

# Structural Modeling of Marine Reserves with Bayesian Estimation

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**Abstract** *Structural models can assess the effectiveness of fishery management prospectively and retrospectively. However, when only fishery-dependent data are available, structural econometric models are highly nonlinear in the parameters, and maximum likelihood and other extremum-based estimators can fail to converge. As a solution to these estimation challenges, we adapt Bayesian econometric methods to estimate a dynamic structural model of marine reserve formation. Using simulated data, we find that our approach is able to recover structural biological and economic parameters that classical estimation procedures fail to recover. We apply the approach to real data from the Gulf of Mexico reef-fish fishery. We test the effects of the Steamboat Lumps Marine Reserve on population growth and catchability for gag, a species of grouper. We find that after four years, the reserve has neither produced statistically significant losses in sustainable yield nor statistically significant gains in biological production.*

**Key words** Marine reserves, marine protected areas, Bayesian econometrics, Markov Chain Monte Carlo.

JEL Classification Codes C11, Q22.

## Introduction

There are precious few retrospective analyses of the fishery benefits of marine reserves. This fact has raised concerns amongst fisheries scientists (Hilborn *et al.* 2004; Sale *et al.* 2005). The policy reality is that reserves continue to be established in spite of gaps in our scientific knowledge, and they are supported by conceptual models in fisheries science that predict harvest gains (or only modest harvest losses)

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when large areas are closed to fishing (Polacheck 1990; Bohnsack 1993; Walters 2000). However, most economic models articulate a limited set of bioeconomic conditions under which reserves would enhance fisheries (Holland and Brazee 1996; Sanchirico and Wilen 2001; Anderson 2002; Smith 2004), conditions that appear even more limited in models that incorporate the harvest sector's behavior (Smith and Wilen 2003, 2004; Dalton and Ralston 2004).<sup>1</sup>

Do actual marine reserves stimulate fisheries productivity? As more reserves are formed throughout the world, how might we answer this question in the future? In this paper, we take steps toward filling this knowledge gap by adapting new methods from Bayesian econometrics to estimate a dynamic structural model of the impacts of marine reserves on fishery outcomes. As a starting place, our outcome of interest is a change in the sustainable yield of the fishery, which necessarily involves a tradeoff of lost fishing area with a potential increase in biological productivity. We use both simulated data and real data from the Gulf of Mexico reef fish fishery, and we explicitly test hypotheses about the effects of marine reserves.

To evaluate the effectiveness of existing marine reserves retrospectively, there are two statistical approaches available: descriptive and structural. The descriptive approach uncovers structural breaks and trend changes in the bioeconomic system by examining the signs of particular parameters. In previous work, we estimated descriptive panel models of marine reserves in the Gulf of Mexico that approached the problem from the perspective of program evaluation (Smith, Zhang, and Coleman 2006a). This allowed us to incorporate a large number of regressors, seasonal effects, area-specific shifters and trends, and vessel-specific fixed effects. A limitation of this approach, however, is that it can only tell us what has happened and has no ability to forecast the future effects of keeping a policy in place. For a bioeconomic system, dynamics may unfold for decades beyond the sample period. Thus, the descriptive model approach may leave one with an incomplete picture of the long-run treatment effects from a policy intervention.

Compared to a descriptive approach, structural modeling has some advantages. Using simulated data, we found that a descriptive model can sign policy treatment effects correctly but cannot estimate the magnitudes consistently due to the latency of the state variable; *i.e.*, the fish stock (Smith, Zhang, and Coleman 2005). In contrast, a structural model accounts for the latent state variable and can estimate unknown biological and economic parameters consistently—as well as the direct structural impact of a policy—with non-experimental data. As a result, the same model can be used to analyze the effects of an existing policy and forecast the future effects of that policy as dynamics continue to unfold.

The advantages of a dynamic structural model come at a cost. In a dynamic bioeconomic system, elements are generally related nonlinearly, imposing a heavy burden on the estimation process. Models become highly nonlinear in the parameters when the analyst uses fishery-dependent data to resolve both economic and biological parameters of the system. Because the fish stock is not directly observed, backwards recursion is necessary to generate an estimation equation in terms of observable quantities and parameters. Such complexity may account for the relatively small number of empirical bioeconomic papers in the fisheries literature that are dynamic and simultaneously estimate biological and economic parameters (Wilen

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<sup>1</sup> Some of the more favorable bioeconomic predictions about marine reserves explicitly account for existence values (*e.g.*, Beattie *et al.* 2002), or explicitly model reserves as a hedge under uncertainty (*e.g.*, Conrad 1999; Grafton, Kompas, and Lindenmayer 2005). We do not model these values in our analysis but note that fishery costs of a policy could be offset by non-fishery conservation benefits.

1976; Homans and Wilen 1997).<sup>2</sup> This complexity may also account for the modeling simplifications that are typically made; *e.g.*, a Schaefer production function.

Bayesian techniques provide a promising new direction for estimating nonlinear dynamic structural models for several reasons. First, the Markov Chain Monte Carlo (MCMC) method simulates, but does not maximize, the likelihood function (Chernozhukov and Hong 2003), an advantage over traditional methods when the objective function is not well behaved. Thus, Bayesian estimation approaches are capable of estimating some models for which extremum-based estimators fail to converge. Second, Bayesian methods have a natural way of incorporating prior information on the parameters (Gelman *et al.* 1995). This is particularly important for incorporating fishery-independent biological information (Hilborn and Mangel 1997), and can be useful for general bounds on the parameter space, such as non-negativity constraints. Third, there may be computational gains from generalizing a Bayesian model to account for economic or biological heterogeneity through random parameters in comparison to introducing simulation-based estimation to an already highly nonlinear maximum likelihood problem.<sup>3</sup>

We estimate two Bayesian dynamic structural models with logistic growth. The first model uses simulated data for which we know all of the true biological and economic parameters, as well as the true policy impact of establishing a marine reserve. The data assume that there is a single representative fishing vessel. We find that the Bayesian model using MCMC converges near the true parameter values in the simulated data exercise, and this exercise serves as a proof of concept. In the second model, we estimate biological and economic parameters with real data from the Gulf of Mexico reef fish fishery for which we have more than ten years of log-book records. Two marine reserves were established in-sample, so, in principle, we can examine the structural impact on the system. We find that the MCMC approach estimates parameter values for one of the reserves but fails to converge for the other. More specifically, we find in one case that the marine reserve did not reduce fishing area enough to have a net negative effect on catchability. There is some indication that the reserve stimulated biological production of the fishery, but the result is not statistically significant.

In the next section, we describe the Gulf of Mexico reef-fish fishery and the biology of the gag. We then develop a discrete-time dynamic structural model of marine reserve formation that embeds a reserve within a larger, observable harvest area. The following section summarizes our empirical results with both simulated and real data. We then conclude with a discussion of the limitations of our approach and the potential applicability to other fisheries.

## The Gulf of Mexico Reef Fish Fishery and Gag

The Gulf of Mexico reef fish complex is extremely diverse (with 62 commercially harvested reef species), and involves a wide variety of gear types, thus presenting managers with substantial challenges. The most common gear types are hook and line (including handlines, electric bandit reels, buoy gear, and conventional rod and

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<sup>2</sup> An alternative approach is to decouple the biological and economic parameters, *e.g.*, Bjorndal and Conrad (1987). However, this approach assumes a stable production function and stable stock dynamics. We are interested in testing whether reserves affect these relationships and thus cannot decouple the biology and economic model components.

<sup>3</sup> This point is somewhat speculative, but there are results that suggest MCMC estimation estimates faster for some classes of discrete choice models with heterogeneity. See Train (2003).

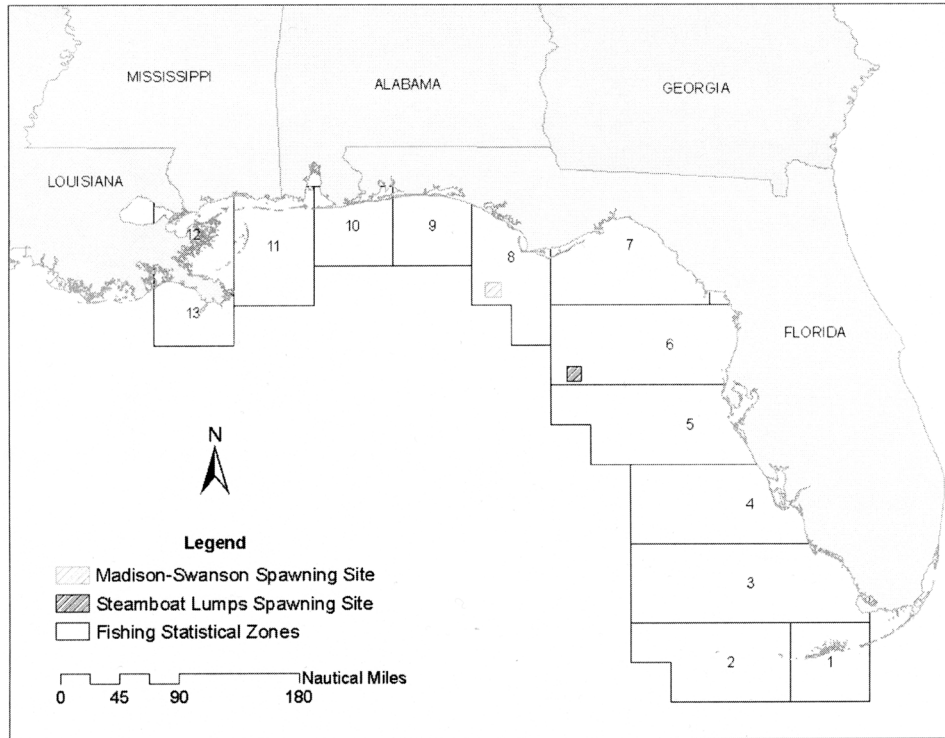
reel), bottom long line, and traps (although traps are being phased out completely in the next couple of years). Existing management includes limited entry (there are currently approximately 1,200 federal commercial Gulf of Mexico reef fish permit holders), size limits, trip limits, season closures, quota management, and more recently, marine reserves. Only a fraction of permitted vessels regularly engage in commercial reef fish fishing. For example, 25% of vessels accounted for 75% of fishing trips over the 1993-2002 period.

Economically important species such as gag (*Mycteroperca microlepis*), scamp (*M. phenax*), and red grouper (*Epinephelus morio*) could gain some long-run biological benefits from marine reserves. These species are long-lived, slow-growing protogynous hermaphrodites (Coleman *et al.* 2000). Protogynous hermaphrodites mature first as females and then transform to males later in life. Because fishing tends to select for larger individuals, it tends to select for males. This selection reduces male-to-female sex ratios (Coleman, Koenig, and Collins 1996; McGovern *et al.* 1998), and some traditional fisheries management tools, particularly size limits, may exacerbate this effect. For Gulf of Mexico gag, the percentage of males from the 1970s to the 1990s has declined from 17% to 2% (Coleman *et al.* 2000). The same decline does not appear in red groupers, which do not aggregate to spawn (Coleman, Koenig, and Collins 1996). Thus, we focus on gag in this paper. An empirical examination of reserves for the gag fishery is particularly timely, since recent life history modeling of gag population dynamics suggests that, among available management alternatives, closing spawning sites to fishing ranks highest for sex ratio recovery and close to the top for overall growth rate of the population (Heppell *et al.* 2006).

The two marine reserves in the Gulf of Mexico that we study—Steamboat Lumps Marine Reserve and Madison-Swanson Marine Reserve—went into effect in June 2000 to address concerns about this skewed sex ratio. They were announced to the fishing community one year before being established. They were authorized as experimental reserves with a sunset of four years, and were recently reauthorized for an additional six years, based exclusively on biological data within and outside of each reserve and anecdotal information about the fishery outside each reserve. Systematic evaluations of these reserves as management tools are only beginning to emerge (Smith, Zhang, and Coleman 2006a), and understanding their performance will be critical for future reauthorizations.

The reserves are located in two of the thirteen distinct National Marine Fisheries Service (NMFS) fisheries statistical zones in the Gulf of Mexico (figure 1). These two zones represent the heart of the gag fishery in the Gulf of Mexico. Steamboat Lumps is located in zone 6, comprising 104 NM<sup>2</sup> of this 8,100 NM<sup>2</sup> zone, whereas Madison-Swanson is located in zone 8, comprising 115 square nautical miles (NM<sup>2</sup>) of this 9,570 NM<sup>2</sup> zone. Each reserve captures 1.3 and 1.2%, respectively, of the total area in the NMFS statistical zone within which they occur. There is, thus, substantial fishable area left open within each of the statistical zones, as well as elsewhere on the West Florida Shelf. However, percentage area is misleading in a fisheries context because not all ocean bottom is alike. The reserves in question are located in deep water along the continental shelf edge and contain distinct patch reef formations where reef fish aggregate in general and many grouper species aggregate to spawn (Koenig *et al.* 2000).

There is not a one-to-one relationship between NMFS fishing zones and what we might reasonably deem a patch from a bioeconomic perspective. The spatial resolution of the logbook data is extremely coarse, which is typical, and the NMFS fishing zones are spatial aggregates of the underlying biological and economic processes. The empirical challenge is to use this coarse information to infer how policy changes affect fishery outcomes. In our model (next section), we exploit the fact that gag have high site fidelity. As such, the effects of a reserve are likely to remain within the same NMFS fishing zone that contains the reserve.



**Figure 1.** Gulf of Mexico Reef No-take Marine Reserves Established in June 2000  
Source: Adapted from Smith, Zhang, and Coleman 2006a.

Complete fishing logbook data exist for all reef species in the Gulf of Mexico from 1993 through 2004. Thus, there are substantial data before and after the policy change to assess reserve performance. We cut the data after October 2004 because some logbook records for 2004 may not have been submitted or processed in the most recent database that we received in February 2005. This leaves us with 142 months of data.

### A Discrete-Time Model of Marine Reserve Formation

In this section, we develop a stylized dynamic structural model to understand how a reserve might appear in a fishery that extends over a large contiguous region. While some might argue that this exercise attempts to re-invent the wheel, the existing literature does not match the spatial scale of available data for doing *ex post* assessment of marine reserves. Specifically, we do not directly observe data at the scale of a bioeconomic patch. In many cases, a reserve will be formed within an observational unit that constitutes a much larger area than the reserve itself. In some cases, we may only observe the entire fishery and will want to infer the reserve effect on the remaining open area in aggregate. These conditions motivate our empirical model below. We begin with a discrete-time ( $t$ ) lumped-parameter model of the fish stock ( $X$ ) and harvest ( $H$ ) in each fishing zone ( $j$ ):

$$X_{j,t+1} = X_{j,t} + r_j \gamma_1^{Z_{j,t}} X_{j,t} \left( 1 - \frac{X_{j,t}}{K_j} \right) - H_{j,t}. \quad (1)$$

The parameters  $r$  and  $K$  are the conventional intrinsic growth and carrying-capacity parameters.  $Z$  is an indicator variable that denotes when a reserve is in effect such that:

$$Z_{j,t} = \begin{cases} 1 & \text{if there is a reserve in } j \text{ at } t \\ 0 & \text{if no reserve or pre-reserve} \end{cases}. \quad (2)$$

Thus,  $\gamma_1$  scales intrinsic growth when a reserve is established somewhere within the zone. The magnitude of  $\gamma_1$  will be a function of the size of the reserve, the reserve placement, and the connectivity of the reserve with areas outside the reserve. Our model will be able to estimate  $\gamma_1$  conditional on a particular reserve in place, but will not provide a means of comparing  $\gamma_1$ 's across fisheries. As seen in figure 1, the Steamboat Lumps and Madison-Swanson reserves are located within larger fishing areas. The idea is that equation (1) forms a lumped-parameter description of how biological returns would operate on the surrounding area of a reserve. That is, if a reserve generates spillovers, it would appear to stimulate population growth in the zone that contains the reserve. However, the reserve also closes off part of the fishing area, which might affect the production function for fishermen. As such, harvest is given by the following function of stock and effort ( $E$ ):

$$H_{j,t} = q(E_{j,t})^\alpha \gamma_2^{Z_{j,t}} X_{j,t}. \quad (3)$$

In this form,  $q$  is a catchability coefficient,  $\alpha$  is a Cobb-Douglas production parameter (the corresponding parameter on  $X$  is assumed to be one), and  $\gamma_2$  scales the production function to account for reduced fishing area when a reserve is in place.<sup>4</sup> As above, the magnitude of  $\gamma_2$  relates to a particular fishery. We expect that a larger reserve will shrink  $\gamma_2$ , but given heterogeneity in habitat, this relationship is not necessarily linear and limits comparisons across fisheries.<sup>5</sup>

In essence, this model allows the reserve to influence biomass in the larger zone within which the reserve is embedded, but scaling the harvest function only permits harvesting in the open portion of the zone. This setup is consistent with many log-book data sets for which reserves do not correspond to an entire fishing zone.

As a first step, we take fishing effort as given and focus on estimating the biological and production parameters. This means that we do not present a fully bioeconomic description of this system and focus only on positive analysis of the biological system coupled with the economic production function. Quantifying these features is necessary but not sufficient for normative analysis; to characterize the

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<sup>4</sup> It is also possible that the reserve could appear to increase catchability if reserve establishment provides spatial information to the fleet that was not common knowledge previously. This information gain would likely apply to only a subset of fishing vessels. Our model is only able to test the net effect of reduced fishing area and increased information.

<sup>5</sup> An assumption throughout our structural modeling is that production relationships—both biological and economic—are stable and only are influenced by the formation of a marine reserve. This means that the effects of other policy instruments are assumed not to affect the analysis. At least for total allowable catch (TAC), this assumption is innocuous in our case study. Though a TAC exists for all shallow-water groupers, it does not bind in-sample.

optimal policy one would need to measure prices, costs, and the discount rate as well. So, our model should be viewed as a step towards an empirical Bayesian bioeconomics.<sup>6</sup> Our simplification allows us to derive and estimate a single-equation model where the goal is to use data on catch and effort alone to infer the latent stock dynamics. Through recursive substitution of (3) into (1), we are able to predict the catch ( $H$ ) in period  $t + 1$  without knowing the stock ( $X$ ):

$$H_{t+1} = (1 + r\gamma_1^{Z_t} - qE_t^\alpha\gamma_2^{Z_t})\gamma_2^{Z_{t+1}-Z_t}H_t\left(\frac{E_{t+1}}{E_t}\right)^\alpha - \frac{r}{qK}\gamma_1^{Z_t}\gamma_2^{Z_{t+1}-2Z_t}H_t^2\left(\frac{E_{t+1}}{E_t^2}\right)^\alpha. \quad (4)$$

This model is equivalent to the original setup, and we will use this one as our data generating process in both the simulated data analysis and the real data analysis. At this stage, two comments are worth mentioning. First, even without the complication of a reserve effect, estimating intrinsic growth and carrying capacity jointly in a surplus production model is problematic because the data often do not span the population range (Hilborn and Mangel 1997). Second, introducing marine reserves puts sharp edges in this model. While this is what our theoretical model predicts, it may create difficulties as a practical matter for estimation.

We add an error term ( $\epsilon_t$ ) to the above model with the assumption that it is independently and identically distributed normal with zero mean and variance ( $\sigma^2$ ). Variance is assumed to be known in the simulated data Monte Carlo experiment just for simplicity and assumed to have a diffuse distribution in the analysis of real data. The model to be estimated is thus:

$$H_{t+1} = \gamma_2^{Z_{t+1}-Z_t}H_t\left(\frac{E_{t+1}}{E_t}\right)^\alpha + r\gamma_1^{Z_t}\gamma_2^{Z_{t+1}-Z_t}H_t\left(\frac{E_{t+1}}{E_t}\right)^\alpha - q\gamma_2^{Z_{t+1}}H_tE_{t+1}^\alpha - \frac{r}{qK}\gamma_1^{Z_t}\gamma_2^{Z_{t+1}-2Z_t}H_t^2\left(\frac{E_{t+1}}{E_t^2}\right)^\alpha + \epsilon_{t+1}. \quad (5)$$

To simplify notation, we define the following:

$$A_{t+1} = \gamma_2^{Z_{t+1}-Z_t}H_t\left(\frac{E_{t+1}}{E_t}\right)^\alpha, \quad (6)$$

$$B_{t+1} = \gamma_1^{Z_t}\gamma_2^{Z_{t+1}-Z_t}H_t\left(\frac{E_{t+1}}{E_t}\right)^\alpha, \quad (7)$$

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<sup>6</sup> Smith, Zhang, and Coleman (2005) take the extra step of closing this model with a Vernon Smith (1968) effort adjustment equation and derive some basic theoretical predictions based on a single-area fishery.

$$C_{t+1} = -\gamma_2^{Z_{t+1}} H_t E_{t+1}^\alpha, \quad (8)$$

and

$$D_{t+1} = -\gamma_1^{Z_t} \gamma_2^{Z_{t+1}-2Z_t} H_t^2 \left( \frac{E_{t+1}}{E_t^2} \right)^\alpha. \quad (9)$$

To reduce some of the nonlinearity in estimation, we re-parameterize the model as follows:

$$k = \frac{r}{qK}. \quad (10)$$

Then the model can be rewritten as:

$$H_t = A_t + rB_t + qC_t + kD_t + \varepsilon_t. \quad (11)$$

One favorable feature of the above model is that it is linear in the parameters  $r$ ,  $q$ , and  $k$ . This will allow us to use Gibbs sampling to estimate some of the parameters and thus reduce some of the computational burden of our model.

### Model Estimation and Results

In the simulated data analysis, we use 500 periods for one fishing zone. A reserve is formed after 300 periods, so it is in place for the remaining 200 periods. For prior information we make conservative assumptions but still impose more structure than we will impose for the analysis of real data. Defining  $I$  as the indicator function, we first assume  $I(q > 0)$  and  $I(k > 0)$ . These are the least restrictive assumptions. Given that groupers are slow growing, we restrict the possibilities for intrinsic growth  $I(0 < r < 1)$ . Prior biological knowledge could be used in a similar fashion for other species. We assume diminishing returns to fishing effort  $I(0 < \alpha < 1)$ . Finally, we assume that the impact of the reserve on population growth is positive (growth is scaled upward) but less than 100%  $I(1 < \gamma_1 < 2)$ , and the reduction in fishing area is no more than 50%  $I(0.5 < \gamma_2 < 1)$ .

Given our parametric assumption on the error term, the unnormalized posterior distribution for the parameters of the simulated data model is:

$$p(r, q, k, \alpha, \gamma_1, \gamma_2 | H, E, \sigma^2) \propto \quad (12)$$

$$\exp \left\{ - \frac{\sum_{t=1}^T [H_t - (A_t + rB_t + qC_t + kD_t)]^2}{2\sigma^2} \right\}$$

$$\times I(0 < r < 1)I(q > 0)I(k > 0)I(0 < \alpha < 1)I(1 < \gamma_1 < 2)I(0.5 < \gamma_2 < 1).$$

The exact conditional posterior distributions of  $r$ ,  $q$ , and  $k$  are given by:



$$r|\cdot \sim TN \left( \frac{\sum_{t=1}^T B_t [H_t - (A_t + qC_t + kD_t)]}{\sum_{t=1}^T B_t^2}, \frac{\sigma^2}{\sum_{t=1}^T B_t^2} \right) I(0 < r < 1), \quad (13)$$

$$q|\cdot \sim TN \left( \frac{\sum_{t=1}^T C_t [H_t - (A_t + rB_t + kD_t)]}{\sum_{t=1}^T C_t^2}, \frac{\sigma^2}{\sum_{t=1}^T C_t^2} \right) I(q > 0), \quad (14)$$

and

$$k|\cdot \sim TN \left( \frac{\sum_{t=1}^T D_t [H_t - (A_t + rB_t + qC_t)]}{\sum_{t=1}^T D_t^2}, \frac{\sigma^2}{\sum_{t=1}^T D_t^2} \right) I(k > 0), \quad (15)$$

where  $TN$  is a truncated normal distribution.  $TN$  is a continuous distribution that both allows us to impose inequality constraints and permits estimation through Gibbs sampling. We assume that the variance is known in the simulated data model, an assumption that we will relax in the analysis of real data. In MCMC estimation, the three parameters in equations (13) through (15) are estimated through Gibbs sampling. Because it is difficult to find the exact conditional posterior distributions of  $\alpha$ ,  $\gamma_1$ , and  $\gamma_2$ , these parameters are estimated through Metropolis-Hastings sampling. Appendix A contains a brief overview of the estimation procedure, and further details on Gibbs sampling and Metropolis-Hastings can be found in a textbook on Bayesian statistics (*e.g.*, Gelman *et al.* 1995).

The results of the simulated data exercise with 2,000,000 MCMC simulations (discarding the first 1,000,000 as burn in) are summarized in table 1. Since the data are simulated, we know the true value of each parameter. True values are reported in the second column. The estimates are in the third column along with standard errors in the fourth column. Qualitatively, none of the estimates are far from their true values, and none are statistically different. This suggests that the MCMC methods work well on this difficult estimation problem, at least when the data set is ideal. Figure 2 shows the empirical distributions for each parameter.

Turning to the real data, we restrict the analysis to gag fishing. As discussed above, gag is the species that the two marine reserves are most likely to enhance through recovery of the sex ratio. There are 142 months of data, and we define effort as total crew days at sea. Though not a perfect measure, this allows us to aggregate across gear types for the gag fishery. Compared to the simulated data exercise, we make even more conservative assumptions about priors. In particular, we now assume diffuse priors for all parameters, and, with the exception of  $q$ —which we force to be strictly positive—we do not force the other parameters to be within specified ranges. In the analysis of real data, we also assume the prior distribution of  $\sigma^2$  is diffuse; that is,  $p(\sigma^2) \propto 1/\sigma$ . These more conservative assumptions change the unnormalized posterior distribution for the parameters to:

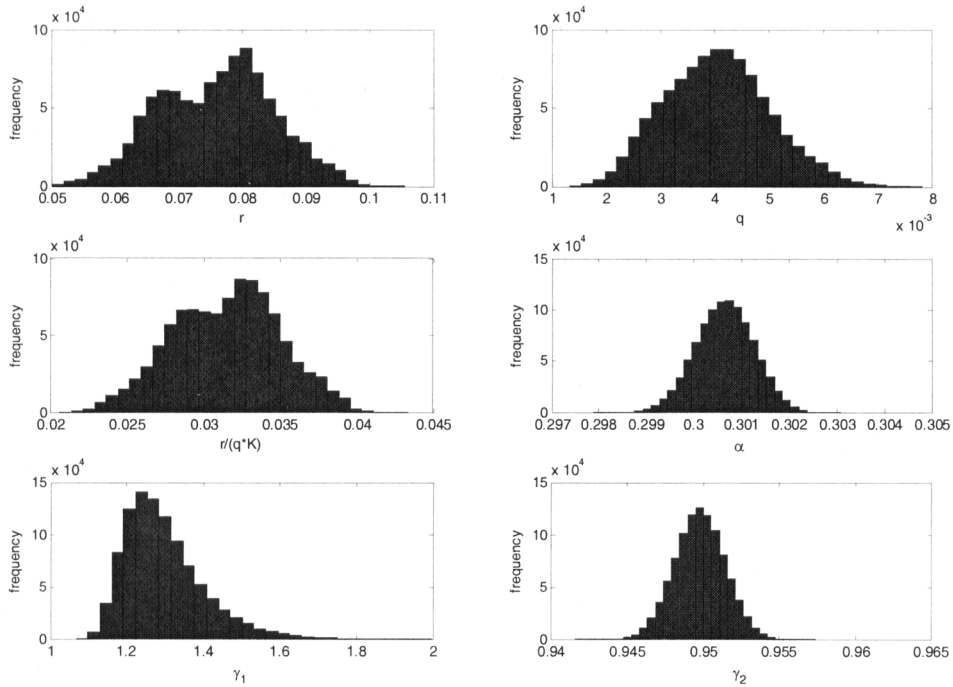
$$p(r, q, k, \alpha, \gamma_1, \gamma_2, \sigma^2 | H, E) \propto \exp \left\{ - \frac{\sum_{t=1}^T [H_t - (A_t + rB_t + qC_t + kD_t)]^2}{2\sigma^2} \right\}, \quad (16)$$

$$\times \frac{1}{\sigma^{T+1}} \times I(q > 0),$$

**Table 1**  
Results of MCMC Estimation on Simulated Data

Parameter	True Value	Estimated Value	St. Error
$r$	0.08	0.076	0.0091
$q$	0.005	0.0041	0.001
$k$	0.032	0.0315	0.0035
$\alpha$	0.3	0.3006	0.0006
$\gamma_1$	1.2	1.2993	0.1078
$\gamma_2$	0.95	0.9498	0.0017

Note: Results are based on 2,000,000 simulations in the Markov Chain and discarding the first 1,000,000.



**Figure 2.** Empirical Distributions of MCMC Simulations on Simulated Data

with corresponding changes in equations (13) through (15). With our diffuse prior assumption on the variance, the conditional posterior for the variance is:

$$\sigma^2 | \sim IG \left( T, \sum_{t=1}^T [H_t - (A_t + rB_t + qC_t + kD_t)]^2 \right), \tag{17}$$

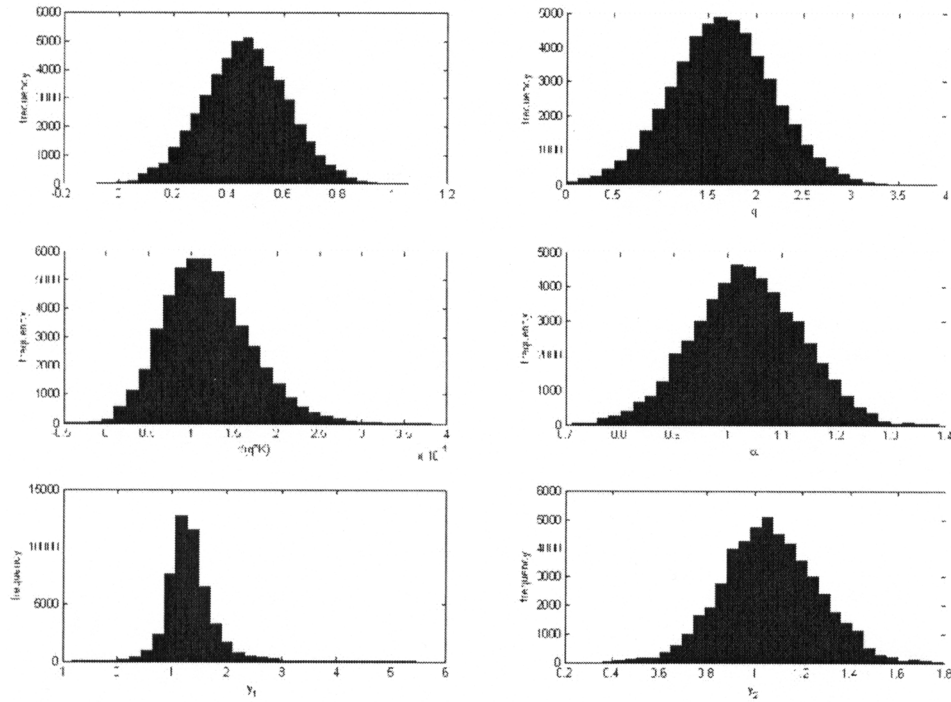
where *IG* is an inverted gamma distribution. *IG* is a standard parametric assumption for variance in Bayesian estimation because it does not force one to incorporate strong prior information but is easy to draw from in the MCMC routine.

We estimate the MCMC model on NMFS Zone 6 data to measure the effects of the Steamboat Lumps Marine Reserve. Table 2 reports estimates and standard errors, while figure 3 shows the empirical distributions for each parameter. All of the parameters are statistically significant; *i.e.* they are statistically different from zero. The magnitudes of  $\gamma_1$  and  $\gamma_2$  are of greatest interest. Under the null hypothesis that the marine reserve has no effect on population growth of gag,  $\gamma_1 = 1$ . Though the mean of the distribution of  $\gamma_1 > 1$ , this result is not statistically significant ( $t = 0.70$ ). Thus, we fail to reject the hypothesis that the reserve has no effect on gag population growth. Similarly, under the null hypothesis that the reserve does not have a net effect on catchability,  $\gamma_2 = 1$ . Here again, we fail to reject this hypothesis ( $t = 0.21$ ). Table 2 also reports implied carrying capacity and maximum sustainable yields (MSY) without and with the marine reserve. Here we take the point estimates as given, and thus the MSY with the reserve is 35% higher.

Though the signs of the parameters are sensible, the intrinsic growth parameter appears unrealistically high. After all, gag is known to be a relatively slow growing fish. Similarly, the implied carrying capacity appears unrealistically low. Taken together, these parameters suggest that the fishery is taking a large portion of the total biomass in each period, and the population is replenishing rapidly. These problems illustrate a classic problem in empirically resolving logistic growth parameters from fishery-dependent data (Polacheck, Hilborn, and Punt 1993; Hilborn and Mangel 1997). Data are often consistent with two possibilities: (*i*) a low carrying capacity and high intrinsic growth rate, and (*ii*) a high carrying capacity and low intrinsic growth rate. The two parameters are theoretically identified, and the analysis of the simulated data illustrates this fact. Empirically, however, there may be insufficient

**Table 2**  
MCMC Results for the Gag Fishery in NMFS Zone 6

Parameter	Estimate	St. Error
<i>r</i>	0.46083	0.15457
<i>q</i>	1.65410	0.54001
<i>k</i>	0.00012	0.00005
$\alpha$	1.03811	0.10200
$\gamma_1$	1.35215	0.50517
$\gamma_2$	1.04560	0.19261
$\sigma^2$	8,579	1,059
Implied Carrying Capacity in Zone 6 (pounds)		234,774
Implied MSY for Zone 6 (no reserve)		27,048
Implied MSY for Zone 6 (with reserve)		36,573



**Figure 3.** Empirical Distributions of MCMC Simulations on Gulf of Mexico Gag Fishery Data (NMFS Zone 6 Only)

variation in the data to resolve both intrinsic growth and carrying capacity because the analyst often observes data only from a narrow range of the net growth function of a stock. With simulated data, one can ensure that observations are drawn from the entire range of the net growth function.

We next attempt to estimate the model for NMFS Zone 8 to capture the effects of the Madison-Swanson Marine Reserve. However, the model fails to converge. We tried a number of approaches, including putting more restrictive priors on the model based on the parameter estimates that we obtained for Zone 6. One possible explanation is that the error term does not enter additively. The error entered additively by construction in the simulated data analysis, but for the real data, it could enter in any number of ways. Another possibility is simply that there are too many confounding factors that are not controlled for in the estimation. This illustrates a fundamental tension between structural and non-structural modeling. Non-structural approaches often can accommodate a wide range of covariates without complicating the estimation problem. In contrast, it is more problematic to build other shifters and trends into the structural model.

## Discussion

Many authors have used modeling to predict that marine reserves enhance population growth of fish species, but demonstrating actual growth empirically in a functioning marine reserve is the real currency of a reserve effect. Only a handful of

papers have conducted retrospective analyses of the empirical effects of marine reserves on fisheries (McClanahan and Kaunda-Arara 1995; Murawski *et al.* 2000; Roberts *et al.* 2001; Russ and Alcala 1996; Russ *et al.* 2004; Smith, Zhang, and Coleman 2006a). To our knowledge, no previous paper has done so with a structural model. Our structural approach uses a simple surplus production model and adds two features to account for the effects of marine reserves. Although our model cannot measure the mechanisms through which reserves could contribute to fish population growth, it serves as an important step towards assessing the net effect of a policy change in a bioeconomic system. In contrast, non-structural approaches may be subject to bias due to the presence of nonlinearities, dynamics, and latent state variables.

Although our approach works well on simulated data, the results on real data from the Gulf of Mexico are inconclusive. We are unable to obtain results for the Madison-Swanson Marine Reserve, suggesting that either the model does not work for this location or that the signal to noise ratio is simply too small. We do find results for the Steamboat Lumps Marine Reserve; it neither produces a statistically significant increase in population growth nor a statistically significant decrease in catchability associated with decreased fishing area. These results may simply be the truth of the matter with regard to gag; the reserve has had neither positive nor negative effects on gag fishing. It is also possible that we need more than 4.5 years of data post-reserve to resolve the treatment effects that we are trying to measure empirically.

We recommend that policy-makers maintain and continue to enforce Steamboat Lumps and Madison-Swanson Marine Reserves. In a descriptive (or quasi-structural) statistical model, we found that these reserves produced modest catch decreases for all reef fish lumped together (Smith, Zhang, and Coleman 2006a), but we were unable to make any statements about the future effects of the reserves. In the current paper, we present a model that, in principle, can make statements about the future of reserves. It focuses on just one species, and for one of the reserves, finds no statistically significant gains or losses in sustainable yield. Taken together, these results suggest that there is much we still do not know about the fishery effects of these reserves. As marine reserves gain policy momentum, it is important not only to develop tools for measuring their effects but also to keep them in place long enough to measure these effects. Otherwise, managers will continue to be in the dark about how actual reserves affect actual fisheries.

One might reasonably argue that logistic growth is simply the wrong model for gag population dynamics. In fact, we have parallel empirical bioeconomic modeling underway that draws on recent work in fisheries ecology (Heppell *et al.* 2006), specifies gag population dynamics with age structure, and includes gag's unique reproductive characteristics (Smith, Zhang, and Coleman 2006b). This work relies on a substantial amount of fishery-independent data that is unavailable for most exploited fish species. This is especially true for reef-fish species in developing countries where marine reserves are so heavily touted as a policy solution. We submit that understanding the importance of marine reserves is of such great policy significance that it is worthwhile to pursue multiple modeling strategies, including both non-structural analyses of treatment effects and diverse structural ways of capturing dynamics. We also note that in many fish stock assessments, analysts frequently use multiple models of population dynamics to ask different sorts of questions about the stock or to explore the robustness of policy recommendations.

While no model is ever perfect, we believe that if a marine reserve generates large, long-run catch changes, and the reserve has been in effect long enough for these impacts to materialize, these changes would show up in a lumped-parameter model like the one in this paper. With the steady emergence of new marine reserves

throughout the world, it is important to develop tools for assessing them that match the likely spatial and temporal scales of data collection. The spatial resolution of fishery data is likely to be coarse, and managers will be forced to infer effects of a reserve from data on a much broader spatial area. Our model is not the only possibility for addressing this problem but serves as an example.

The approach in this paper is potentially applicable to a wide range of bioeconomic problems. By focusing on the biological system and the economic production function, our model structurally characterizes the effects of a policy change on two critical components of the bioeconomic system. The advantage of Bayesian estimation in our case is that it can handle the highly nonlinear estimating equation that emerges from recursive substitution of the dynamic structural model. This is potentially applicable to analyzing a wide range of policy interventions in bioeconomic systems such as territorial use rights, gear restrictions, and seasonal closures. Nevertheless, we study only a portion of the bioeconomic system. A full description would also include a model of harvest sector behavior. Thus, our model is only a step towards a Bayesian bioeconomics.

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## Appendix A

### Details on MCMC Estimation for Known $\sigma$

The MCMC estimation algorithm uses the following steps:

1. Start at an initial parameter vector  $\theta^0 = (r^0, q^0, k^0, \alpha^0, \gamma_1^0, \gamma_2^0)$ ;
2. Generate  $\theta^{i+1}$  from  $p(\theta_j|\theta_j^i, x)$  sequentially, which includes two parts in this study:
  - 2.1 Gibbs sampling (for  $r, q,$  and  $k$  with exact posterior distributions):

$$\begin{aligned} r^{i+1} &\sim p(r|q^i, k^i, \alpha^i, \gamma_1^i, \gamma_2^i, H, E, \sigma^2), \\ q^{i+1} &\sim p(q|r^{i+1}, k^i, \alpha^i, \gamma_1^i, \gamma_2^i, H, E, \sigma^2), \\ k^{i+1} &\sim p(k|r^{i+1}, q^{i+1}, \alpha^i, \gamma_1^i, \gamma_2^i, H, E, \sigma^2). \end{aligned}$$

- 2.2 Metropolis-Hasting sampling (for  $\alpha, \gamma_1,$  and  $\gamma_2$ ):

2.2.1 With  $r^{i+1}, q^{i+1},$  and  $k^{i+1}$  generated in the last step, draw  $\theta_{new}(\alpha, \gamma_1,$  and  $\gamma_2)$  from a proposal density  $q(\theta_{new}|\theta_{old})$  sequentially. We adopt the random walk sampler with a normal kernel:

$$q(\theta_{new}|\theta_{old}) \propto \exp\left(-\frac{(\theta_{new} - \theta_{old})^2}{\sigma_{proposal}^2}\right),$$

2.2.2 Set  $\theta^{i+1} = \theta_{new}$  with a probability of  $u$ , and  $\theta^{i+1} = \theta_{old}$  with a probability of  $1 - u$ , where:

$$u(\theta_{new}|\theta_{old}) = \min\left[1, \frac{p(\theta_{new})q(\theta_{old}|\theta_{new})}{p(\theta_{old})q(\theta_{new}|\theta_{old})}\right].$$

3. Increase  $i$  and repeat step 2.