overfished or if overfishing is taking place. A diagram of a limit control rule (or phase plot, Figure 6.6) is a useful tool to determine stock status, and to assess the performance of management actions. The stock is **OVERFISHED** if biomass falls below the Minimum Stock Size Threshold (MSST) [a proxy of  $MSST/B_{MSY} = 1-M$  (natural mortality rate)]. **OVERFISHING** occurs if a stock exhibits fishing mortality rates greater than  $F/F_{MSY}$ , equivalent to the Maximum Fishing Mortality Threshold (MFMT). Any combinations of relative  $B$  and  $F$  above or to the left of the limit control rule are situations to be avoided; combinations to the right and below the limit control rule line are acceptable and sustainable.

## 6.7 Examples: Fitting ASPIC to queen conch data

If a time series of catch, effort, and/or relative abundance index exists, and there is enough contrast in the data to represent different stages of the stock and the fishery, it should be possible to fit ASPIC. The purpose of this section is to illustrate the use of the ASPIC software to perform production model assessments of queen conch. Guided examples are presented, using some of the options that are useful to analyze fishery data for this species.

Examples<sup>3</sup> are used to illustrate ASPIC assessments with: 1) simulated and 2) real conch fishery data. The objectives, in each case are to:

- 1) Simulated data- Present a case where adjusting the model is relatively simple, and assessment results can be evaluated directly by comparison with the simulated stock.
- 2) Real data- Apply the model to a real queen conch assessment and show the difficulties that the (ASPIC) analyst can face when confronted with real (conch) data, which may be limited and may not conform entirely to the model assumptions.

### 6.7.1 Conch simulated data

The examples in this section are based on simulated data. The behavior of the stock and the fishery are modeled after queen conch population dynamics and fishery operations. The hypothetical stock was generated using the Gompertz function under the equilibrium Fox production model [generalized form (Equation 5), with shape parameter  $p > 0$ ; see sections 6.3.3 and 6.3.4]. Parameters for the base model were calculated using equilibrium estimators for the Pella-Tomlinson form of the biomass-dynamic function (see Appendix A in Hilborn and Walters, 2005). The ranges for fishing effort and yield are loosely based in the Puerto Rican fishery (Valle-Esquivel, 2002a,b; McCarthy, 2007), as presented in the real case example. Fishing pressure is applied monotonically, through a constant increase in fishing effort.

Simulated data consists of a conch population (in biomass), yield, effort, and catch rates. Two data sets are derived from the base-case production model: (1) deterministic data, and (2) stochastic data. An ASPIC stock assessment is performed in each case and results are compared. Results from the stochastic case are subsequently bootstrapped to obtain confidence intervals of the parameters. These examples illustrate the use of main ASPIC program modes FIT and BOT and the option to select the model shape (appropriate for conch). Also, program ASPICP is used to project the bootstrapped population under two different management regimes: TACs (total allowable catch) and effort controls. The concepts of “overfishing” and “overfished” are introduced in the context of production model analysis. Finally, the interpretation of phase plots (Figure 6.6) is provided with the examples.

#### Base Model

The parameters of the generalized Pella-Tomlinson biomass dynamic model used for the simulation of conch fishery data are given in Table 6.1. The resulting surplus

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<sup>3</sup> Example input and output files are provided in the attached disk, under the ‘Conch ASPIC files’ folder.

production, yield and CPUE curves of the Fox model are illustrated in Figure 6.7. This base model was used to generate a ‘realistic’ subset catch and effort data.

### 1) Deterministic example

Consists of a subset of catch, effort, and CPUE index data drawn from the base-case Fox production model, and attempts to represent a plausible (i.e., realistic) range of values. Effort is constrained between 500 and 12,000 units, which produce yields between 250 and 900 metric tons per year (assuming each catch unit equals 1kilogram). Beyond that effort, yield and CPUE would be greatly reduced, so a fishery is not likely to continue expanding effort under those circumstances (Figure 6.7). A 24-year time series with constantly increasing effort was constructed (Table 6.2, Figure 6.8).

### Inputs/Options

- Input file: ‘Fox\_conch1.inp’
- Program mode: FIT
- Model shape: FOX
- Base-model parameters  $K$ ,  $q$ ,  $MSY$  (from Table 6.1) can be used as a reference for starting guesses. Give  $K$  and  $MSY$  reasonable ranges based on the (known) hypothetical population (Figure 6.7). \*\*Note: this not an option in real cases because the population is not known; seeking these parameters is the goal of the assessment. Other options to calculate starting guesses and bounds are given in Section 6.6.

### Results and Interpretation

- Output: ‘Fox\_conch1.fit’
- Parameter estimates are given in Tables 6.3 and 6.4, and resulting CPUE, relative biomass and fishing mortality trajectories are shown in Figure 6.9
- Normal convergence is attained, with the Fox model providing a better fit than the logistic (see values of the objective function in the comparison of Logistic and Fox models) (Table 6.3).
- The fit of the model to CPUE data is excellent ( $R^2$  in CPUE= 0.997). Observed and estimated values of CPUE are nearly identical because the data are simulated, and was generated with the same functions used in the ASPIC estimator.
- Resulting ASPIC trajectories (Figure 6.9) show that CPUE declines exponentially as a result of monotonically increasing effort under the Fox model. This effort trend is also reflected upon the relative fishing mortality trend, which also increases at a constant rate. Relative  $F$  crosses the  $F_{MSY}$  level in 1990, and shows that OVERFISHING ( $F/F_{MSY} > 1$ ) is occurring since then.
- The yield trajectory shows that yield exceeded  $MSY$  between 1986 and 1997.
- CPUE is an index of relative abundance, thus the trend in absolute biomass with respect to  $MSY$  follows the same trajectory, with an exponential decline in abundance.
- From 1992 onward, absolute biomass falls below the biomass at  $MSY$ , and reaches very low levels by the end of the time series.
- This trend ( $B/B_{MSY} < 1$ ) indicates that the stock is OVERFISHED since 1992.

## 2) Variable data example

Consists of the same set of deterministic data, with added random variability in catch (C.V.=15 %) and CPUE. Only a set random catch was used in this example. The purpose of this scenario is to add noise to the data to present a more realistic case and to verify if ASPIC converges to similar values as in the previous example, and approaches “reality” (the simulated population in this case).

### Inputs/Options

PROGRAM	ASPIC	ASPIC	ASPIC	ASPICP
Mode	FIT	FIT	BOT	
Description	Point estimates	Point estimates	Bootstrapped estimates	Projections of management controls
Model shape	LOGISTIC	FOX	FOX	
Input Files	Logistic_conch2.inp	Fox_conch2.inp	Fox_conch2_boot.inp	2a) Fox-conch2a-boot.ctl 2b) Fox-conch2b-boot.ctl
Output Files	Logistic_conch2.fit	Fox_conch2.fit	Fox_conch2_boot.bot Fox_conch2_boot.bio Fox_conch2_boot.det	2a) Fox-conch2b-boot.prj 2b) Fox-conch2a-boot.prj

- With the initial guesses provided for the parameters, normal convergence was attained, with the Fox model providing a better fit than the logistic (Table 6.3). In this example, the logistic and Fox models were fit separately, although a comparison of fit and parameters is made automatically when the Fox shape option is used.
- The Fox exponential-yield model showed a better fit (Table 6.4). A bootstrap run was performed with the results from this model, providing parameter estimates, and 50%, and 80% confidence intervals (Table 6.5). The bootstrap option (BOT) produces a main output file (\*.bot) and 2 additional outputs (\*.BIO, and \*.DET), which are later used in ASPICP.
- ASPICP was used to project the bootstrapped model for 10 years under 2 management scenarios:  
2a) Catch quota: uses constant catch at 50% of last year ( $C=50\%$  of  $C_{2006}=1.7E+05$ ).  
2b) Effort control: uses a gradual reduction in fishing effort of 10% for 5 years, and 5% thereafter. This strategy reduces effort to 20% of the 2006 value by the end of the management period (year 2017).
- Projections of the yield or the effort from the final year of data (2006) are not presented, as maintaining those (unsustainable) fishing mortality levels causes the hypothetical stock to collapse, with very limited possibility of recovery.

### Results and Interpretation

- Resulting ASPIC trajectories (Figure 6.9) show similar trends to Example 1, with some fluctuation around the estimated CPUE, relative biomass and relative F. Relative F exceeds the FMSY level in 1988, and shows that OVERFISHING ( $F/FMSY > 1$ ) has been occurring since then. Fluctuations in relative F and B values indicate that the model

captured the observed variability in catch and catch rates. The yield trajectory shows that yield significantly exceeded MSY between 1986 and 1999.

- Bootstrapped CPUE, relative biomass and fishing mortality trajectories (with 80% confidence intervals) are illustrated in Figure 6.10.
- From 1993 onward, absolute biomass falls below the biomass at MSY, and reaches very low levels ( $B_{2007}/B_{MSY} = 1.86E-01$ ) by the end of the time series (or 18.6% of the biomass needed for MSY). This trend ( $B/B_{MSY} < 1$ ) indicates that the stock is OVERFISHED since 1993, and depleted to unsustainable biomass levels.

## **2a) Projections of a constant catch quota**

- Bootstrapped trajectories with constant catch (Example 2a, Figure 6.10), as expected, also show that fishing mortality and catch significantly exceeded MSY for most of the time series, resulting in OVERFISHING and in a severely OVERFISHED stock. To rebuild the stock, a drastic management measure is implemented: catch is reduced to half the level of the final year and maintained at that level through the 10-year management period. This strategy rapidly rebuilds the stock above the  $B_{MSY}$  level and reduces  $F$  significantly, to levels well below  $F_{MSY}$ .
- The control rule plot (Figure 6.10) shows that almost from the beginning, the fishery is exceeding the MFMT, and crosses the MSST between 1994-1995, thus becoming overfished and with overfishing occurring since 1996 and through the end of the historical series.
- The drastic reduction in catch and the constant quota policy applied in the 10-year management period result in a rapid recovery. Under this strategy, the stock returns to the “safe zone” of the phase plot (above MSST and below MFMT) within ten years.

## **2b) Projections of gradual reductions in effort**

- An example of an effort management control (Example 2b) is illustrated in Figure 6.11. While the use of this milder policy does reduce fishing mortality over the 11-year management period, stock recovery is slow. At the end of this period,  $F$  is successfully reduced to levels near  $F_{MSY}$ , and  $B$  approaches  $B_{MSY}$ . Yield remains stable, at levels similar to the yield of the final year of the assessment ( $Y_{2006}$ ).
- The phase plot shows a gradual but successful recovery into the “safe zone” (above MSST and below MFMT) within eleven years.
- More drastic measures or a longer rebuilding period are needed for complete recovery of the stock.

## **Final notes on simulated examples**

- Example 1 illustrates the use of the basic ASPIC options and the interpretation of output from the FIT program mode. Results showed that ASPIC easily converges when “good data”, with sufficient contrast in the relative abundance index, are used as inputs.
- Example 2 illustrates the implementation of more advanced ASPIC tools to calculate confidence intervals of the estimated parameters and to project bootstrapped trajectories under selected management schemes. Results showed that ASPIC can converge when there is some noise in the input data, as long as it continues to meet the assumptions of production models.

- Two data sets were tested to evaluate how close assessment results were to the “true” population (the simulated base-model here), given a range of observations with and without variability. Formal statistical analyses to compare ASPIC results against the “true” population are beyond the scope of this manual, and therefore are not presented.
- Model comparison was not a goal of these examples. Formal model comparisons can, however, be performed with the FTEST program, included in the ASPIC suite, which can aid in the final model selection.

### 6.7.2 Fitting ASPIC to real data: the Puerto Rico fishery

The data analyzed in this example consists of catch and CPUE data from the commercial conch fishery of Puerto Rico. Landings include years 1993-2005 (data taken from NMFS, 2007). The standardized catch rate includes years 1983-2004, and was obtained using an updated index, calculated with the methods described in Valle-Esquivel (2002b). This assessment is based on previous assessments by Valle-Esquivel (2002b, and 2006, unpublished). The purpose of this example is to use ASPIC to illustrate the stock-assessment process and some of the difficulties that can be encountered when performing a real queen conch assessment (as presented in Valle-Esquivel, 2002b, 2003)<sup>4</sup>. ASPIC did not find a stable solution without imposing constraints on parameters. This example shows some of the most consistent and informative results obtained and illustrates the projection of some simple management alternatives. A brief discussion of results is presented.

#### Inputs/Options

- Input data for ASPIC: conch landings and an index of relative abundance. The standardized, scaled CPUE index is used (Figure 6.12). The data used in the model projections is not included.

PROGRAM	ASPIC	ASPIC	ASPIC
Mode	FIT	FIT	BOT
Description	Point estimates	Point estimates	Bootstrapped estimates
Model shape	LOGISTIC	FOX	FOX
Input Files	pr83_05_logistic.inp	pr83_05_fox.inp	pr83_05_logistic.inp (* Change mode to BOT)
Output Files	pr83_05_logistic.fit	pr83_05_fox.fit	pr83_05_logistic.bot pr83_05_logistic.bio pr83_05_logistic.det

<sup>4</sup> This example is not an official assessment of the conch fishery of Puerto Rico. Results should not be used to describe stock status or to provide management advice. They are intended to illustrate the use of production models in a real-case scenario.



- CPUE Standardization was conducted using a generalized linear mixed model approach (GLMM), under the lognormal assumption (Valle-Esquivel, 2006, unpublished data.) Only trips with positive catch greater than 5 pounds were considered, unsuccessful trips were not, so effort may be underestimated and CPUE overestimated. The explanatory variables used in the final Lognormal GLM model were:

$$\text{Ln CPUE} = \text{year} + \text{month} + \text{gear} + \text{coast} + \text{yr} * \text{month} + \text{yr} * \text{coast} \quad (7)$$

- It is important to look at patterns in the available data to assess if a production model is a feasible alternative. In this case, there is an unclear trend in the landings and in the CPUE series. Landings appear to decline through 1992, and to increase and stabilize thereafter, at about 200,000 kg per year. Landings follow the trend in fishing effort closely, but some fluctuations may be explained by a variety of other factors: economic, environmental, reporting, in addition to stock abundance.
- There is not enough contrast in the CPUE index, it shows a very smooth decline, but remains flat through most of the time series, with only a small peak in 1988. The average standardized CPUE was. 55 lb/trip, with a range 44-86 lb, and an average c.v. of 13%.

## Results and Interpretation

- ASPIC did not converge when it was allowed to run without constraints. It could not obtain reasonable results for all parameters at a time, often hitting parameter bounds. A number of different starting guesses were attempted without success.
- To obtain reasonable solutions, constraints had to be imposed on parameter values. Constraints went from non-informative (a broad range of values) to more informative to narrow down the search for reasonable values that allowed the model to converge.
- The Fox model only provided a slightly better fit to the data. To avoid overparameterization, the logistic model was chosen as the best alternative.
- Sensitivity trials were used to evaluate the effect of changing one parameter at a time, with a range of values tested. Fixed values for  $MSY$ ,  $B1/K$ , and  $q$  were used. Trials with fixed  $MSY$  or  $q$  gave the best fits.
- Point estimates from a single assessment were not produced. The most consistent and informative results were achieved with a fixed catchability of  $q=2E-07$ .
- Relative biomass and fishing mortality trajectories suggest that the stock is in decline and very close to falling below  $B_{MSY}$ , and that fishing mortality has increased rapidly, exceeding  $F_{MSY}$  since 1993 (Figure 6.13). The stock appears to be nearly overfished, and overfishing is clearly occurring.
- There is a large uncertainty regarding the initial biomass value. ASPIC found a solution with a large  $B1/K$  ratio, but considering that the fishery started long before 1983, it is possible that biomass is actually more depressed than it appears. Management decisions should be based on this premise. A plan to eliminate overfishing and prevent the stock from becoming overfished is imminent.
- Simple management scenarios were applied to the fishery. 20-year stock projections are based on hypothetical catch or effort quotas (Figure 6.13). The following conclusions were drawn from these scenarios (only no management and catch quotas are depicted):

- Continuation of current fishing practices for 10 more years would deplete the stock even further, and overfishing would continue to occur, at levels well above  $F_{MSY}$ .
- Gradual reductions in catch can rapidly stop overfishing and allow the stock to remain stable (or recover) above  $B_{MSY}$ .
- Gradual reductions in effort can be as effective, but more difficult to implement than catch quotas.
- Closures (no fishing) are a more drastic, but a more effective and rapid strategy to rebuild the stock and prevent overfishing.

## Conclusions

- Assessment results were highly dependent on constraints imposed on initial parameter values, thus limiting the value of the assessment.
- Limited data constrained results. Catch rates were not informative, so there were no clear trends in abundance, possibly declining. The lack of contrast in the CPUE series does not allow simple estimation of population parameters  $R$  and  $K$ .
- Insufficient/ inadequate data rendered unclear and inconclusive results. However, population trajectories and phase plots suggested that overfishing is occurring and that the stocks are approaching an overfished state. This situation calls for immediate reduction in fishing effort to prevent a further decline in abundance, to eliminate overfishing, and to allow the population to recover to sustainable levels within a ten-year frame.

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### Tables and graphs from ASPIC examples

Table 6.1. Parameters of the Pella-Tomlinson biomass dynamic model used for simulation of a conch fishery.

Parameter	Simulated PM (EQUILIBRIUM)
K	6.00E+06
r	0.4
p	0.0001
q	1.00E-04
MSY	882867
fMSY	4000
BMSY	2.21E+06

Table 6.2. Data from production model simulation used to fit ASPIC.

Example		DETERMINISTIC		STOCHASTIC	
Year	Effort	Catch1	CPUE1	Catch2(+15% CV)	CPUE2
1983	500	264749	529	249067	498
1984	1000	467279	467	449218	449
1985	1500	618556	412	466236	311
1986	2000	727828	364	728651	364
1987	2500	802876	321	878894	352
1988	3000	850236	283	1099642	367
1989	3500	875377	250	714362	204
1990	4000	882867	221	1102916	276
1991	4500	876506	195	852966	190
1992	5000	859447	172	911390	182
1993	5500	834292	152	1029211	187
1994	6000	803178	134	778946	130
1995	6500	767854	118	866523	133
1996	7000	729739	104	695016	99
1997	7500	689976	92	539569	72
1998	8000	649479	81	630227	79
1999	8500	608971	72	832071	98
2000	9000	569012	63	583319	65
2001	9500	530033	56	415847	44
2002	10000	492356	49	469848	47
2003	10500	456213	43	481308	46
2004	11000	421764	38	358063	33
2005	11500	389110	34	399476	35
2006	12000	358306	30	341783	28

Table 6.3. Comparison of Logistic and Fox estimated ASPIC parameters from Examples 1 (deterministic data) and 2 (stochastic data). The Fox model provided a better fit than the logistic in both cases.

**COMPARISON OF LOGISTIC AND FOX MODELS**

Model	Details	Example 1		Example 2	
		LOGISTIC	FOX	LOGISTIC	FOX
Code	Convergence=0	0	0	0	0
Exponent	"m" in Pella-Tomlinson Function	2	1	2	1
Bmsy/K		0.5	0.368	0.5	0.368
B1/K		1.54E+00	1.09E+00	1.37E+00	1.03E+00
MSY		4.22E+05	6.94E+05	4.37E+05	5.91E+05
K		7.91E+06	3.69E+06	8.47E+06	6.30E+06
q1		3.68E-05	1.30E-04	3.68E-05	7.03E-05
Objective function	Minimize	6.24E-01	1.48E-02	9.35E-01	5.31E-01
R2 in CPUE		9.34E-01	9.97E-01	9.16E-01	9.47E-01

Table 6.4. Estimated ASPIC parameter estimates from Examples 1 (deterministic data) and 2 (stochastic data).

**Point estimates from ASPIC in FIT mode**

Parameter	Estimate	Example 1 Simulated data Deterministic	Example 2 Simulated data Stochastic
<b>Model parameters</b>			
*B1/K	Starting relative biomass	1.09E+00	1.03E+00
K	Carrying capacity	3.69E+06	6.30E+06
q(1)	Catchability coefficient	1.30E-04	7.03E-05
phi	Shape of production curve (fixed for Fox model)	0.3679	0.3679
<b>Management and derived parameters</b>			
MSY	Maximum sustainable yield	6.94E+05	5.91E+05
Bmsy	Stock biomass giving MSY	1.36E+06	2.32E+06
Fmsy	Fishing mortality rate at MSY	5.11E-01	2.55E-01
B./Bmsy	Ratio: B(2007)/Bmsy	1.59E-01	1.59E-01
F./Fmsy	Ratio: F(2006)/Fmsy	3.05E+00	3.37E+00
Fmsy/ F.	Ratio: Fmsy/ F(2006)	3.28E-01	2.97E-01

Table 6.5. Bootstrapped parameter estimates from Example 2 (stochastic data).

**ESTIMATES FROM BOOTSTRAPED ANALYSIS\***

Param name	Point estimate	Bias in estimate	Relative bias	Bias-corrected confidence limits				Inter-quartile range	Relative IQ range
				Approx 80% lower CL	Approx 80% upper CL	Approx 50% lower CL	Approx 50% upper CL		
<b>B1/K</b>	1.03E+00	-6.52E-02	-6.31%	9.14E-01	1.12E+00	1.01E+00	1.09E+00	7.42E-02	0.072
<b>K</b>	6.30E+06	-3.78E+05	-6.00%	5.20E+06	8.97E+06	5.93E+06	7.97E+06	2.04E+06	0.324
<b>q(1)</b>	7.03E-05	1.26E-05	17.88%	4.29E-05	9.39E-05	5.07E-05	7.67E-05	2.61E-05	0.37
<b>MSY</b>	5.91E+05	2.91E+04	4.93%	4.38E+05	6.66E+05	4.96E+05	6.16E+05	1.20E+05	0.203
<b>Ye(2007)</b>	2.67E+05	5.31E+03	1.99%	2.10E+05	3.23E+05	2.33E+05	2.96E+05	6.34E+04	0.237
<b>Y.@Fmsy</b>	9.42E+04	1.63E+03	1.73%	6.87E+04	1.24E+05	8.04E+04	1.10E+05	2.91E+04	0.309
<b>Bmsy</b>	2.32E+06	-1.39E+05	-6.00%	1.91E+06	3.30E+06	2.18E+06	2.93E+06	7.52E+05	0.324
<b>Fmsy</b>	2.55E-01	4.74E-02	18.59%	1.34E-01	3.47E-01	1.71E-01	2.85E-01	1.14E-01	0.446
<b>fmsy(1)</b>	3.63E+03	-1.10E+01	-0.30%	3.28E+03	3.86E+03	3.45E+03	3.74E+03	2.93E+02	0.081
<b>B./Bmsy</b>	1.59E-01	-3.89E-03	-2.44%	1.23E-01	2.08E-01	1.41E-01	1.87E-01	4.63E-02	0.291
<b>F./Fmsy</b>	3.37E+00	6.60E-02	1.96%	2.74E+00	4.22E+00	3.00E+00	3.79E+00	7.85E-01	0.233
<b>Ye./MSY</b>	4.52E-01	-1.08E-02	-2.39%	3.81E-01	5.34E-01	4.16E-01	5.00E-01	8.40E-02	0.186

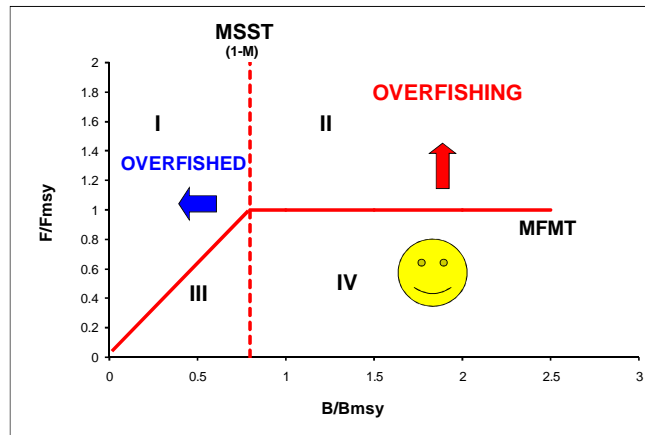


Figure 6.6. A diagram of a generic default limit control rule (or phase plot) (with  $M=0.2$ ). MSST= Minimum Stock Size Threshold; MFMT=Maximum Fishing Mortality Threshold. The stock is overfished if biomass falls below MSST; overfishing occurs if MFMT is exceeded. Acceptable relative biomass and  $F$  combinations occur to the right and below the limit control rule line (represented by a smiley face).

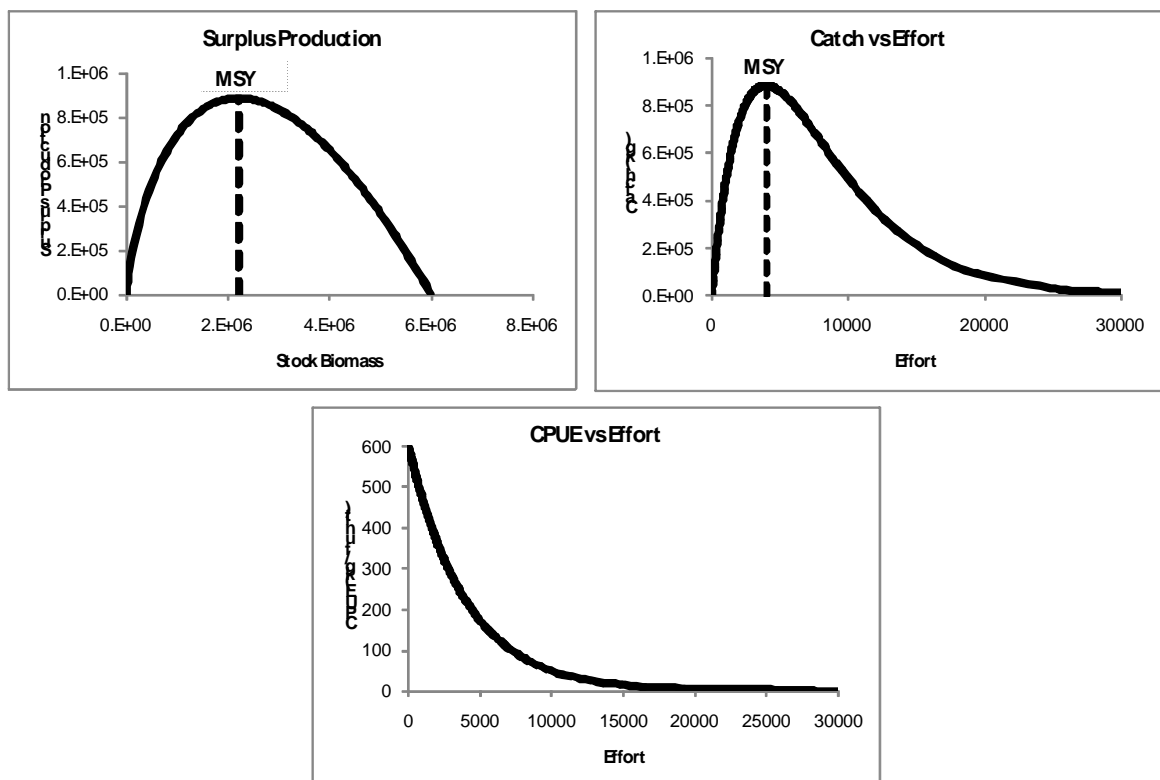


Figure 6.7. Surplus production, yield and CPUE curves for a hypothetical population constructed under the Fox model assumptions.



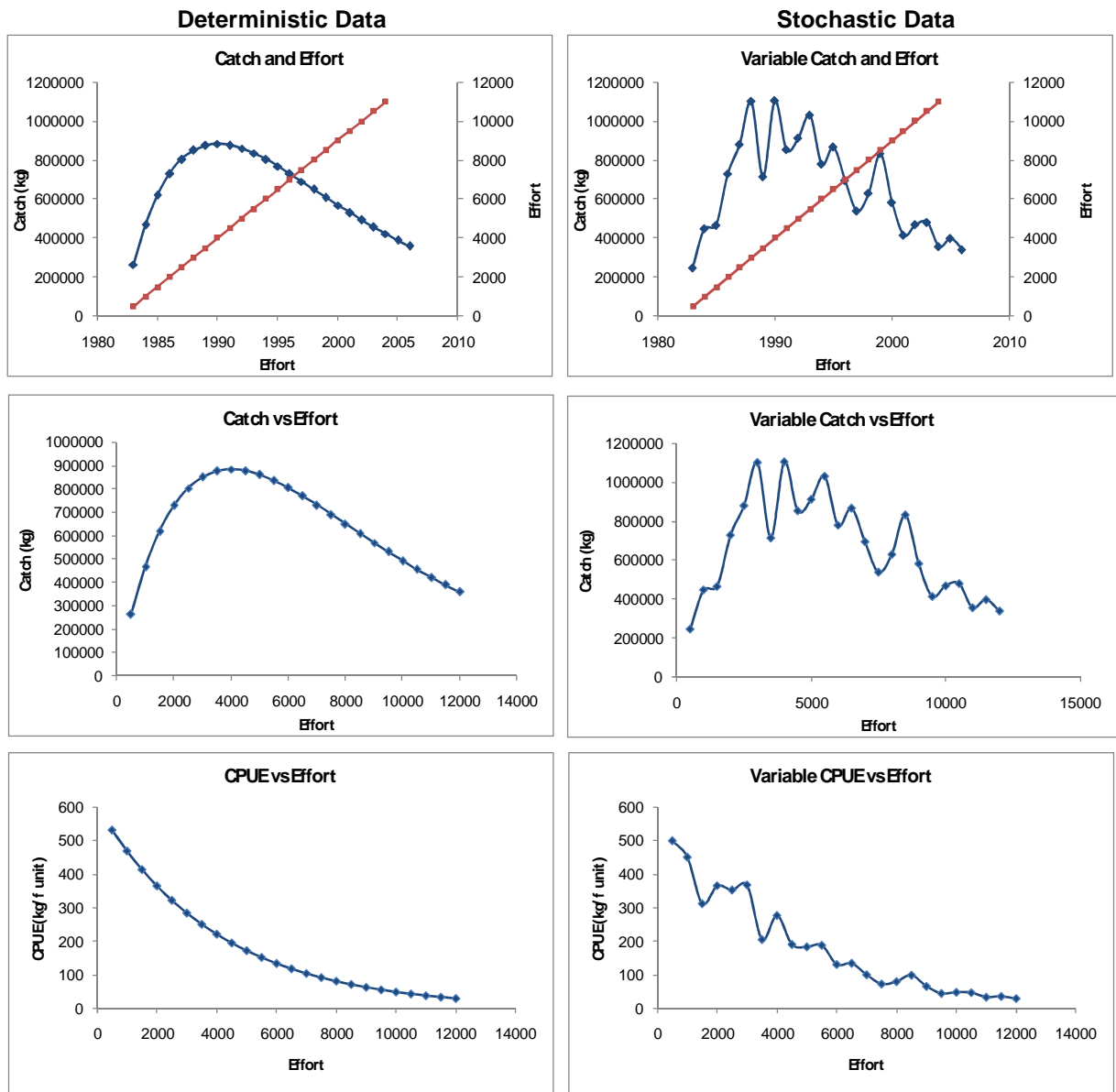


Figure 6.8. Plots of simulated deterministic (left panel) and stochastic (right panel) data used to fit ASPIC.

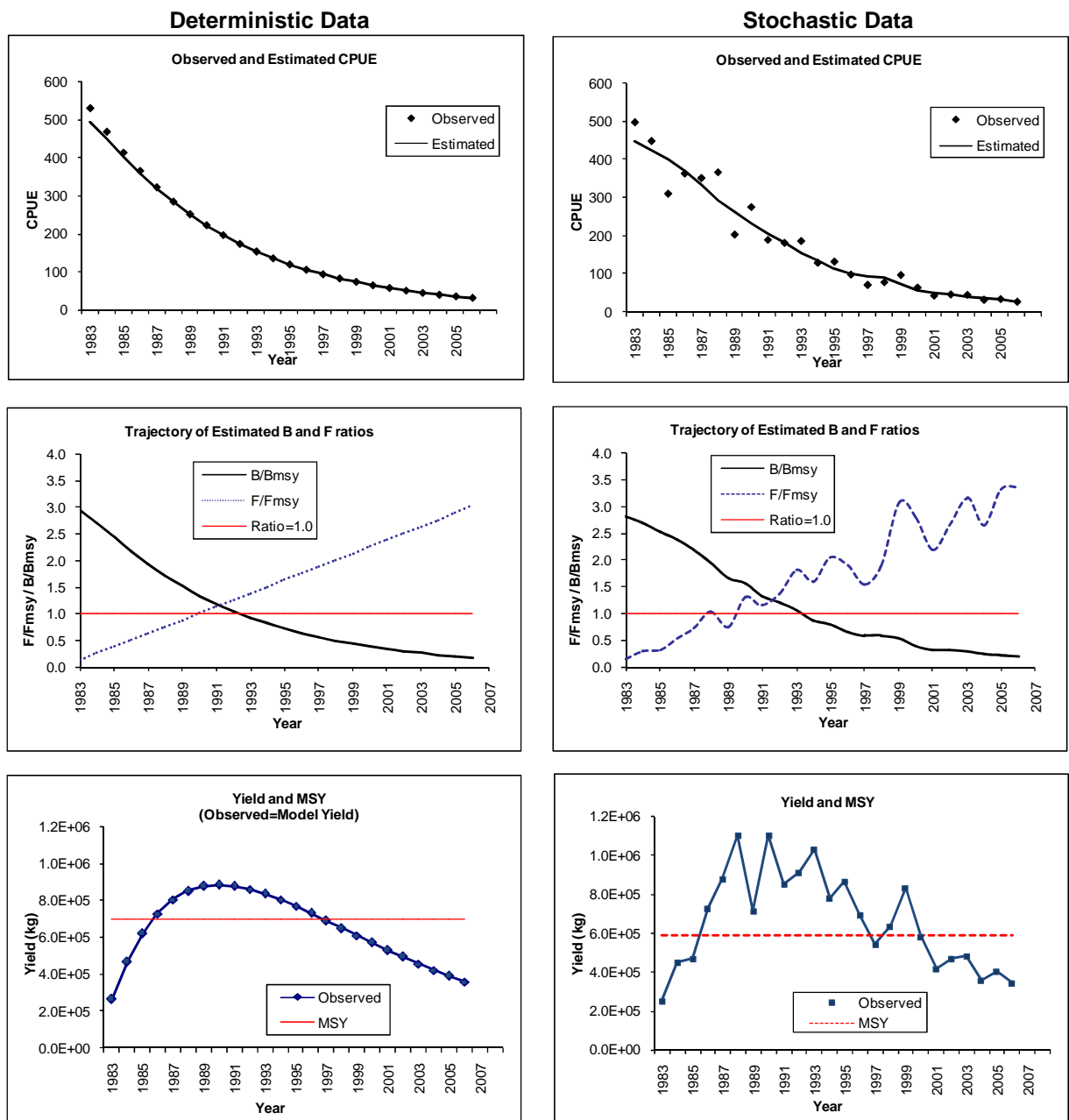


Figure 6.9. Resulting trajectories from ASPIC, simulated Examples 1 (left panel) and 2 (right panel).

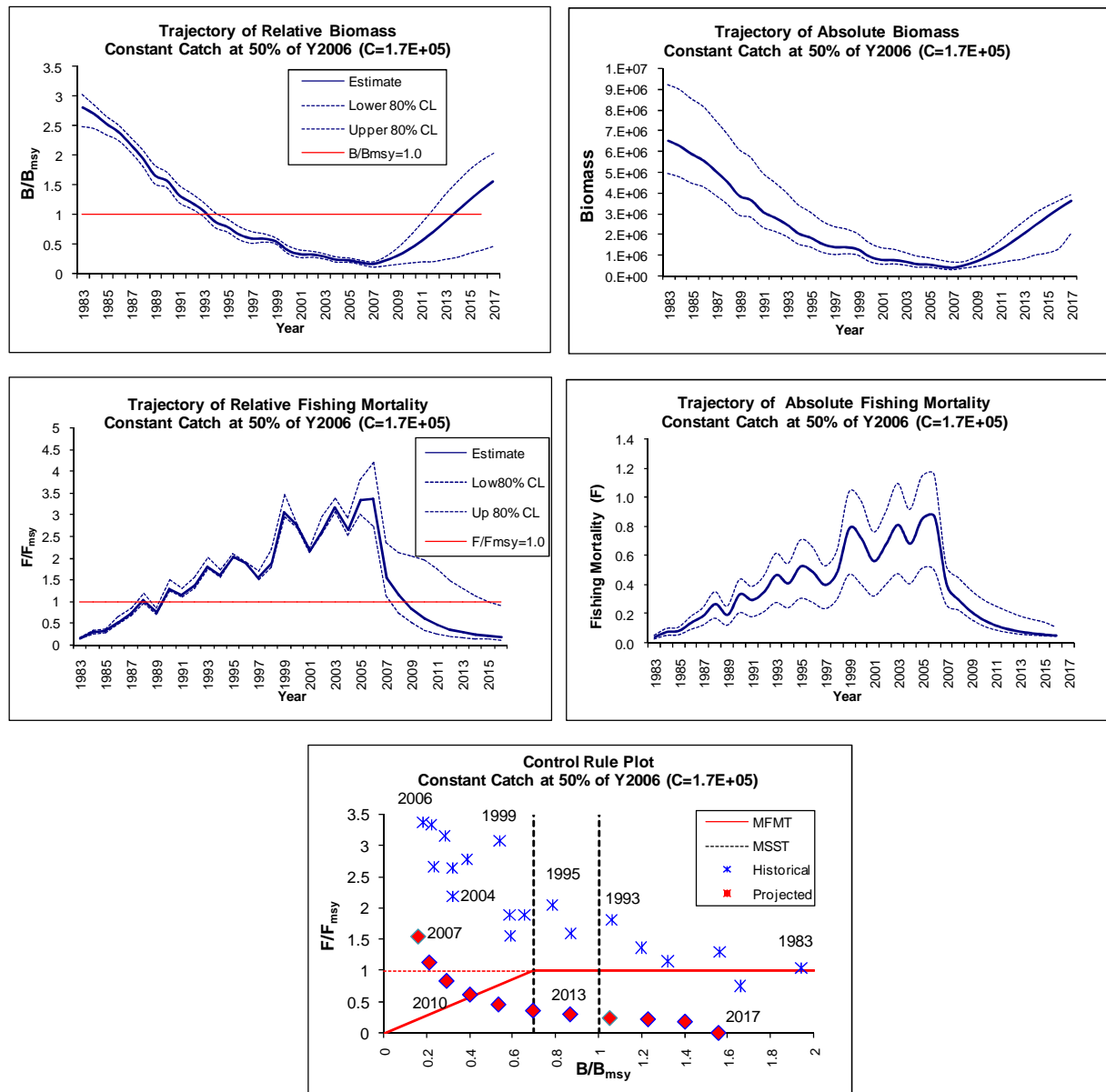


Figure 6.10. Bootstrapped model projections of simulated data (Example 2) under a constant catch scenario, with catch equivalent to 50% of the yield in the last year observed ( $C=50\%$  of  $3.4E+05=1.7E+05$ ). Plots show trajectories of relative biomass ( $B/B_{MSY}$ ), absolute biomass ( $B$ ), relative fishing mortality ( $F/F_{MSY}$ ), and absolute fishing mortality ( $F$ ). The final control rule plot illustrates the position of the stock with respect to MFMT and MSST. Historical years are 1983-2006, projected years are 2007-2017.

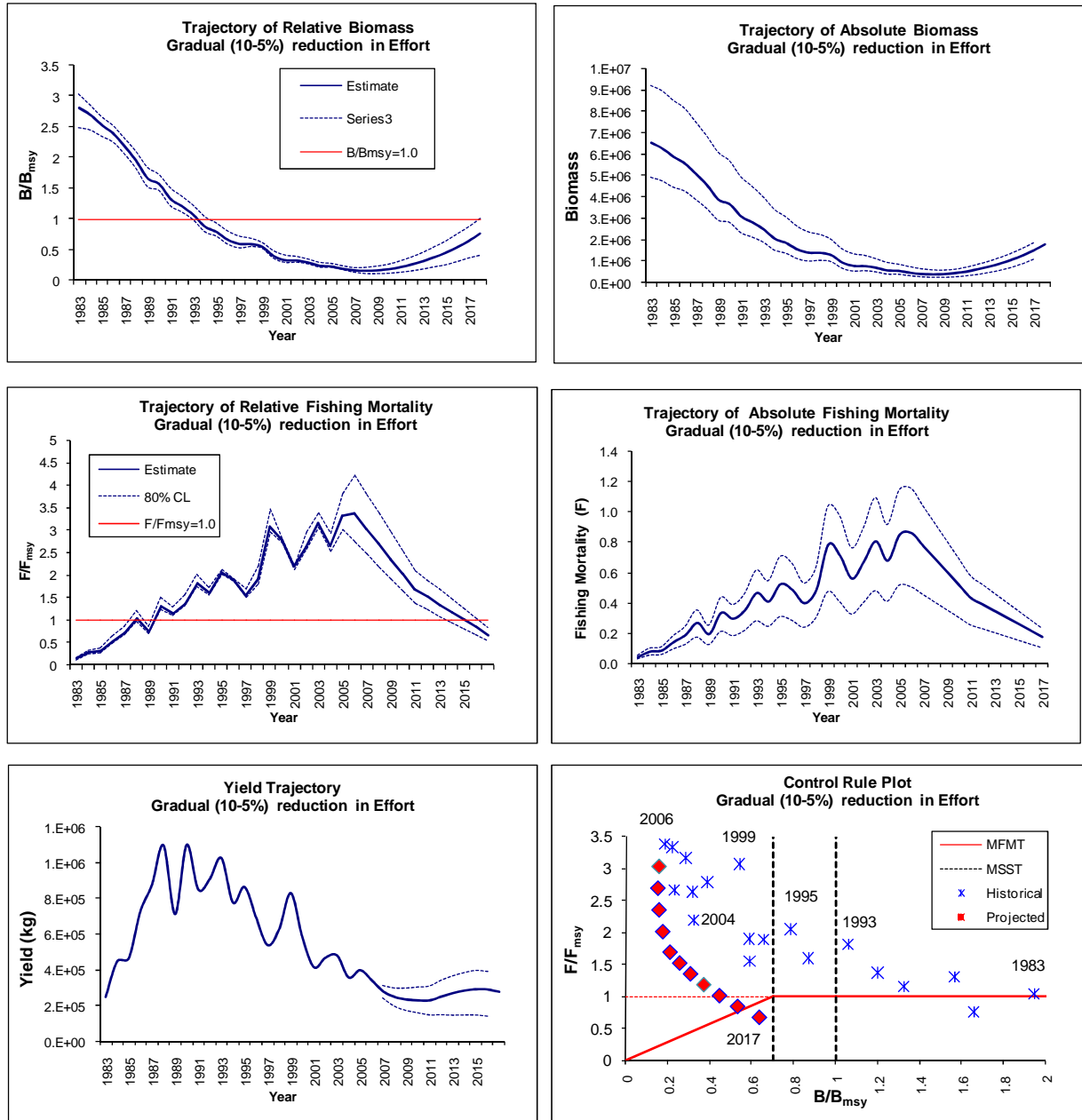


Figure 6.11. Bootstrapped model projections of simulated data (Example 2) under a gradual reduction in fishing effort of 10% for 5 years, and 5% thereafter. This strategy reduces effort to 20% of the 2006 value by 2017. Plots show trajectories of relative biomass ( $B/B_{MSY}$ ), absolute biomass ( $B$ ), relative fishing mortality ( $F/F_{MSY}$ ), absolute fishing mortality ( $F$ ), and yield. The final control rule plot shows the position of the stock with respect to MFMT and MSST. Historical years are 1983-2006, projected years are 2007-17.

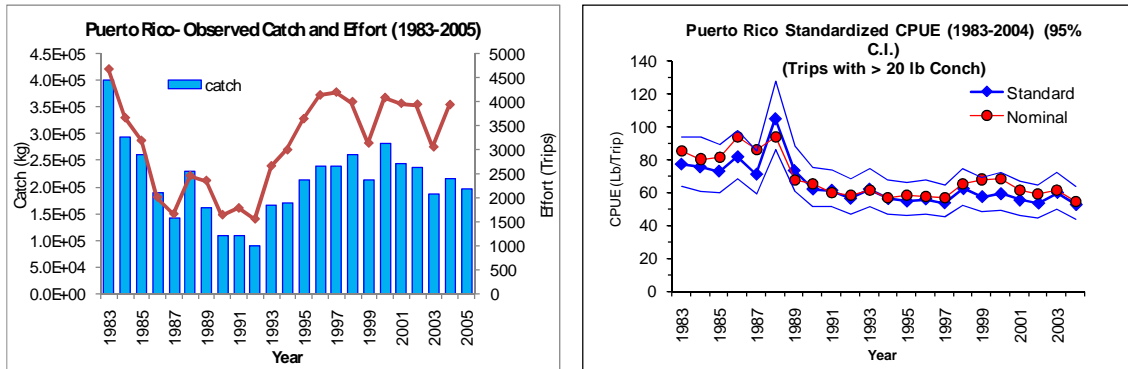


Figure 6.12. Real data used in ASPIC Example 3. Puerto Rico commercial queen conch landings, effort, and standardized CPUE index. Reported data from NMFS (2007), and index values from CPUE analysis (Valle-Esquivel, 2002b, and 2006, unpublished data).

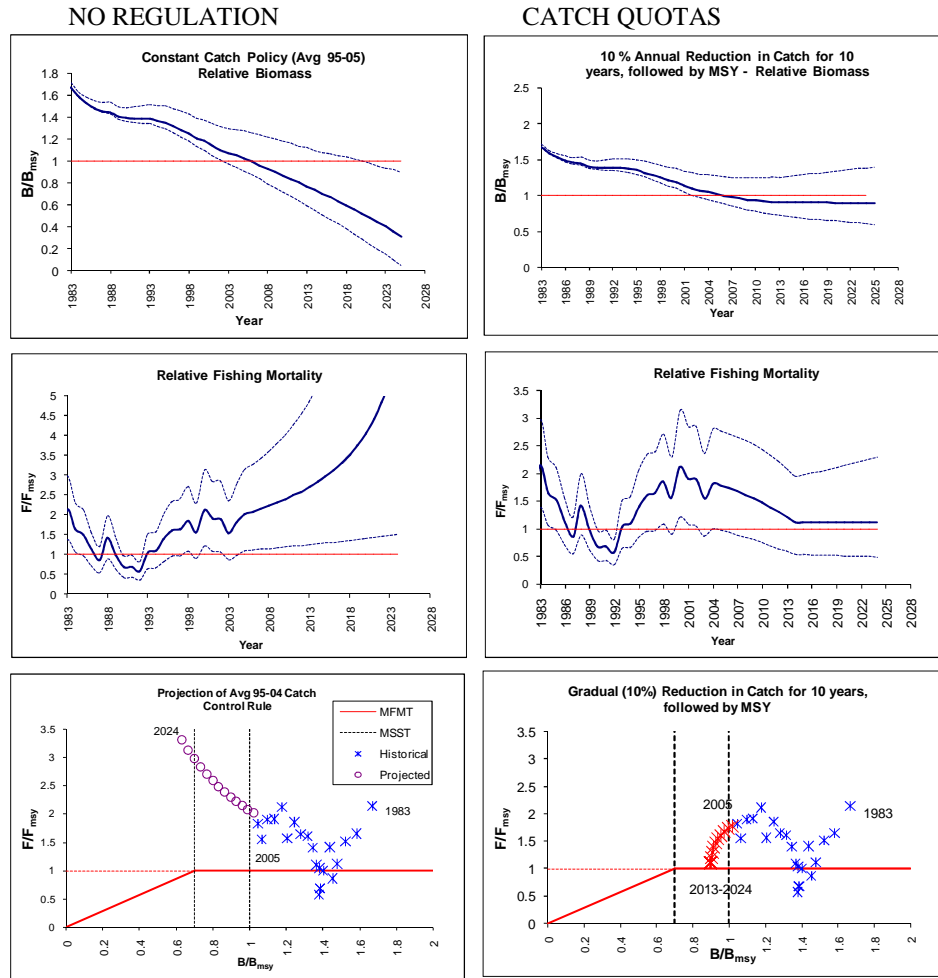
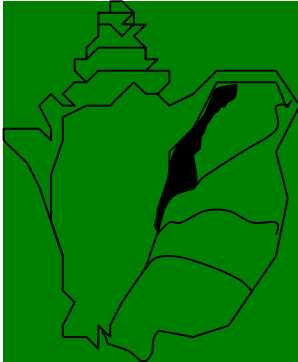


Figure 6.13. Bootstrapped model projections of Puerto Rico data (Example 3) under no regulation (left panel) and a gradual reduction of 10% in catch for 10 year years, followed MSY (right panel). Plots show trajectories of relative biomass ( $B/B_{MSY}$ ) and relative fishing mortality ( $F/F_{MSY}$ ), and phase plots. The control rule plot illustrates the position of the stock with respect to MFMT and MSST. Historical years are 1983-2005, projected years are 2006-2017.



## 7. QUEEN CONCH SIMULATOR

### 7.1. Introduction

A simulation model, 'ConchMgtSim' (Conch Management Simulator) (Valle-Esquivel, 2003), that incorporates the most important characteristics of the biology, population dynamics, and fisheries of queen conch was used to develop test-data bases that can be used in queen conch stock assessment. The model can simulate different scenarios of a conch fishery and can be applied to evaluate the effect of simple management regulations (e.g., reductions in effort, size limits, seasonal closures). The model configuration used here incorporates meat weight to describe the size-structure of the population and the landings. 'ConchMgtSim' is a general model, with some flexibility to represent different scenarios regarding the population and the fishing operation.

The essential value of any fisheries simulator relies on the fact that experiments cannot be conducted with real fish (or shellfish) populations, or with the users of that resource. Controlled experiments to evaluate the impacts of different fishing patterns (effort, catch, seasons of operation, areas fished, etc.) are not feasible in reality.

A simulation model is a computer representation of a complex reality. Simulation models are an essential tool in fisheries management because a variety of hypothetical experiments can be conducted very rapidly on a personal computer and can incorporate and analyze the prevailing uncertainty in all fishery systems. Basic knowledge of the biology of the stock (i.e., growth, reproduction, recruitment, distribution, abundance, longevity, migration patterns, etc.) and of the characteristics of the fishery (i.e., catch, effort, catch rates, selectivity, management regulations, etc.) is sufficient to develop a fishery simulation model. The models become more robust as more information is available, but ultimately, models can only be schematic and simplified representations of reality.

### 7.2. Value and Purpose of the Model

The conch simulator consists of a (virtual) conch population, that undergoes recruitment, growth, natural, and fishing mortality. The population (in numbers and clean meat weight) can be tracked down at any moment in time, under different biological and fishing scenarios. The outputs produced by the model include: population numbers and biomass by year, catch and yield by age and month/year, spawning stock size and recruits by year, and final population age/weight structure.

The general purpose of the model is to test hypotheses regarding conch stock behavior under different population dynamic characteristics, different fishery operations, and different management regimes. In addition, the data generated with this simulator can be used to test different stock assessment models, given that assessment results can be compared against the “true” (virtual) conch population. The simulator was used in this manual to:

- Generate a hypothetical queen conch stock that accurately reflects the population dynamics of the species and the characteristics of conch fisheries.
- Generate (simulated) age/weight structured data to perform stock assessment analysis under controlled experimental conditions.

The objective of this section is to introduce the concept of a simulation model as a tool to analyze fisheries with limited data, as is the case with the large majority of queen conch fisheries. The conch simulator is described and simple applications of the model are illustrated. The original ‘ConchMgtSim’ program is a complex algorithm written in Fortran 90. A simplified version was developed in Microsoft Excel to make the program available and accessible to a larger audience, and is provided with this manual.

## **7.3 Description of the Conch Simulator**

### **7.3.1 Model Components**

The conch simulator used to generate test-databases for this manual consists of the model CONCHMGTSIM ©, developed by Valle-Esquivel (2003), with a few simplifications and modifications. A detailed description of the model and documentation of the Fortran 90 program are provided in the cited reference. The main configuration, parameters, and applications relevant to the objectives of this manual are described here.

The main simplification of the model consisted in reducing the number of array dimensions from three to two. Originally, the simulator generates conch populations and catch structured by age and two size-dimensions (shell-length, and shell-lip thickness); in this version, the population and the catch are structured by age and one size dimension (meat weight). This simplification was based on two facts:

- 1) Assessing growth in two phases (shell length as juveniles, shell-thickness as adults) is cumbersome; conversely, growth in weight is a continuous process that can be modeled with a single function; and,
- 2) Most conch fisheries discard the shells and clean the meat at sea, even when size-based regulations may be in place. Thus, the only observable dimension of the individuals fished is often the clean meat filet. It must be noted, however, that a large variability is attached to this “Meat Weight” dimension, when linked to age or shell dimensions, and that it is virtually impossible to assess age or the state of maturity from meat weight data alone. To run this model configuration, a number of assumptions had to be made to apply and parameterize a Gompertz growth-in-meat weight model.

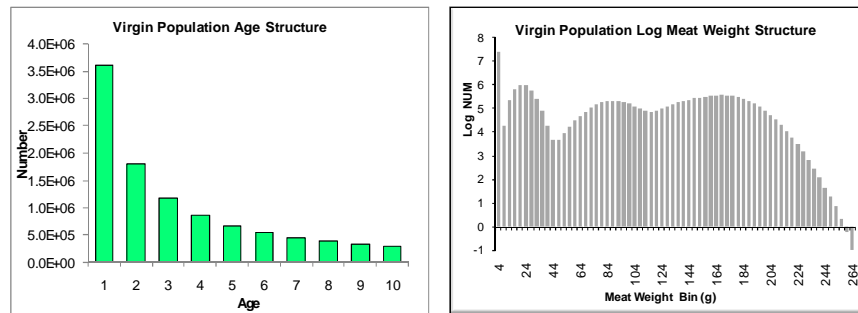
The simulator consists of an age and weight structured population, where recruitment, growth, maturity, natural mortality, and fishing mortality occur at known rates, and can be adjusted to desired levels. Variability can be added to some of these functions. A monthly time step is used to exploit the conch, with annual summaries of numbers of conch, catch and yield by age and meat weight compiled in output files. A



brief description of the general configuration (from Valle-Esquivel, 2003) and of the current parameterization follows.

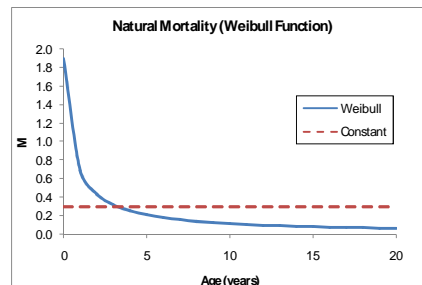
**1. Dimensions:** ages 0-10, 80 sizes (1-320 grams in 4 gram bins), one gear, year-round fishery (12 months of operation), maximum of 50 years in one run.

**2. Virgin Population:** Equilibrium-state, with constant recruitment at  $2.4 \times 10^7$  recruits.



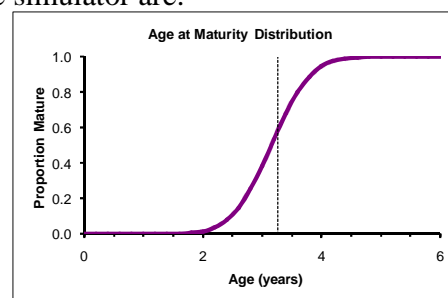
**3. Natural Mortality:** 2 options:  
 1) Constant  $M=0.3 \text{ year}^{-1}$   
 2) Decreasing  $M$  at age, according to a Weibull function (Appeldoorn, 1988a):

$$M = 4.001 * (\text{Age} + 0.5)^{(0.0774 - 1)} \quad (1)$$



**4. Maturity:** Queen conch become sexually mature after the maximum siphonal length is reached, with the lip becoming fully-flared and subsequently increasing in thickness (Appeldoorn 1998). The proportion of mature individuals was based on literature values (Appeldoorn 1990), with 50% mature at age 3.25 years. The cumulative probability distribution and the values used in the simulator are:

AGE	% Mature
0	0.0%
1	0.0%
2	1.49%
3	38.46%
4	94.35%
5	99.97%
6	100.00%



**5. Number of Age Classes:** Longevity estimates for queen conch that have been reported in the literature range from 7 to 30 years, according to the location of the population sampled and the method used to age the conch. To Ten age classes are used in this model configuration.

**6. Recruitment:** 4 options.

- 1) Constant recruitment
- 2) Random about a mean
- 3) Deterministic stock recruitment relationship, and
- 4) Random about a stock-recruitment curve.

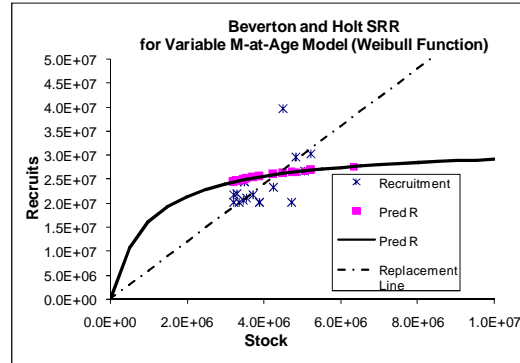
The Base-Case runs used option 3, in the form of a deterministic Beverton-Holt (1957) stock-recruitment curve. Stock-recruitment parameters were estimated by scaling standardized catch rates from Puerto Rico, using the method described in NFSC (2002) and Valle-Esquivel (2002b). Recruitment levels were scaled to produce reasonable yields (at levels resembling those of Puerto Rico over the catch history of the species, within a range of 75-200 MT/year). The equation and parameters are:

$$N_{y,0} = \frac{\alpha S_y}{\beta + S_y} \quad (2)$$

where  $N_{y,0}$  are the number of recruits (age 0 conchs) on year  $y$ ;  $S_y$  is the spawning stock size (in numbers) at the start of year  $y$ , and  $\alpha$ ,  $\beta$  are the stock-recruitment parameters. For an average of  $2.4\text{E}+07$  recruits:

$$\text{Alpha}=\alpha=3.2\text{E}+07$$

$$\text{Beta}=\beta=1.0\text{E}+06$$



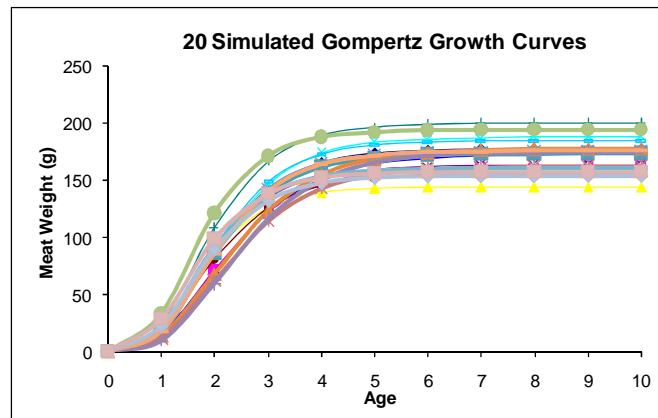
**7. Growth.** A Growth Transfer Matrix was created using the method of Legault (1996). The Gompertz equation was selected to simulate growth in meat weight:

$$W_t = W_\infty e^{\left[ \ln \frac{W_0}{W_\infty} e^{(-Gt)} \right]} \quad (3)$$

Parameter	Mean	VAR (10%CV)	Cov ( $W_{\infty}$ -G)	Distribution
$W_{\infty}$	172.67	298.16		$N(172.7, 17.3)$
G	1.156	0.0134	-0.6	$N(1.156, 0.116)$
$W_0$	0.19	Low 0.05	High 0.35	$U(0.05, 0.35)$

These parameters were obtained from multiple regression analysis of morphometric data from the Bahamas (length-MW, lip-MW) collected by Ehrhardt and colleagues (1996-1998), and based on the method described by Appeldoorn (1992). Multiple-regression equations were combined through simulation with a generalized growth in length function (based on parameters for the whole Caribbean, in Valle-Esquivel, 2003) and Appeldoorn's (1988b) growth in lip function for adults. Other trials can include other parameters [i.e., growth in weight parameters for Puerto Rico estimated by Appeldoorn (1992)], or the use of different growth equations.

The probability distributions give the range of values used for each parameter in 10 million stochastic projections of growth trajectories. A matrix of growth probability values that incorporates uncertainty is produced with this method (Legault, 1996), and is used as an input in the conch simulator<sup>5</sup>. The graph below shows twenty sample growth patterns that would occur within the simulations.



Standard equations from the fisheries literature are used to calculate and fishing (F) and total mortality (Z), abundance (N), catch in numbers (C), and yield in weight(Y).

**8. Fishing Mortality.** The fully selected fishing mortality rate (F) for any age-meat weight cell in the simulation is calculated as the product of effort (f), catchability (q), and selectivity (S)

$$F = f * q * S$$

(4)

- Effort and catchability values are adjusted in the simulations to obtain the desired depletion level at the end of the exploitation period.

<sup>5</sup> A Gompertz growth simulator is included in electronic format under folder 'CH7-Conch Simulation Model'.

- Effort is input for each year, can be constant, increase, or decrease over time. Currently set at levels resembling those of the Puerto Rico fishery, averaging 4000 effort units/ year (i.e., number of fishing trips).
- Selectivity is knife-edge, fixed in time, and size (weight) specific, starting at Meat Weight=80 grams. Knife-edge selectivity can be manipulated to change the size of recruitment into the fishery (i.e., minimum meat weight regulations).
- Constant catchability, currently  $q= 5.5e-05$ .

**9. Total Mortality Rate.** Calculated by adding the natural and fishing mortality rates per cell

$$Z_t = M_t + F_t \quad (5)$$

**10. Population Abundance.** The abundance of the first age/size class is generated using one of the stock-recruitment relationships described above. The abundance of the other age classes follows the exponential decline equation, where population abundance (N) is reduced over time from the combined effects of natural and fishing mortality:

$$N_t = N_{t-1} e^{-Z_t} \quad (6)$$

**11. Catch in Numbers and Yield.** The catch equation is used to calculate the total catch from any cell during the month:

$$C_t = \frac{N_t F_t (1 - e^{-Z_t})}{Z_t} \quad (7)$$

**Yield** is calculated as the sum of the meat weights of all the individuals in a cell, divided by 1000 to obtain weight in kilograms. The total catch-by- meat weight for the year is the sum of the catches over all meat weight bins and months. The total yield for year is the sum of all monthly yields.

**12. Sectors of the Fishery and Season of Operation.** A single fishery is used, with its corresponding selectivity, fishing effort, and season of operation (with the option to open or close the fishery during certain months of the year).

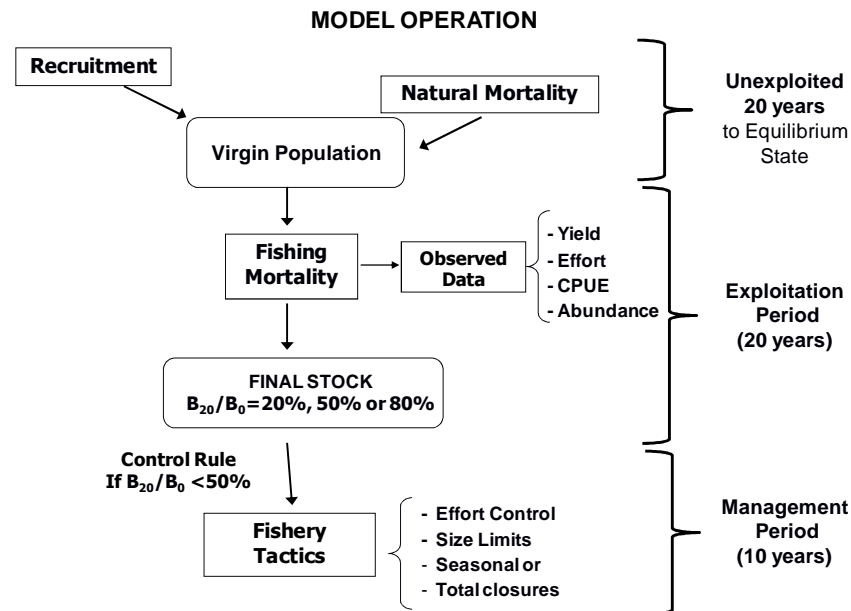
**13. Data Generated.** The main outputs produced by the model include: population numbers, biomass, final age/meat weight structure, and annual and monthly summaries of catch and yield. Simulated age/weight structured catches were used elsewhere in this manual to test the validity of assessment models.

**14. Historical Condition and Management.** Simulation of historical catches can lead to an unexploited, fully-exploited, or over-exploited population. Reductions in fishing effort, size-limits (i.e., limits on minimum meat weight), and seasonal closures can be implemented for a selected management period, by extending the number of years in the simulation.

### 7.3.2 Model Operation

A virgin population is created by adding a constant number of recruits to Age 0 bins, and following this cohort under natural mortality for 20 years until equilibrium

conditions are met. This generates an unexploited stock. Fishing mortality is introduced according to a desired pattern of exploitation to produce different depletion levels (e.g., 20%, 50%, 80% of the unfished stock) at the end of the exploitation period. If the stock is depleted (e.g., under a control rule of  $B_{20}/B_0 < 50\%$ ), fishery tactics are applied for a 10-year management period (Figure .



### 7.3.3 Computer Programs and Limitations

CONCHMGTSIM is a FORTRAN 90 application for PC computers. There is a main program that calls a number of subroutines, modules and functions to perform different tasks and calculations required by the simulator. The program uses several input files, and produces several output files, which can be summarized and plotted for interpretation. Some of the fishery and management-related inputs are flexible (M, SRR and parameters, fishing effort,  $q$ , selectivity, season of operation), but other, critical inputs such as the growth transfer matrix and the initial population, are not. The major limitation of this program is its complexity: it is not user-friendly, and requires a certain level of expertise in programming languages. CONCHMGTSIM and extensions were developed for a specific purpose (generation of age/weight structured catch data in this manual), so in the present configuration, application to other case studies is limited<sup>6</sup>.

A simplified version of the Fortran program simulator was developed in Microsoft Excel to make the program available and accessible to a larger audience<sup>7</sup>.

### 7.4 Model Implementation

<sup>6</sup> Some of the subroutines have licensing restrictions or are the intellectual property of other authors (MAKEGTM, Legault 1996; Valle-Esquivel, 2003), so only compiled versions of the program may be available upon request.

<sup>7</sup> An Excel version of the conch simulator is included with this manual in the electronic folder 'CH7-Conch Simulation Model'.

### 7.4.1 Simulation Experiments

#### Factors and Levels

Many factors may affect the structure of a queen conch stock that is subject to exploitation, but it is virtually impossible to examine every possibility. Four factors can be considered to perform simulation experiments with this model: (1) the rate of natural mortality, (2) the rate of recruitment, (3) the selectivity, (4) the level of depletion at the end of the exploitation period. Alternative growth models (Ehrhardt, in. prep.) may also be tested. Experiments consist in creating different scenarios of the population and the fishery through the combination of factors and levels. In the examples presented here, other factors of interest were held constant to simplify the experiments: the age at maturity, the growth function, the number of gears, and the season of operation of the fishery. Alternatives for fixed and experimental factors and levels are outlined in the following tables.

FIXED FACTORS	LEVELS/ OPTIONS
1) Natural Mortality (M)	1. Age-specific 2. Constant: M=0.2, 0.3,0.5
2) Recruitment (R)	1. Constant 2. Variable 3. SRR-Deterministic 4. SRR-Random
3) Age at Maturity (AM)	AM~N(3.25,0.32)
4) Growth Transfer Matrix	1. Stochastic Gompertz MW-at-Age function
5) Number of fleets (Gears)	1
6) Fishing Season	1. Year-round fishery 2. Seasonal

\*\*Shaded areas show options used in the scenarios presented here.

EXPERIMENTAL FACTORS	LEVELS
7) Effort (f)	1. Constant over time 2. Increasing 3. Decreasing
8) Catchability (q)	Constant
9) Selectivity (S) (in Meat Weight, MW)	1. Knife-edge: MW=80 g 2. Knife-edge: MW=120 g 3. Knife-edge: MW= 160 g
10) Depletion Level (DL) (at END of exploitation period) DL= Bfinal / B0	1. Low= 80% of initial stock 2. Intermediate= 50% of initial stock 3. High= 20% of initial stock

\*\*Effort and Catchability are adjusted in each scenario to obtain the desired F and and depletion level at the end of the exploitation period.

#### Simulation Scenarios

Four simulation scenarios are presented to illustrate the implementation of the conch simulator. The assumptions and inputs used in each case, the main outputs produced and a short interpretation of results are provided. These scenarios are only a

few of many possibilities, but intend to demonstrate the value of the simulator to test hypotheses about exploitation and management of queen conch stocks. The simulation scenarios described below are provided as examples of the conch simulator (in electronic folder 'Ch7-Conch Simulation Model').

**I) Scenarios to illustrate the effect of different fishing mortality levels:**

- 1) Base-Case Scenario (Scenario 1-Case2)- Intermediate Depletion Level
- 2) Case 1- Low Depletion Level,
- 3) Case 3- High Depletion Level

**II) Scenarios to illustrate implementation of management regulations on a severely depleted stock:**

- 4) Meat Weight Limit
- 5) Fishing Effort Reduction
- 6) Seasonal Closures

### **I) Fishing Mortality/ Depletion Level Scenarios**

**1) Base-Case Scenario (Scenario 1-Case2)-**'Intermediate Depletion Level' was created and used as a reference for all subsequent trials, with Age-Specific Natural Mortality (M) and Deterministic Beverton-Holt SRR. Only variability in the growth model is incorporated under this set-up. Base-case conditions are outlined below.

Construction of other scenarios included changes in the fishing mortality pattern, implemented through changes in effort, selectivity, and final depletion levels. Further analyses could make different assumptions regarding key population dynamic processes: recruitment, mortality, and growth, as suggested in the fixed factors table. Each simulation trial involves the exploitation of a conch population in equilibrium for a period of 20 years. Depending on the final depletion level, a subsequent 10-year management period can be implemented to rebuild the stock and/or to stop overfishing.

<b>FACTOR</b>	<b>SCENARIO I (Base-Case)</b>
Natural Mortality	Age-specific
Recruitment	Deterministic Beverton-Holt SRR
Virgin Population	Constant recruitment= 2.4E+07
Age Classes	0-10
Maturity	50% Mature @ Age=3.25
Growth	Stochastic Gompertz
Exploitation Period	21 years
Fleets	1
Fishing Season	Months 1-12
Catchability	Constant, $q=5.5E-05$
*Effort	Constant $f=4000$ units/yr
*Selectivity	Knife-edge= 80 g
*Depletion Level	Intermediate, DL=50%

The other two depletion scenarios are based on different fishing mortalities, applied at a constant rate over the time series. Parameters for these three F/Depletion scenarios are given below. Case 3 is used later to test management regulations.

- 2) **Case 1-** 'Low Depletion Level', and
- 3) **Case 3-** 'High Depletion Level'

Parameters	Scenario I	Scenario I	Scenario I
	Case 1	Case 2 – Base case	Case 3
	Constant F Low DL	Constant F Intermediate DL	Constant F High DL
Final DL= $B_{21}/B_1$	80%	50%	20%
F(yr)	0.085	0.22	0.44
Effort (f) units/yr	1550	4000	8000
Catchability (q)	5.50E-05	5.50E-05	5.50E-05
Selectivity (MW)	80g	80g	80g

The data generated under this base-case scenario is used to illustrate the main model outputs: time series of catch, yield, population size, biomass and age/ meat weight structure (in the Fortran90 application) (Figures 7.1- 7.6).

### Scenario 1- Interpretation of results

- Fishing effort and fishing mortality rate are maintained at constant levels to produce a depletion of 50% at the end of the historical time series (year 21) (Figure 7.1).
- Stock biomass is thus, declines exponentially to 50% of the unfished biomass by year 21. The spawning stock also declines, to 37% of the virgin spawning biomass. The effect of overfishing on reproductive adults is more severe (Figure 7.2)
- The age structure is modified by fishing. From the exponential decline equation, there are naturally more young individuals than old ones in the virgin stock. The relatively unselective fishery catches conch at 80 grams, thus reducing the abundance of most age-classes over time. By year 21, very few conch ages 7-10 remain. (Figure 7.3).
- Biomass by age also declines within a year and over time, but given the large variability of MW-at-age, the annual distributions do not change the shape over time (Figure 7.3)
- Catch-at-age distributions show that age-2 conch are the most abundant in the catch, with older ages in smaller proportions (Figure 7.4).
- The meat-size structure of the catch clearly shows knife-edge selectivity at 80g. The annual catch distributions have a peak at 160 grams, and decline in bigger sizes. This pattern remains stable over time (Figure 7.4).
- Yield declines at the beginning of the series, and remains stable thereafter (Figure 7.5).
- The comparison of the final age and meat weight structure among the stocks fished at different F levels shows that the effects of fishing are more severe at greater fishing mortalities. The disappearance of large age/size classes and a greater reduction in stock size are clear as F increases (and the depletion level increases) (Figure 7.6).

The next three scenarios, introduce different types of management regulation to a severely depleted stock (Scenario I-Case3-DL=20%):



**4) Meat Weight Limit- Case 1- 'H120'** - A meat weight selectivity of 120 g is applied during the historic period, instead of the base-case selectivity of 80g, which considered non-selective. Size-based management occurs during the historic period, so there is no additional 10-yr management series.

**Meat Weight Limit- Case 2- 'H80M120'** – A meat weight selectivity of 80 g during the historic period (base-case), and of 120g during an extended, 10-year management period.

**5) Fishing Effort Reduction- 'F10% Red'**- Fishing effort is reduced by 10%each year during the management period, to reach  $F=0$  in the last year.

**6) Seasonal Closures- 'Close\_4mo'** – A 4-month closure is implemented each year during the management period. This is another form of effort-reduction strategy.

#### A brief comparison of management scenarios

A comparison of the effects of management regulations upon the stock (in terms of biomass, age/size structure, and yield) at the end of the management period can provide information to select the best management option. Regulations are listed below, in order of effectiveness, for each management objective (from Figures 7.7, 7.8, and 7.9):

MANAGEMENT OBJECTIVES					
	Place	Biomass reconstruction	Reconstruction of Age Structure	Reconstruction of Size (MW) Structure	Increase Yield
<b>Best</b>	1	F Reductions	Improve historical MW limits	F reduction	Seasonal closures- maintain historical levels
	2	Seasonal (4-month) closures	F reductions	Seasonal closures	Improve historical MW limits
	3	Improve MW limits (to larger MW=120g) in historical period	Seasonal closures	Improve historical MW limits	MW limits only in management period*
	4	MW limits only in management period. * Need more time or combine with other regulations	MW limits only in management period*	MW limits only in management period* .	Status quo
<b>Worst</b>	5	Status quo	Status quo	Status quo	Effort reductions- reduce yield significantly; at $F=0$ no yield

#### A final note on conch fisheries management

These examples are only a few of hundreds of possibilities that can be attempted with conch simulation models. The ultimate aim of such exercises is to find a compromise among objectives to elucidate the best set of management options to rebuild overexploited queen conch stocks and to stop overfishing. In the face of the enormous uncertainties associated with queen conch biology, assessment and management, it is recommended that scientists and managers start making use of this and all the other tools available to make more informed decisions. Hopefully, manual users will start viewing conch fisheries management from a different perspective after understanding the great challenges and opportunities that this species represents.

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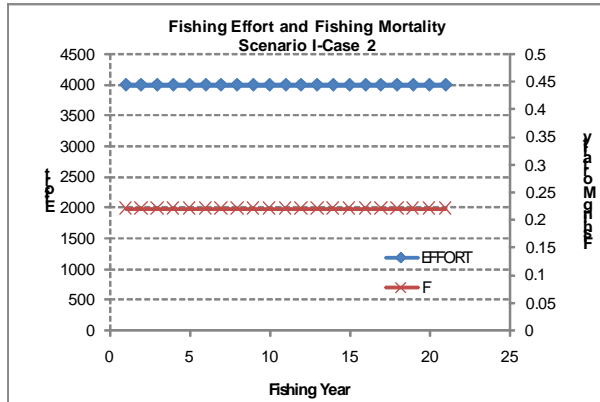


Figure 7.1 Constant fishing effort and fishing mortality needed to create the base-case scenario with DL=50% (Scenario I- Case 2).

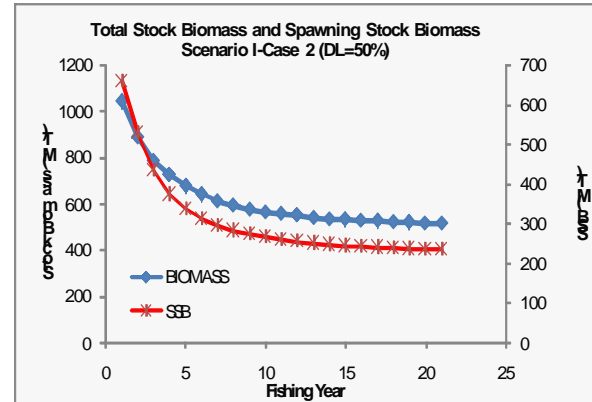


Figure 7.2 Biomass depleted to 50% by the end of the exploitation period ( $DL=B_1/B_{21}=0.5$ , Scenario I-Case2). Spawning stock also shown (depleted to 37%).

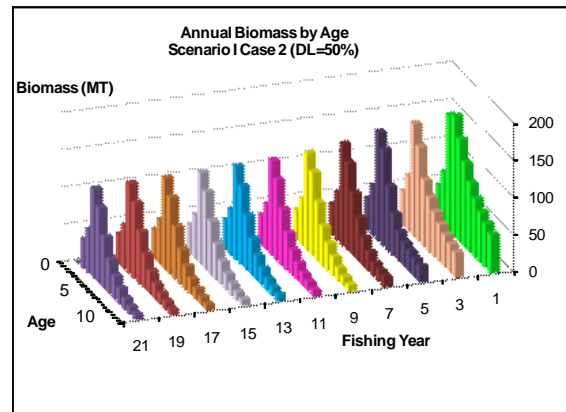
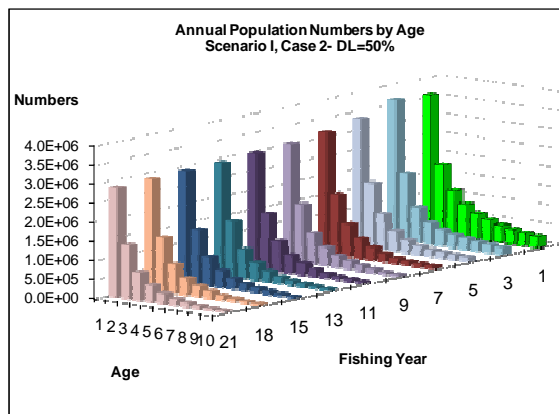


Figure 7.3 Annual age-structure of population numbers and biomass under Scenario I-case 2 (DL=50%).

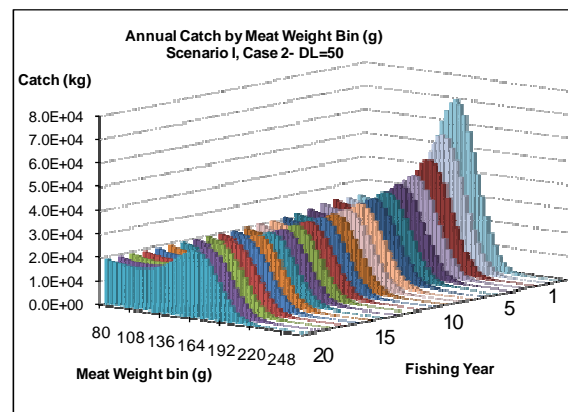
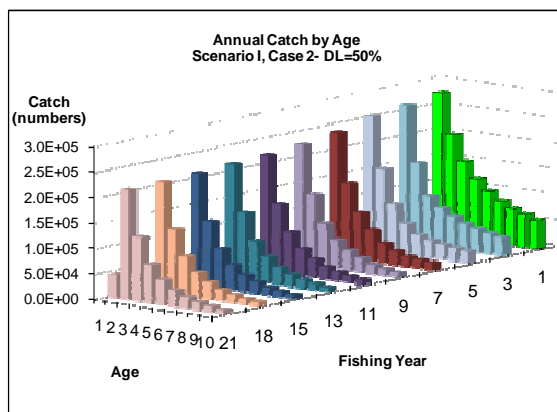


Figure 7.4 Annual catch in numbers by age and annual catch in numbers by meat weight bin (4 gram bins).

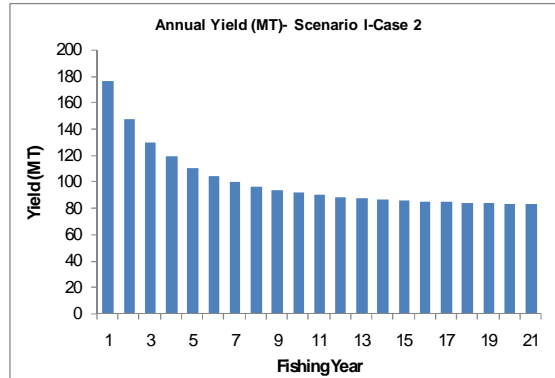


Figure 7.5 Annual yield (MT) under Scenario I-case 2 (DL=50%).

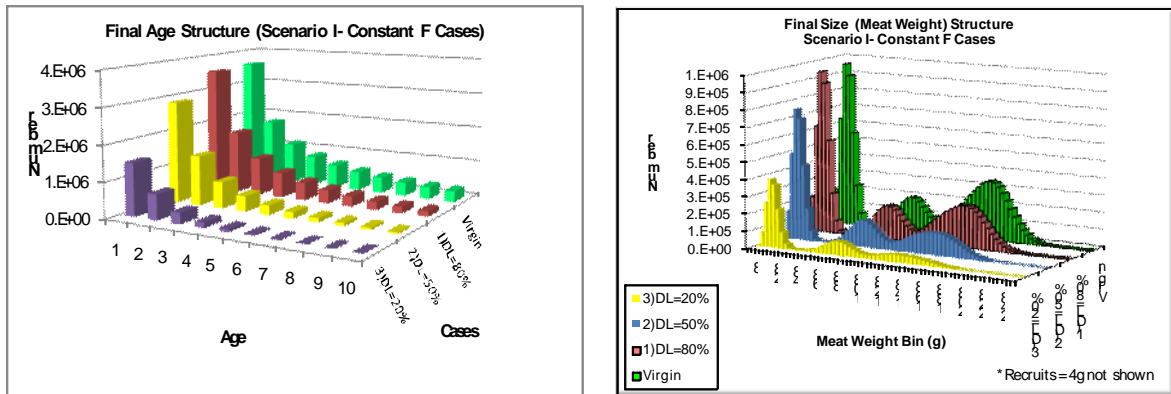


Figure 7.6. Comparison of the final age and meat weight structure among the simulated stocks fished to different depletion levels (DL=80%, 50%, 20%) under Scenario I (cases 1- 3).

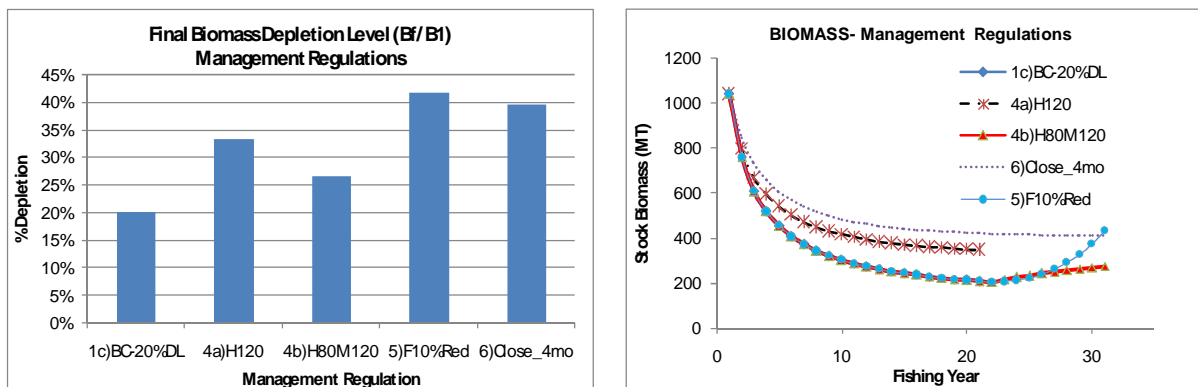


Figure 7.7. Final biomass depletion level and biomass trajectories under different management regulations. Depicted scenarios are: 1c) BC-20% DL=Base-case; 4a) H120=Historic MW limit =120g; 4b) Management MW limit=120g; 5) F10%Red= 10% effort reduction per year; 6) Close\_4mo= 4- month seasonal closures.

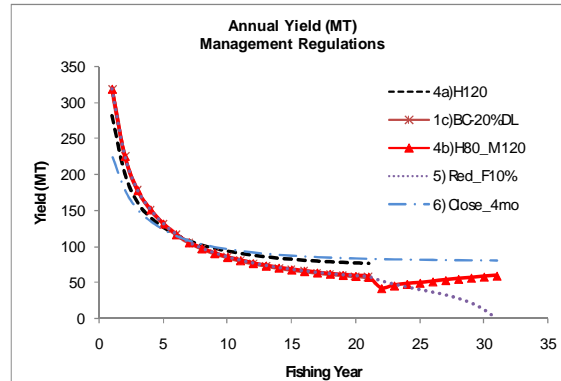


Figure 7.8. Annual yield trajectories under different management regulations. Depicted scenarios are: 1c) BC-20%DL= Base-case ; 4a) H120=Historic MW limit =120g; 4b) Management MW limit=120g; 5)F10%Red= 10% effort reduction per year; 6) Close\_4mo= 4-month seasonal closures.

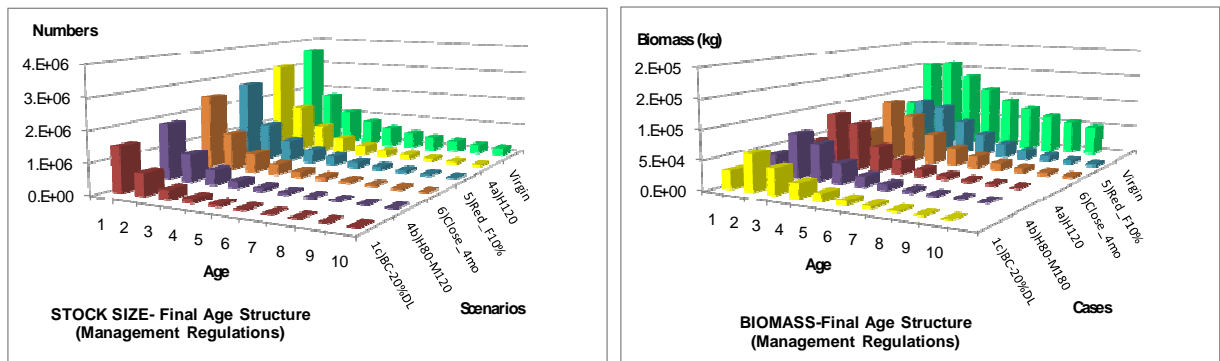
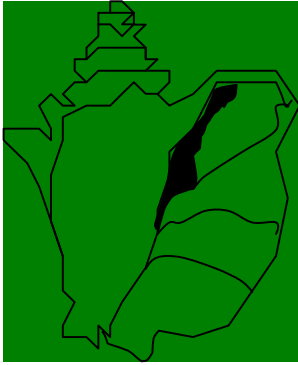


Figure 7.9. Final age structure in numbers and biomass under different size limit regulations, at constant  $F=0.4$ . Depicted scenarios are: After 21 years: 1c) BC-20%DL=Historic MW limit=80g; 4a) H120=Historic MW limit =120g, and after 31 years, 4b) H80M120= Historic MW limit=80g, Management MW limit=120g.



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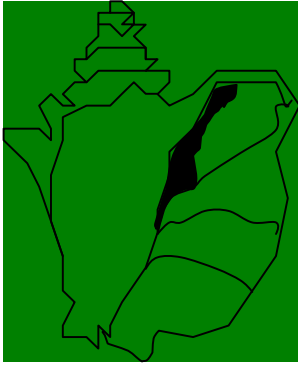
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## APPENDICES

Back cover



Aztec Queen Conch Sculpture from Templo Mayor Tenochtitlan (Mexico City) Archeological Museum, Mexico City. Photo by Monica Valle-Esquivel.