2.0 Estimation and Projection Methodology

As described in section 1.6, methods for management reference point estimation and predictions of stock status through 2009 have been classed into three categories, depending on the availability of data: age-based reference points; surplus production estimators, and index-based approaches. The theory and specific application of methods associated with the three approaches are summarized below.

2.1 Age-based assessments of reference points

Both a parametric and an empirical non-parametric approaches to age based production analyses were employed to derive F_{MSY} and B_{MSY} or their proxies, and to conduct projections for evaluating rebuilding plans if required. The two approaches were applied to each stock (where appropriate) so as to be potentially complementary and supportive and because using both should build confidence in the results. Where results differ appreciably, the results of the empirical approach were used as a component in final model selection. Automatic objective application these techniques is often compromised by lack of sufficient observation on stock and recruitment over a suitable range of biomass to provide suitable contrast. Thus it is often necessary to extrapolate beyond the range of observation and to infer the shape of the stock recruit relationship, within the range of observation, from limited and very variable data. Subjective judgement, drawn from collective scientific experience, was used to establish the following guidelines for applying both of these approaches. Unless there is convincing evidence to the contrary, the shape of the stock recruit relation will be assumed to be asymptotic. This assumption leads to an adaptive management approach to test the strength of supercompensatory mechanisms at higher stock sizes that should permit gradual accumulation of information at higher biomass, facilitating subsequent refinement of reference points (section 4.4). Making the assumption of increasing recruitment as biomass increases can result in predicting recruitment outside the range of observation and can result in unreasonably large estimates of B_{MSV} . Alternatively, making the assumption that recruitment varies inversely with biomass beyond some point result in a more aggressive harvesting strategy which might not permit learning about the potential productivity of the resource at higher biomass. In the absence of a plausible mechanism for overcompensation (cannibalism, spatial interference between adults and progeny, etc.) an asymptotic relationship is preferred as a basis for reference point estimation and projections.

For stocks that have been consistently growth overfished, if the estimate of Fmsy is substantially greater than Fmax or F40% msp, the basis of this needs to be closely examined for possible model mis-specification.

The specific procedures used for age-based reference point estimation are described below. We emphasize again that reference point estimates will periodically be updated and possibly change substantially as we learn more about stock dynamics at higher biomass. Parametric and non-parametric approaches should be attempted in parallel, if re-enforcing, either approach can be used for projections.

2.1.1 Empirical Non-parametric Approach

The general approach of the empirical non-parametric method is to evaluate various statistical moments of the observed series of recruitment data and to apply the estimated biomass per recruit associated with common F reference points to derive the implied spawning stocks and equilibrium yields. For this purpose, we developed a consistent format ("4-panel plots", see Figure 3.1.2 for the example of Gulf of Maine cod). The 4-panel plots includes the time series of spawning stock biomass and recruitment (plots a and b) and the scatterplot of stock-recruit data (plot c). A lowess smoother is fit to the s-r data as a visual guide to any trend in the relationship between stock and recruitment. If this trend is flat, then the mean or median recruitment is chosen for biomass calculation, depending on the leverage exerted by outliers (usually very large year classes). In the lower right corner of the 4-panel plot the moments of the recruitment series are multiplied by the BPR at F0.1 and F40% msp to give point estimates of associated spawning biomasses. For example, in Figure 3.1.2 the mean of all recruitment values in the series is 7.67 million fish. If this value is multiplied by 11.412 kg/fish at F40% msp, this results in a spawning biomass of 87,580 metric tons. This value is compared to the results from parametric analyses of model fits. The full bpr/ypr analysis for this stock is given in Table 3.1.2.

Several types of analyses of the recruitment * BPR analysis are undertaken, depending on the shape of the relationship between stock and recruitment:

• For cases where recruitment appears to be impaired at lower biomass, the average recruitment at a higher biomass stanza is evaluated as the proxy for recruitment at MSY, otherwise the average recruitment over all observations will be used.

• The B_{MSY} proxy will be calculated from the spawning biomass per recruit at $F_{40\%}$ and the proxy for recruitment at MSY. This assumes that compensatory mechanisms such as impaired growth or maturity schedules or reduced recruit survival are negligible over the range of expected biomass considered. All of these parameters can be monitored, consisted with the recommended adaptive approach to increasing stock biomass.

• Projections to evaluate rebuilding plans incorporate uncertainty in the current population estimate (either bootstrap replicates or suitable variance simulation) and stochasticity in predicted recruitment (see section 2.4.1 below). Recruitment stochasticity is accommodated by either resampling from observed recruitment, r/ssb or their CDFs, (as long as the s-r model used is consistent with that used for estimating reference points).

• The use of $F_{40\%}$ as a proxy for F_{MSY} is likely to maintain adequate spawning potential for most primary New England groundfish based on the results of Clark (1993) and Mace (1994). This choice represents a more conservative spawning potential ratio than recommended by Clark (1991), and is consistent with the analyses of Thompson (1993) who suggested that fishing mortality rates be set no greater than $F_{30\%}$ and with the review of spawning-per-recruit requirements by Mace and Sissenwine (1993), who found that, on average, stocks require threshold spawning potential ratio values of at least 31% for sustainability. Overall, these results suggest that an F_{MSY} proxy of $F_{35\%}$ may be too high to sustain stocks in the long term. Based on the results of Dorn (2002), $F_{40\%}$ appears to be too aggressive a harvest rate for long-lived West Coast *Sebastes* spp., and therefore the use of $F_{50\%}$ as a proxy for F_{MSY} is considered to be appropriate for Acadian redfish.

2.1.2 Parametric Model Approach

The parametric model approach uses a fitted parametric stock-recruitment model along with yield and spawning biomass per recruit information to calculate MSY-based references points using a standard algorithm. A key difference between the nonparametric proxy and the parametric approach is that the parametric approach produces a direct estimate of F_{MSY} in contrast to using an assumed proxy value. A key similarity between the nonparametric proxy and the parametric approach is that both use yield and spawning biomass per recruit analyses to determine MSY and B_{MSY} values. Descriptions of the stock-recruitment models, estimation of stock-recruitment model parameters, and computation of maximum sustainable yield are given below.

Stock-Recruitment Models

The stock-recruitment models for estimation of MSY-based reference points were chosen to allow for compensatory and overcompensatory stock-recruitment dynamics. This choice provided two competing hypotheses about the possible forms of density-dependence. Both compensatory and overcompensatory models included a deterministic component to describe equilibrium stock-recruitment dynamics. Similarly, the models included an observation error term to account for randomness in the stock-recruitment data.

Deterministic Component

The Beverton-Holt curve (Beverton and Holt 1957) was used to model compensatory stockrecruitment dynamics where recruitment increases with spawning stock to an asymptote at large spawning stock size. This curve has a sound theoretical basis as a model of stock-recruitment dynamics. The Beverton-Holt curve arises naturally when density-dependent effects are critical at some early life history stage (see, for example, Quinn and Deriso 1998) and can also arise as a result of adaptation to balance predation and foraging risk in a variable environment (Walters and Korman 1999). This model was considered to be the null hypothesis in the absence of evidence that it was inconsistent with the observed data.

The modified Beverton-Holt curve (Mace and Doonan1988) was used for parameter estimation:

$$R = \frac{4z_{MAX}R_{MAX}S}{S_{MAX}(1 - z_{MAX}) + S(5z_{MAX} - 1)}$$

where S_{MAX} = maximum observed level in the stock-recruitment data; R_{MAX} = maximum expected recruitment; and z_{MAX} = steepness of the modified Beverton-Holt curve computed as the ratio of R at 20% of S_{MAX} to R_{MAX} .

A standard form of the Beverton-Holt curve was used for projections:

$$R = \frac{\alpha S}{\beta + S}$$

The parameters of the standard and modified curves were related as:

$$\alpha = \frac{4z_{MAX}R_{MAX}}{5z_{MAX} - 1}$$

and

$$\beta = \frac{S_{MAX}(1 - z_{MAX})}{5z_{MAX} - 1}$$

For the purposes of using the results of Myers et al. (1999) to determine appropriate prior distributions for the steepness parameter, the steepness calculated relative to the unfished spawning stock size, S_{UNFISHED} , denoted as z, was related to unfished equilibrium recruitment, R_{UNFISHED} , and the parameters of the standard curve via:

$$z = \frac{\frac{\alpha S_{UNFISHED} 0.2}{\left(\beta + S_{UNFISHED} 0.2\right)}}{R_{UNFISHED}}$$

For stocks that had short time series of stock-recruitment data and had relatively high NEFSC autumn survey biomass indices during the 1960s, values of S_{MAX} were computed as the product of average spawning biomass times the ratio of average NEFSC autumn survey biomass indices during 1963-1970 to the average biomass indices during 1990 to the most recent year for which stock-recruitment data were available. This computation was done for Gulf of Maine cod (S_{MAX} =77,500 mt), Georges Bank cod (S_{MAX} =104,200 mt), Georges Bank (S_{MAX} =36,200 mt) and Southern New England (S_{MAX} =64,400 mt) yellowtail flounder. For the other three stocks where parametric models were investigated, the maximum spawning biomass value in the stock-recruitment time series was S_{MAX} ; these were Georges Bank haddock (S_{MAX} =199,500 mt), Cape Cod yellowtail flounder (S_{MAX} =5,000 mt), and Southern New England winter flounder (S_{MAX} =14,600 mt). Here it is important to note that S_{MAX} was simply a fixed value for which to estimate the R_{MAX} parameter.

The Ricker curve (Ricker 1954) was used to model overcompensatory stock-recruitment dynamics where recruitment decreases with spawning stock as stock size becomes large. The form of the Ricker model used for parameter estimation was:

$$R = Se^{\alpha + \beta S}$$

where α = the slope at the origin and β = the strength of density-dependence in the relationship.

Stochastic Component

The stochastic component was represented by a multiplicative lognormal or an autoregressive, multiplicative lognormal error structure with a lag of one year. The stochastic component was multiplied by the deterministic component, denoted as $f(S_i)$ for the ith data point, to obtain the stock-recruitment model:

$$R_i = f(S_i)e^{\varepsilon_i}$$

For uncorrelated errors, the ϵ_i were iid Gaussian random variables with zero mean and constant variance σ^2 . In this case, the error variance (σ^2) was a parameter to be estimated. For autoregressive lag-1 errors, the ϵ_i were distributed as:

$$\varepsilon_i = \phi \varepsilon_{i-1} + w_i$$
, where $|\phi| < 1$, $Var(\varepsilon) = \sigma^2$,
 $w_i \sim N(0, \sigma_w^2)$, and $\sigma_w^2 = (1 - \phi^2)\sigma^2$

and the autoregressive coefficient and the error variance were additional model parameters to be estimated. The multiplicative lognormal error term was used because this positively-skewed distribution arises naturally when groundfish survival rates during early life history are affected by numerous independent random events represented as multiplicative log-scale effects. In this context, as the number of random events becomes large, the distribution of the mean of the logscale multiplicative process approaches a normal random variable under the central limit theorem. The autoregressive error term was included to model serial correlation in random environmental variation because this allowed successive recruitments to be correlated when the effects of environmental forcing were strong, e.g., periods of good recruitment followed by periods of poor recruitment, regardless of the deterministic component.

Estimation of Stock-Recruitment Model Parameters

Maximum Likelihood Estimation

Parameter estimates were computed using maximum likelihood estimation conditioned on the stock-recruitment model (see, for example, Brodziak et al. 2001). The support function, or loglikelihood (log*L*), for a total of n stock-recruitment data points (R_i , S_i) with uncorrelated lognormal errors was:

$$\log L(\underline{\theta}, \sigma^2) = -\frac{n}{2}\log(2\pi) - n\log\sigma - \sum_{i=1}^n \log R_i - \frac{1}{2\sigma^2} \sum_{i=1}^n \left(\log R_i - \log f(S_i)\right)^2$$

For models with autoregressive lag-1 correlated lognormal errors (see, for example Seber and Wild 1989) the loglikelihood was:

$$\log L(\underline{\theta}, \sigma^2, \phi) = -\frac{n}{2}\log(2\pi) - n\log\sigma_w - \sum_{i=1}^n \log R_i + \frac{1}{2}\log(1-\phi^2)$$

$$-\frac{1}{2\sigma_w^2}\sum_{i=2}^n \left(\log R_i - \phi \log R_{i-1} - \log f(S_i) + \phi \log f(S_{i-1})\right)^2 - \frac{(1-\phi^2)}{2\sigma_w^2} \left(\log R_1 - \log f(S_1)\right)^2$$

Maximum likelihood estimates (MLEs) of model parameters were computed using these support functions and the time series of stock-recruitment data. The AD Model Builder software package (Otter Research Ltd. 2001) was used to compute the MLEs.

Bayesian Priors on Steepness, Slope at the Origin or Unfished Recruitment

Because it was recognized that there would be limited information on the value of the steepness parameter of the Beverton-Holt curve or the slope at the origin of the Ricker curve, we borrowed from the strength of meta-analyses of numerous fish populations (Myers and Mertz 1998) to help to determine these parameters in a Bayesian statistical estimation framework (Gelman et al.1995; Hilborn and Mangel 1997; Punt and Hilborn 1997). In this context, an informative prior on the steepness or slope at the origin was determined using results of Myers et al.'s (1999) meta-analysis of a large number of stock-recruitment data sets. In a frequentist estimation framework, the use of such a prior would be conceptually equivalent to applying a penalty function to the support function to constrain parameter estimates (e.g., Edwards 1992).

The prior on steepness of the Beverton-Holt curve was based on values of z reported in Table 1 of Myers et al. (1999). The informative prior was assumed to be distributed as a normal random variable. Thus, the negative log of the prior on steepness (P(z)) was:

$$-\log P(z) = 0.5\log(2\pi) + \log(\sigma_z) + \frac{(z - \mu_z)^2}{2\sigma_z^2}$$

The mean of the informative prior was taken to be the median point estimate of steepness (z). The standard error of the informative prior was computed from the upper and lower values of the 60% confidence interval for steepness and the assumption that the steepness was normally distributed. This led to informative priors for the steepness of Atlantic cod, haddock, yellowtail flounder, and winter flounder (Table 2.1.2.1).

Similarly, the prior on the slope at the origin of the Ricker curve was based on values of α =logA and standard errors reported in Table 1 of Myers et al. (1999). As with the steepness parameter, the informative prior was assumed to be distributed as a normal random variable so the negative

log of the prior on the slope at the origin $(P(\alpha))$ was:

$$-\log P(\alpha) = 0.5\log(2\pi) + \log(\sigma_{\alpha}) + \frac{(z - \mu_{\alpha})^2}{2\sigma_{\alpha}^2}$$

The parameters of the informative priors for the slope at the origin of Atlantic cod, haddock, yellowtail flounder, and winter flounder (Table 2.1.2.1).

Bayesian Prior on Recruitment

It was also recognized that there could be limited information on recruitment at high spawning stock sizes because the assessment time horizons of most stocks were short in comparison to their historic period of exploitation. For example, Georges Bank cod had been fished since the 1700s but the assessment time horizon begins in the late-1970s. As a result, an empirical Bayesian statistical estimation approach (Carlin and Louis 2000) was used to determine informative priors for the distribution of unfished recruitment, $R_{UNFISHED}$. The informative prior for $R_{UNFISHED}$, denoted by $P(R_{UNFISHED})$, was assumed to be normally distributed so that the negative log prior had form:

$$-\log P(R_{UNFISHED}) = 0.5\log(2\pi) + \log(\sigma_R) + \frac{(z-\mu_R)^2}{2\sigma_R^2}$$

The mean and standard error of the informative prior on $R_{UNFISHED}$ was determined using the empirical data on recruitment at high spawning stock size. For stocks that had a pattern of increasing recruitment with increasing spawning stock size, either in the hindcast or observed recruitment data, an appropriate subset of the observed recruitment data was used to determine the mean and standard error of the prior. These stocks were: Georges Bank haddock, Georges Bank cod, Southern New England winter flounder, and Georges Bank and Southern New England yellowtail flounder. For Georges Bank haddock, recruitment values during 1931-1960 were used to determine the prior parameters. For Georges Bank cod, recruitment values for spawning stock sizes in the top quartile of the spawning stock distribution were used to determine the prior parameters. For Southern New England winter flounder, recruitment values for spawning stock sizes were used to determine the prior parameters. For Southern New England winter flounder, recruitment values for the five highest observed spawning stock sizes were used to determine prior parameters; this was done because the data series was short (n=17). For the Georges Bank and Southern New England yellowtail flounder, recruitment values for spawning stock sizes in the top quartile of the hindcast spawning stock sizes in the top quartile of the spawning stock sizes in the top quartile of the hindcast spawning stock distribution were used to determine prior parameters; this was done because the data series was short (n=17). For the Georges Bank and Southern New England yellowtail flounder, recruitment values for spawning stock sizes in the top quartile of the hindcast spawning stock distribution were used to determine the prior parameters.

For stocks that had no discernable trend in recruitment with spawning stock size, the entire set of observed recruitment values were used to compute the mean and standard error of the prior. These stocks were: Gulf of Maine cod and Cape Cod yellowtail flounder.

Bayesian Estimation of Parameter Uncertainty

We used a Bayesian approach to characterize the uncertainty in output parameters of the parametric model to compute MSY-based reference points. This was done to give estimates of precision and Bayesian credibility intervals (confidence intervals) for the key output parameters. The AD Model Builder software package (Otter Research Ltd. 2001) was applied with an informative prior on either steepness, slope at the origin, or unfished recruitment, depending upon model configuration and with an uninformative prior on the remaining model parameters. In this approach, the posterior distribution of model parameters is assumed to be multivariate normal with mode equal to the MLE. The observed Hessian matrix at the MLE is used to estimate the covariance of the posterior distribution and samples from the posterior distribution are calculated using a Markov Chain Monte Carlo (MCMC) algorithm based on the Gibbs sampler (Gelman et al. 1995). The MCMC algorithm was run for 500,000 iterations to obtain representative samples from the posterior distribution with a sampling interval of every 100th value to reduce autocorrelation in the series of samples. Thus, there were 5,000 posterior samples available for inference.

Computation of Maximum Sustainable Yield

Maximum sustainable yield for a fixed equilibrium stock-recruitment curve combined with yield and spawning biomass per recruit information was computed using a standard algorithm (Sissenwine and Shepherd 1987; Clark 1991; Brodziak 2002). In this approach, equilibrium yield is determined for a uniform grid of fishing mortality values. In this case, we used a grid of F ranging from 0 to 2 in 0.005 increments. The first step of the algorithm is to compute yield per recruit (Y/R) and spawning biomass per recruit (S/R) for each value of F. In this case, standard procedures to compute YR and S/R were applied (Gabriel et al. 1989). The second step of the algorithm is to determine the equilibrium spawning biomass based on the spawning biomass per at F and the stock-recruitment parameters over the grid of F values. For the Beverton-Holt model, the equilibrium spawning biomass (S*) is:

$$S^* = \alpha(S / R) - \beta$$

while for the Ricker model, it is:

$$S^* = \frac{-1}{\beta} \left(\log(S / R) + \alpha \right)$$

The third step of the algorithm is to compute equilibrium recruitment (R^*) from equilibrium spawning biomass and the stock-recruitment parameters over the grid of F values. For the Beverton-Holt model, R^* is:

$$R^* = \frac{\alpha S^*}{\beta + S^*}$$

while for the Ricker model, R* is:

$$R^* = S^* e^{a + \beta S^*}$$

The fourth step of the algorithm is to compute equilibrium yield (Y*) over the grid of F values as the product of equilibrium recruitment and yield per recruit:

$$Y^* = (R^*)(Y / R)$$

The last step of the algorithm is to determine MSY as the maximum value of Y* over the grid of F values; this also determines the value of B_{MSY} and F_{MSY} .

Use of Median Stock-Recruitment Curve

Applying a logarithmic transformation to either parametric stock recruitment model leads to a nonlinear regression equation:

$$Z = \log(F(S)) + \varepsilon$$

where $Z=\log R$. This provides a way to estimate the parameters of F(S) in a logarithmic scale which is natural approach to rescaling the estimation equation.

In log-scale, any estimate of Z calculated from the parameters of F(S) for a particular value of S is an unbiased estimate of the expected value of Z, E[Z]. In contrast, any estimate of F(S) computed from the parameters of F(S) under inverse transformation to the original measurement scale is a biased estimate of the expected value of F(S). This bias is approximately equal to the exponential function of the population error variance divided by 2 and it applies only to the statistical expectation of F(S). In fact, the estimate of F(S) computed from the parameters of F(S) under inverse transformation to the original measurement scale is equal to the estimate of F(S). Some transformation of F(S) is expected value of F(S) computed from the parameters of F(S) under inverse transformation to the original measurement scale is equal to the median of the distribution of the estimator of F(S) (see, for example Seber and Wild 1989, pp. 86-87).

For the purposes of evaluating whether MSY-based reference points are achieved, the median value of the distribution of any skewed estimator has been considered preferable to the mean. For example, projections are conducted to determine the fishing mortality that would lead to B_{MSY} being achieved with a 50% probability in a given year. In practice, the achievement of management targets under simulation has been consistently evaluated with respect to the 50% probability or median level for New England groundfish stocks. This implies that, to be consistent with the interpretation of achieving reference points under projection, the median stock-recruitment curve, as estimated under a logarithmic or any other monotonic transformation of the data, may be used as the basis for reference point computations. As a result, the median stock-recruitment curve is used for MSY-based reference point computations, in contrast to the expected value which would be subject to accurate estimation of the population error variance and correct specification of the observation error distribution.

	Steepness		Slope at the origin	
Species	Mean	SE	Mean	SE
Atlantic cod	0.84	0.08	1.37	0.15
Haddock	0.74	0.11	0.72	0.21
Yellowtail flounder	0.75	0.07	0.79	0.34
Winter flounder ¹	0.80	0.09	0.79	0.18

Table 2.1.2.1 Parameters of informative prior distributions for steepness and slope at the origin.

¹ Based on reported values for Pleuronectids

Hierarchical Criteria for Comparing Parametric Stock-Recruitment Model Fits

For each of the candidate stock-recruitment models, an hierarchy of criteria is applied to determine whether the maximum likelihood model fits are consistent with auxiliary information and with respect to model goodness-of-fit measures. These criteria are used as a quality control check to ensure that the individual model outputs make sense.

A priori, it is required that the estimated MLE from the model fit satisfies first- and second-order derivative conditions required for a strict maximum. These are that the gradient of the loglikelihood is identically zero at the MLE and that the Hessian matrix of second derivatives of the negative loglikelihood is positive definite.

In addition to satisfying the derivative conditions, each model must satisfy the following hierarchy of criteria to be considered credible:

- 1. Parameter estimates must not lie on the boundary of their feasible range of values
- 2. The estimate of MSY lies within the range of observed landings
- 3. The estimate of S_{MSY} is not substantially greater than the nonparametric proxy estimate
- 4. The estimate of F_{MSY} is not substantially greater than the value of F_{MAX}
- 5. The dominant frequencies for the autoregressive parameter, if applicable, lie within the range of one-half of the length of the stock-recruitment time series
- 6. The estimate of recruitment at S_{MAX} , the maximum spawning stock size proxy input to the stock-recruitment model, is consistent with the value of recruitment used to compute the nonparametric proxy estimate of S_{MSY}

For the subset of models that satisfy these criteria, Akaike's Information Criterion (AIC) can be used to assign relative probabilities to each model based on loglikelihood values (Brodziak et al. 2001). In this approach, each candidate model is assigned an equal prior probability of being the true state of nature. Model likelihood ratios are then compared using Bayes' Theorem to

compute the posterior probability that each model represents the true state of nature. Last, the most likely model is selected as the best parametric model from which to base reference point calculations and stochastic projections. Further details of these calculations are provided below.

A bias-corrected form of the AIC criterion, known as AIC_C (Burnham and Anderson 1998 and references therein), was computed for each candidate model fit to data set D, with K parameters, n data points and, likelihood value $L(D | \underline{\Theta})$ at the MLE $\underline{\Theta}$.

$$AIC_{C} = -2\log L(D \mid \underline{\Theta}) + 2K + \frac{2K(K+1)}{n-K-1}$$

In theory, the best model has the lowest AIC_c value. However, when AIC_c values were very similar among models, support for a single best model was limited.

Given the AIC_c values, Bayes' theorem was applied to evaluate the relative goodness of fit of each model. The probability that each candidate model was the true state of nature was computed for the available stock-recruitment data. Estimated AIC_c values were used to measure the relative likelihood of each model, with a penalty applied for the number of parameters which differed according to the assumed error structure. In particular, let $\underline{M} = \{M_k\}$ denote the set of models and let M_{MAX} denote the model with the maximum AIC_c value; M_{MAX} is the least likely model in \underline{M} . Thus, for a given set of stock-recruitment data D and model M with corresponding AIC_c value of AIC_c(D|M), the likelihood ratio of model M to the least likely model is $\Lambda(D|M,M_{MAX})$ where:

$$\Lambda(D|M, M_{MAX}) = \frac{L(D | \Theta_{M})}{L(D | \Theta_{M_{MAX}})} \propto \frac{e^{-AIC_{C}(D|M)}}{e^{-AIC_{C}(D|M_{MAX})}}$$

The posterior distribution of relative model credibility was calculated from the likelihood ratio form of Bayes' Theorem using the model likelihood ratios relative to the least likely model and the prior distribution of each model, $Pr(M_k)$. The posterior probability of model M, denoted by Pr(M|D), is the product of its likelihood ratio and prior probability divided by a normalizing constant

$$\Pr(M|D) = \frac{\Lambda(D|M, M_{MAX}) \Pr(M)}{\sum_{M_k \in \underline{M}} \Lambda(D|M_k, M_{MAX}) \Pr(M_k)}$$

In the absence of any prior information on the credibility of candidate models, we assumed equal prior probabilities for each them. Models that did not satisfy first- or second-order derivative conditions at the calculated maximum or that did not satisfy one or more of the hierarchical criteria were assigned a prior probability of zero.

Model Name Decoder

Model names were built iteratively as more analyses were conducted (For example, see table 3.1.1 for Gulf of Maine cod). To decode the model name:

1. Start at the right, the last two letters are either BH (Beverton and Holt) or RK (Ricker), which distinguish the two possible underlying stock recruitment relationships.

2. If there is an A just before either BH or RK this means that an autoregressive error term was assumed in the model.

3. All the remaining models start with a P.

4. If the P is alone except for the letters already examined this means that the model assumed a prior for the steepness parameter in the Beverton and Holt model or the slope parameter in the Ricker model.

5. If the P is followed by R (not part of RK for the Ricker model), then the model assumed a prior for the unfished recruitment from the VPA data.

6. If the P and R are followed by HC, then the model assumed a prior for the unfished recruitment that was derived from hindcast data.

7. If the P is followed by 2, then the model assumed both a prior for unfished recruitment (either from the VPA data, no additional letters, or the hindcast data, HC) and a prior for either the steepness parameter in the Beverton and Holt model or the slope parameter in the Ricker model.

The 24 possible model names (note that all models are not examined for all stocks) are given in the table 2.1.2.2.

			Priors			
					Unfi	shed R
	Stock Recruitment	Auto-				
Name	Relationship	regressive	Steepness	Slope	VPA	Hindcast
BH	Beverton & Holt					
ABH	Beverton & Holt	Yes				
PBH	Beverton & Holt		Yes			
PABH	Beverton & Holt	Yes	Yes			
PRBH	Beverton & Holt				Yes	
PRABH	Beverton & Holt	Yes			Yes	
P2BH	Beverton & Holt		Yes		Yes	
P2ABH	Beverton & Holt	Yes	Yes		Yes	
PRHCBH	Beverton & Holt					Yes
PRHCABH	Beverton & Holt	Yes				Yes
P2HCBH	Beverton & Holt		Yes			Yes
P2AHCBH	Beverton & Holt	Yes	Yes			Yes
RK	Ricker					
ARK	Ricker	Yes				
PRK	Ricker			Yes		
PARK	Ricker	Yes		Yes		
PRRK	Ricker				Yes	
PRARK	Ricker	Yes			Yes	
P2RK	Ricker			Yes	Yes	
P2ARK	Ricker	Yes		Yes	Yes	
PRHCRK	Ricker					Yes
PRHCARK	Ricker	Yes				Yes
P2HCRK	Ricker			Yes		Yes
P2AHCRK	Ricker	Yes		Yes		Yes

Table 2.1.2.2. Definition of model names for fitting stock-recruitment data.

2.2 Surplus Production Assessments

Biomass Dynamics Analyses

A nonequilibrium surplus production model incorporating covariates (ASPIC; Prager 1994, 1995) was applied to each stock using landings (and discards where available) and multiple survey indices of stock biomass. The model assumes logistic population growth, in which the change in stock biomass over time (dB_t/dt) is a quadratic function of biomass (B_t):

$$d\mathbf{B}_{t}/dt = \mathbf{r}\mathbf{B}_{t} - (r/K)\mathbf{B}_{t}^{2}$$
(1)

where r is intrinsic rate of population growth, and K is carrying capacity. For a fished stock, the rate of change is also a function of fishing mortality (F):

$$dB_{t}/dt = (r-F_{t})B_{t} - (r/K)B_{t}^{2}$$
(2)

Biological reference points can be calculated from the production model parameters:

MSY	= K r / 4	(3)
B_{MSY}	= K / 2	(4)
F _{MSY}	= r / 2	(5)

Initial biomass (expressed as a ratio to B_{MSY} : *B1R*), *r*, MSY, and catchability of biomass indices (*q*) were estimated using nonlinear least squares of survey residuals. Biomass indices from research surveys or commercial catch rate contributed as independent biomass indices. Survey residuals were randomly resampled to approximate precision and model bias through bootstrap analysis.

Biomass dynamics models are simpler than age-based models such as VPA with relative advantages (e.g., they require only aggregate catch and biomass indices, and make simple assumptions about population dynamics) and disadvantages (e.g., they may ignore important age-based dynamics; National Research Council 1998a). With reliable observations of catch and biomass indices and a wide range of observed stock conditions, nonequilibrium models of biomass dynamics can provide reliable perspectives on stock status relative to MSY reference points (Hilborn and Walters 1992).

2.3 Index-based Assessments

Application of Index Methods: Catch and Fishery Independent Abundance Surveys

One of the core problems in fisheries science is the estimation of the scaling factor between estimates of relative abundance and true population size. This scaling factor is generally called the catchability coefficient. Assessment models that rely on VPA utilize the record of age-specific catches to approximate the virtual population. The utility of the virtual population as a means of estimating catchability rests on assumptions that the losses due to fishing are both known and large relative to natural mortality. Age structured assessments are data intensive and their scope is restricted to years in which both catch and abundance indices can be aged. In this section we explore the general trends in abundance and fishing mortality deducible from a time series of catch (or landings for some species) and survey indices. For all stocks, only the total catch (mt) and autumn and spring research trawl survey indices (kg/tow) are utilized. We explore the relative fishing mortality rate, defined as the ratio of catch to survey index, and relate it to what we call the replacement ratio. The replacement ratio is introduced here as an analytical tool for examining the historical behavior of a population and any potential influence of removals due to fishing activities. To test these concepts and to facilitate comparisons, the analyses were applied to both the aged and un-aged stocks.

The replacement ratio draws from the ideas underlying the Sissenwine-Shepherd model, delaydifference models, life-history theory, and statistical smoothing. We begin by defining $I_{j,s,t}$ as the j-th relative abundance index for species-stock unit s at time t and $C_{s,t}$ as the catch (or landings) of species-stock unit s at time t. The simple relative fishing mortality rate with respect to index type j, stock s and time t is defined as the ratio of $C_{s,t}$ to $I_{j,s,t}$. This ratio can be noisy, owing to imprecision of survey estimates, and the variation can be damped by writing the relative F as a ratio of the catch to some average of the underlying indices. Following the recommendation of the previous reference point panel review team, relative F is defined as the ratio of catch in year t to a centered 3-yr average of the survey indices:

$$relF_{j,s,t} = \frac{C_{s,t}}{\left(\frac{I_{j,s,t-1} + I_{j,s,t} + I_{j,s,t+1}}{3}\right)}$$
(1)

Note that under this definition, the estimates of relative F for the first and last years of a time series are based on only 2 years of data.

Noise in the survey indices also affects the ability to relate inter-annual changes in abundance estimates to removal from fishing. The general approach of averaging adjacent years to estimate current stock size underlies statistical smoothing procedures (e.g., LOWESS) as well as formal time series models (e.g., ARIMA methods). One of the difficulties of applying such approaches in the present context, is that the derived parameters, if any, are unrelated to the species' biology or any aspect of the fishery. Moreover, we are interested in a basic questions of whether the current stock is replacing itself and whether the current level of catch is too high or low. Population dynamics models usually come to the rescue and allow approximate answers to these questions. However, if age-structure models cannot be applied, and more importantly, if the recent history of the fishery is uninformative, then most mathematical models will fail. The underlying reasons for model failure may not be immediately obvious from analysis of standard diagnostic measures. Of greater concern is the issue of the model mis-specification, wherein an inappropriate model adequately fits the data but leads to deductions inconsistent with basic biology and the fishery. The proposed replacement ratio is a "data-based" technique relying on fewer assumptions. No technique however, can fully compensate for model mis-specification errors.

If we assume that the survival from eggs to the juvenile stage is largely independent of stock size, then the number of recruits will be proportional to stock size. Locally, (i.e, in the neighborhood of any give stock size) this assumption holds for any stock-recruitment function. Since a population is a weighted sum of recruitment events, the interannual change in total stock size tends to be small relative to the total range of stock sizes (at least in the Northeast USA). Recruitment in any year is likely to be small relative to the biomass of the total population. Thus, the change in total biomass is likely to be small relative to the change in annual recruitment. Although the mathematics are more complicated than this ,the argument is based on the premise that if $Var(x/1) = \sigma^2$ then $Var(\Sigma x/n) \sigma^2/n$. Of course, the magnitude of such changes depends on the variation of recruitment and the magnitude of fishing mortality.

Using the linearity assumption defined above, we can employ basic life history theory to write abundance at time t as a function of the biomasses in previous time periods. The number of recruits at time t (\mathbf{R}_t) is assumed to be proportional to the biomass at time t (\mathbf{B}_t). More formally,

$$R_t = S_o Egg B_t$$
 (2)

where **Egg** is the number of eggs produced per unit of biomass, and S_0 is the survival rate between the egg and recruit stages. Survival for recruited age groups at age a and time t $(S_{a,t})$ is defined as

$$S_{a,t} = e^{-F_{a,t} - M_{a,t}}$$
 (3)

where F and M refer to the instantaneous rates of fishing and natural mortality, respectively. We also need to consider the weight at age a and time t $(W_{a,t})$ and the average longevity (A) of the species

Using these standard concepts we now write the biomass at time t as a linear combination of the A previous years. Without loss of generality, we can drop the subscripts on the survival terms and assume that average weight at age is invariant with respect to time. Further, set the product S_0 Egg equal to the coefficient α . The biomass at time t can now be written as

$$B_{t} = R_{t-1}S^{1}W_{1} + R_{t-2}S^{2}W_{2} + R_{t-3}S^{3}W_{3} + ... + ..R_{t-(A-1)}S^{A-1}W_{A-1} + R_{t-A}S^{A}W_{A}$$
(4)

Substituting Eq. (2) into Eq. (4) leads to

$$B_{t} = \alpha B_{t-1} S^{1} W_{1} + \alpha B_{t-2} S^{2} W_{2} + \alpha B_{t-3} S^{3} W_{3} + ... + .\alpha B_{t-(A-1)} S^{A-1} W_{A-1} + \alpha B_{t-A} S^{A} W_{A}$$
(5)

If the population is replacing itself, then the left hand side of Eq. (5) will equal the right hand side. The replacement ratio Ψ_t can then be defined as

$$\Psi_{t} = \frac{B_{t}}{\alpha B_{t-1} S^{1} W_{1} + \alpha B_{t-2} S^{2} W_{2} + \alpha B_{t-3} S^{3} W_{3} + ... + .\alpha B_{t-(A-1)} S^{A-1} W_{A-1} + \alpha B_{t-A} S^{A} W_{A}}$$
(6)

Further simplifications of the replacement ratio can be obtained by letting $\phi_j = \alpha S^j W_j$ and noting that $\mathbf{I}_t = \mathbf{q} \mathbf{B}_t$ where \mathbf{q} is the catchability coefficient.

$$\Psi_t = \frac{q I_t}{\sum\limits_{j=1}^{A} \phi_j q I_{t-j}}$$
(7)

The q's cancel out such that Ψ_t is represented as a ratio of the survey indices to a weighted average of the previous survey values. The survival term S^{j} is equivalent to the l_{x} term in the Euler-Lotka equation for population growth (l_x is the probability of surviving to age x). For high levels of fishing mortality the S^{j} term is decreasing faster than the average weight W_{j} is increasing. Thus the importance of earlier indices rapidly diminishes. All of the I_t and φ_j terms are positive, and at equilibrium, $\mathbf{I}_t = \mathbf{I}_{t+1}$ and $\mathbf{I}_t = \sum \boldsymbol{\phi}_i \mathbf{I}_{t-i}$ both hold. Therefore, $\sum \boldsymbol{\phi}_i = 1$. It would be desirable to express each of the ϕ_i weighting terms as function of the underlying population parameters. As expected, increases in fishing mortality increase the weight to more recent indices, whereas the converse hold for lower fishing mortality rates. As an approximation for this initial analyses, we assumed that all of the $\phi_i = \phi$ which implies that $\phi = 1/A$. Given the high rate of fishing mortality observed in Northeast stocks, we further assumed that A=5 was a valid approximation. Note that even moderate levels of fishing mortality imply low ϕ_i values beyond the fifth term. (e.g., F=0.5, M=0.2 imply S⁵ = 0.03. For the fifth to be important the ratio of the weights between the youngest and oldest ages would have to be greater than $1/S^5$ which, for this example, would exceed 33. As a first approximation, we defined ϕ_i =1/5 for all j. Thus Eq. 7 becomes the ratio of the current index to the average of the 5 previous years.

Application of any smoothing technique reflects a choice between signal and noise. A greater degree of smoothing eliminates the noise but may fail to detect true changes in the signal. Given the abrupt changes in fishing mortality that have occurred in some Northeast stocks, we chose to utilize the current year in the numerator of the replacement ratio. Use of the current index in the numerator rather than a running average of say k years, increases the sensitivity of the ratio to detect such changes. The penalty for such sensitivity is that the proportions of false positives and false negative responses increase. This penalty was judged acceptable for two reasons. First, it is desirable to detect abrupt changes in resource condition given the magnitude of recent and proposed management regulations. Second, the current formulation of the replacement ratio has a natural relationship to stock-recruitment hypotheses and the ratio can be investigated as a function of variations in underlying parameters, especially survival. Alternative formulations of the replacement ratio, say with a 2-yr average population size in the numerator can (and will) be developed, but their basic properties have not been investigated.

When fishing mortality rates exceed the capacity of the stock to replace itself the population is expected to decline over time. The expected behavior of Ψ_t under varying fishing mortality and recruitment is complicated, but it will have a stable point = 1 when the fishing mortality rate is in balance with recruitment and growth. Variations in fishing mortality will induce complex patterns, but in general terms, Ψ_t will exceed 1 when relative F is too high, and will be below 1 when F is too low. To account for these general properties and to reduce the influence of wide

changes in either Ψ_t or the relative F, we applied robust regression methods (Goodall 1983) to estimate the relative F corresponding to $\Psi_t = 1$. The parameters of the regression model

$$\ln(\Psi_t) = a + b \ln(relF_t) \quad (8)$$

were estimated by minimizing the median absolute deviations. Median Absolute Deviation estimators are known as MAD estimators in the statistical literature (eg.Mosteller and Tukey 1977). Residuals were downweighted using a bisquare distribution in which the sum of the MAD standardized residuals was set to 6. This roughly corresponds to a rejection point of about plus or minus two standard deviations from the mean. (Goodall 1983).

The relative F at which $\Psi_t = 1$ was estimated from Eq. 8. as

$$relF_{threshold} = e^{-a/b}$$
 (9)

where the estimates of **a** and **b** from Eq. 8 were substituted into Eq. 9. This derived quantity may be appropriately labeled as a threshold since values in excess of it are expected to lead to declining populations. Alternatively, populations are expect to increase when $relF_t < relF_{threshold}$

Employing the general standard that managers should attempt to rebuild fish stocks within 10 years, we estimated the relative fishing mortality rate at which the expected value of $\Psi_t = 1.1$ as a measure of **relF**_{target}. Applying a little algebra to the Eq. 8 leads to the following estimator of **relF**_{target}:

$$relF_{target} = e^{\frac{0.09531 - a}{b}}$$
(10)

The asymptotic standard errors of $relF_{threshold}$ and $relF_{target}$ were derived from the Hessian matrix of the regression model.

The usual tests of statistical significance do not apply for the model described in Eq. 8. The relation between Ψ_t and relF_t is of the general form of Y/X vs X where X and Y are random variables. The expected correlation between Y/X and X is less than zero and is the basis for the oft stated criticism of spurious correlation. To test for spurious correlation we developed a sampling distribution of the correlation statistic using a randomization test. The randomization test is based on the null hypothesis that the catch and survey time series represent a random ordering of observations with no underlying association. The randomization test was developed as follows:

- 1. Create a random time series of length T of $C_{r,t}$ from the set $\{C_t\}$ and $I_{r,t}$ from the set $\{I_t\}$ by sampling with replacement.
- 2. Compute a random time series of relative F (relF_{r,t}) and replacement ratios ($\Psi_{r,t}$)
- 3. Compute the r-th correlation coefficient, say ρ_r between $\ln(\text{relF}_{r,t})$ and $\ln(\Psi_{r,t})$.
- 4. Repeat steps 1 to 3 1000 times.
- 5. Compare the observed correlation coefficient r_{obs} with the sorted set of ρ_r
- 6. The approximate significance level of the observed correlation coefficient \mathbf{r}_{obs} is the fraction of values of $\mathbf{\rho}_{r}$ less than \mathbf{r}_{obs}

It should be emphasized that relF is not necessarily an adequate proxy for Fmsy, since this parameter only estimates the average mortality rate at which the stock was capable of replacing itself. Thus, while relF defined as average replacement fishing mortality is a necessary condition for an Fmsy proxy, it is not sufficient, since the stock could theoretically be brought to the stable point under an infinite array of biomass states.

Even with an estimate of relF derived from the above procedure, externally-derived estimates of Bmsy or MSY are necessary in order to develop consistent estimates of all the management reference points: MSY, Bmsy and Fmsy or their proxies. For index-based assessments these terms are related by

$$MSY/I_{Bmsv} = relF$$

where I_{Bmsy} is the survey index associated with Bmsy. Knowledge of any two of these terms allows for estimation of the third. For some index stocks (e.g. Gulf of Maine haddock) an external estrimate of MSY was considered, based on average catches over a stable period. For others, the Ibmsy proxy was considered more reliable and MSY derived from the above equation.

Six-Panel Plots of Catch, Relative F, and Replacement Ratios

The relationships among the catches, abundance indices, relative F, replacement ratios and time are summarized in a series of six-panel plots for each stock (19) and survey type (fall, spring). The panels are aligned to facilitate interpretation of the stock dynamics and to allow for a standard approach for comparison among stocks. The top four panels illustrate the interelationships among $\ln(\text{relF}_t)$, $\ln(\Psi_t)$, I_t , and time t. The variables share axes such that the temporal and phase plane interactions are easily followed. The bottom two panels illustrate the temporal patterns between catch C_t and $\ln(\text{relF}_t)$. Two of the panels warrant special consideration. The upper left panel plots $\ln(\Psi_t)$ vs $\ln(\text{relF}_t)$. The strength of the linear association can be inferred from the shape of the confidence ellipse (or principle component) surrounding the points. When the association is strong the ellipse will be long and narrow; when the association is weak the ellipse will approach a circle. The diagonal line represents the robust regression estimate and the dashed horizontal line represents the replacement ratio of 1.0. The intersection of the diagonal line with the replacement line represents the estimate of $relF_{threshold}$. The intersection of the regression line with a horizontal line at a replacement ratio of 1.1 (not shown) represents the estimate of $relF_{target}$

The middle left panel represents the phase plane relationship between the log of the survey, $ln(I_t)$ and the $ln(relF_t)$. Each point is labeled with the survey year and the points are connected to illustrate the temporal sequence. If the population declines with increases in fishing mortality and increases when the fishing mortality is reduced, the population should move up and down a linear isocline. In many species it is interesting to note that the return path for biomass, when F is reduced, tends to deviate sharply from the decline path. This general result may suggest that the rebuilding of stocks will be less predictable than the path of decline. In particular, the influence of truncated age structures on reproduction may be important and certainly, the presence of strong year classes will have a substantial, yet unpredictable influence on stock rebuilding.

Guide to 6 panel plots

The six panel plot developed for the "index" species attempts to show the interelationships among survey estimates of abundance, landings, functions of landings and relative abundance, and time. The two functions of landings and relative abundance considered are the replacement ratio (Eq. 6, section 2.3) and relative F (Eq. 9, section 2.3). The concept of using multiple panels to relate multiple variables over time has been advocated for use in fisheries science (e.g. Clark 1976, Hilborn and Walters 1992) and other fields (e.g. Cleveland 1993). The 6-panel plots attempt to show the logical connections among variables and to estimate underlying biological rates. The example for GOM Haddock (Figure 2.3) will be discussed in detail here.

The first aspect to note about the plots are the shared axes in the top four plots (A,B, C, D) and F. Panels B, D and F show the time series for the replacement ratio, the fall survey index, and the relative F, respectively. The horizontal line in A and B is the replacement ratio =1 line. The relationship between the replacement ratio and relative F in panel A is the key to understanding the influence of fishing mortality on stock size. Panel A is a phase plane that describes the relationship between two variables ordered by time. The degee of association between these variables is characterized by a Gaussian bivariate ellipsoid with a nominal probability level of p=0.6827 equivalent to ± 1 SD about the mean of the x and y variables. The primary and secondary axes of the ellipse are the first and second principal components, respectively. When the degree of association between relative F and replacement ratio decreases, the ellipse becomes more circle-like. The implication is that either the survey is too imprecise to detect changes induced by historical levels of fishing removals, or that the levels of fishing effort have been too low to effect changes in relative abundance. These alternatives can often be distinguished by consideration of the sampling gear and its interaction with the behavior of the species. Similarly incompleteness of the catch record, particularly for species in which the magnitude of discard mortality has varied widely, is another critical factor in the interpretation of the confidence ellipse.

The assumption that the relative F and replacement ratio have a joint bivariate normal distribution in the log –log scale may not hold for all (or any) species. In particular, the



Figure 2.3. Annotated six-panel plot depicting trends in relative biomass, landings, relative fishing mortality rate (landings/index) and replacement ratios for Gulf of Maine haddock. Horizontal dashed (---) lines represent replacement ratios = 1 in (A) and (B), threshold relF in (F) and target relative biomass in (C) and (D). Vertical dashed lines in (A) and (C) represent the derived relF thresholds. Smooth lines in (B), (D), and (F) are Lowess smooths (tension=0.3). The confidence ellipse in (A) has a nominal probability level of 0.68. The regression line in (A) represents a robust regression using bisquare downweighting of residuals. See text for additional details.

replacement ratio model is designed to be sensitive to contemporary changes, so that by definition it will be highly variable. Large changes that are subsequently validated by future observations imply true changes in population status. When the converse is true, it is proper to conclude that the change was an artifact of sampling variation. The degree to which high residuals influence the pattern is tested using the robust regression method of Tukey (Mosteller and Tukey 1977) that downweights large residuals using a bisquare distribution (see Goodall 1983 for details). Thus the regression line in panel A will not be aligned with the primary axis of the ellipse when high residuals distort the confidence ellipse. The expected value of correlation between the replacement rate and relative F is negative. The empirically derived estimate of the sampling distribution for the correlation coefficient , via the randomization test, provides a way of judging the significance of the robust regression line.

The predicted value of relative F at which the replacement ratio is 1 is defined by Eq. 8 and denoted by the vertical line in Panel A and B. The precision of that point depends largely upon where it lies within the confidence ellipse. If the confidence ellipse is nearly centered about the intersection point, then the precision of the relative F threshold will be high. This also indicates that over time, a wide range of F and replacement ratios greater than one have been observed. In contrast, when the intersection point lies in the upper right portion of ellipse, the precision will be low. This is, of course, is a common property of linear regression in which the prediction interval for Y increases with the square of the distance between the independent variable X and its mean. Thus a high degree of correlation between relative F and the replacement ratios greater than one. Panel A demonstrates, in a slightly different way, the implications of the "one-way trip" described in Hilborn and Walters (1992)

Panel C depicts the phase plane for relative biomass (ie. The index) and the relative F. At equilibrium, the population should move up and down a linear isocline. The degree of departure from linearity reflects both sampling variation as well as true variations induced by recruitment pulses and its transient influence on total biomass. Thus the trace of points can give useful insights into parametric model selection of population dynamics under exploitation .

The simple data of catch and survey are generally not sufficient to estimate simultaneously both the threshold F and biomass targets. This property characterizes the common property of indeterminancy of r and K in standard surplus production models. For the GOM haddock example, the relative biomass target is defined external to the model (Panel C and D).

To facilitate the detection of temporal patterns, Lowess smoothing is applied in panels B, D, and F. A relatively low tension =0.3 (i.e., 30% of the span of data are used for the estimate of each smoothed Y value) is used to allow for more sensitive flexing of the smoothed line. As noted earlier, the heightened sensitivity is desirable for this particular application in fisheries management. In a sense, the Lowess smoothing counterbalances the sensitivity built into the definitions of replacement ratio and relative F, by damping the rates of change and allowing for detection of general trends.

The final point to note is that the 6 panel plot may allow one to develop a reasonable picture of the population dynamics in relation to exploitation. With the exception of a brief period in the late 70's the replacement rate for GOM haddock was below one and continued its downward trend until 1990 (Panel A). This was accompanied by a continuously decreasing population size (Panel D). The reduction in landings from nearly 8000 mt in 1984 to less than 500 mt by 1989 (Panel E) greatly reduced the relative F (Panel F) below the threshold level and subsequently led to the replacement ratio exceeding one. The inter-relationships among Panels B, D, and F resemble the kinetics of simple chemical reactions and conceptually one should look for counteracting trends among indices and the influence of the trends in catch and relative survey abundance.

2.4 Projection Methodologies

One principle of conducting stock projections is that the basis for such projections (e.g., stockrecruit model, or emporical approach, production analysis or index method) should be consistent with the approach taken for reference point estimation (see the problems as noted in section 1.5 when this is not the case). Our analyses used consistent projections methodologies in all cases.

2.4.1 Age-Based Projections

Age-based projections are conducted using standard methodology and software (Brodziak et al. 1998; Brodziak and Rago 2002). In this approach, standard statistical techniques of bootstrapping and Monte Carlo simulation are used to project performance measures such as landings, discards, spawning biomass, and recruitment under alternative management policies. The key idea is to propagate variability in estimates of initial stock size forward in stochastic projections of future possibilities based on the same dynamical model and data used in the stock assessment model. Bootstrap replicates of current population size from an age-structured assessment model are combined with a stochastic stock-recruitment relationship to simulate population trajectories through the projection horizon. As a consequence, uncertainties in both initial population abundance and future recruitment are directly incorporated into management advice. The implications of management decisions can be quantified and compared using empirically-derived sampling distributions of catch, landings, discards, spawning biomass, recruitment, and, in the case of management under fixed catch quotas, fishing mortality. Estimates of the probability of exceeding biological reference points or achieving management targets are also quantified.

2.4.2 Surplus Production Projections

Stochastic projection was performed using bootstrap distributions of stock biomass in 2001, and estimated biomass dynamics parameters from ASPIC (Prager 1995). Projections assumed observed catch in 2001 (adjusted upward from January-November data), and the resulting fishing mortality in 2001 was assumed to continue in 2002 (expressed as a ratio to F in the terminal year, 2000). Projections were run through 2010. Results were described using bias corrected confidence intervals of projected biomass and catch.

2.4.3 Projections from Index-Based Methods

Catch Estimation and Projections

The estimates of $relF_{threshold}$ and $relF_{target}$ from Eq. 9 and 10 respectively, can be used to project the expected catches during any forecast period. Under the theory, multiplication of the current abundance index It by $relF_{threshold}$ leads to an estimate of Ct. If the estimate of $relF_{threshold}$ is unbiased then the population is expected to remain constant. This leads to the rather uninteresting forecast of constant catches over any time horizon. Conversely, when the population is fished at $relF_{target}$, the population is expected to grow by an average of 10% per year and the catches will grow at a similar rate. For short time periods and low initial population sizes, this approximation is likely to hold. Results of this approach, summarized in Table 4.1.2, suggest a reasonable degree of coherence with rebuilding schedules and catch projections derived from more complicated age-structured models. Thus, the catch projection estimates for the species without more complicated models may be used for planning and management purposes.

2.5 Mean Generation Times

The calculation of mean generation times for the various stocks is relevant to rebuilding times and rates in as much as life history is a determinant of maximum rebuilding potential and the ability of stocks to recover to Bmsy over a defined time interval (Restrepo et al. 1998). In the context of stocks determined to be unable to meet Bmsy targets in a 10 year time frame once a re-building program has been initiated, the National Standard Guidelines state that the actual rebuilding time plus one mean generation time may be specified as the maximum rebuilding period. The formula of Goodyear (1995) was modified for application to the New England groundfish stocks for which adequate estimates of natural mortality (M) mean weights at age in the stock, and proportion mature at age are available. Generation time, G is the weighted mean age of spawners in a population not subjected to fishing:

$$G = \sum_{a=1}^{A} aE_a N_a / \sum_{a=1}^{A} E_a N_a$$

 N_a is the number at any age in the population, E_a is the weighting factor calculated as the proportion mature at age multiplied by the mean weight at age in the stock, and a is age. For the New England groundfish species, basic data inputs to the calculation are given in the appropriate yield and spawning stock biomass per recruit tables (e.g., Table 3.1.2 for Gulf of Maine cod). The number of ages was determined by applying M to the population numbers at age until there was an insignificant number of fish remaining from the initial assumed cohort size (for redfish we assumed 200 ages, for all others 50 years). Results of the mean generation time calculations are given in Table 2.5. Owing to its low natural mortality rate and delayed maturity, Acadian redfish had the longest mean generation time (30.6 years) while the Georges Bank and Southern New England yellowtail flounder stocks had the lowest G values, under 9 years.

Species	Stock	Mean Generation Time (Years)
Atlantic cod	Gulf of Maine	10.8
	Georges Bank	10.3
Haddock	Georges Bank (current)	8.9
	Georges Bank (1931)	8.8
Yellowtail Flounder	Georges Bank	8.1
	Southern New England	8.3
	Cape Cod	8.8
American plaice	Georges Bank-Gulf of Maine	11.1
Witch Flounder	Georges Bank-Gulf of Maine	12.0
Winter Flounder	Southern New England	8.9
Acadian Redfish	Georges Bank-Gulf of Maine	30.6

 Table 2.5. Calculated mean generation times for Northeast groundfish stocks