SOME BAYESIAN APPROACHES TO ESTIMATION
OF SHRIMP FLEET BYCATCH

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INTRODUCTION:

Estimation of bycatch by the Gulf of Mexico shrimp fleet has been controversial. Historically, observer data were very sparse, unbalanced, and non-random; and existed only for 1972-1982. Better coverage was achieved during the Regional Research Program (1992-97), but even then random sampling of shrimping activity proved impossible, and coverage diminished as the program wound down. Nevertheless, bycatch removals must be accounted for in stock assessments, and a time series for the removals is needed.

Since 1987, a General Linear Model (GLM) approach has been used to provide estimates of bycatch removals [Nichols *et al*. 1987, Nichols *et al*. 1990, Nichols & Pellegrin 1992; see also Ortiz *et al*. 2000 for a modification incorporating the delta distribution]. The GLM combined data from the several shrimp observer programs with research vessel catch rates from the Oregon II, to predict values of (by-)Catch per Unit Effort (CPUE) for the shrimp fleet for all areas and seasons. The model used was perhaps the simplest possible:

$$\log(\mathrm{CPUE}+1)_{ijklmn}=\mathrm{mean}+\mathrm{dataset}_i+\mathrm{year}_j+\mathrm{season}_k+\mathrm{area}_l+\mathrm{depth}_m+\varepsilon_{ijklmn}$$

for each species separately, where CPUE is the catch rate in number of fish per net-hour, mean is an overall mean, dataset is an effect term discriminating shrimp fishing from research survey trawling, the terms year through depth are effects terms for spatial and temporal cells, and the epsilons are error terms assumed to be random, independent, and with equal variance throughout. All terms except epsilon were treated as fixed effects.

The seriously unbalanced database meant that very few interaction terms could be investigated, so estimation was limited to a 'main effects only' model. Because the predicted values are initially on a log scale, an estimator for an arithmetic mean must include a term with the residual variance as well as the log mean. A normal error on the log scale was assumed to complete this step. There is no exact estimator for the variance of the arithmetic mean in this situation, so Arvind Shah derived an approximation [see Nichols *et al*. 1987]. This approximation is probably satisfactory within the context of the model, but it became that clear that the model itself did not capture all the variation in a meaningful manner -- coefficients of variation (CVs) obtained on annual totals were on the order of a few percent for many species, which seemed implausibly small.

To obtain bycatch estimates, the CPUE predictions must be multiplied by estimates of shrimping effort (as two factors: vessel-hours fished, and number of nets per vessel). No estimates of variance for those effort terms existed. Given the problems of implausible CVs, and the absence of components of variance for effort, we followed some advice received in a 1990 peer review [Nichols 1990], and reported point estimates only. We provided separate estimates based on subsetting of data, in part to at least remind users that uncertainty does exist, but was largely unquantified.

Estimates based on the GLM approach have received considerable, well-deserved criticism over the years. In addition to annual discussions by the Council Stock Assessment Panels, three separate peer reviews have considered the issues [Nichols 1990, Gates 1997, Geaghan 1997, Hayne 1997, Hoenig 1997, Lewis 1997, Reeffish Stock Assessment Panel 1997, MRAG Americas Inc. 1997]. The unsatisfactory situation with variance, and the techniques for dealing with observations of zero in a log model may be the most

problematic issues, at least among those issues that might potentially be addressed further. Of course, nothing can be done now for data collected in the past. Most reviewers still identified the GLM as the best approach available, given the state of the underlying data, but nearly all suggested alternative analytical treatments that could be tried. Several families of alternatives were tried (Table 1), with the results summarized in Fig. 1, originally presented in a report to the Reeffish Stock Assessment Panel in February 1997. Fig. 1 illustrates a very fundamental problem – different, plausible analytical treatments gave a huge spread of estimates, implying an uncertainty far beyond that suggested by variance approximations used within any individual analytical approach. Unfortunately, as pointed out by one of our peer reviewers, there are no objective techniques available to choose the best among the analytical alternatives. After a full presentation on the alternatives, the Reeffish Stock Assessment Panel chose to remain with the estimates based on the original GLM structure as the best available [Reeffish Stock Assessment Panel 1997], accepting the caveat that the bycatch was most likely underestimated.

Over the last 10 years, advances in computing power, and theoretical and practical advances in Markov Chain Monte Carlo (MCMC) procedures [Gilks *et al*. 1996] have provided new capabilities, such that we now may be able to address both the 'zero problem' and the 'variance problem' in one new modeling approach. In this paper, I construct a series of Bayesian models for estimation of shrimp fleet bycatch, using the freely available software 'BUGS' [Spiegelhalter *et al*. 1996]. The results are very appealing, in that the uncertainty of the estimates can be much more realistically modeled, and the procedure for dealing with observations of zero seems at least as sound as other available alternatives. The approach also provided insight into the effects of alternative structural assumptions.

METHODS:

The Data:

There are extended discussions of the underlying data available in the several documents and in the material associated with each of the peer reviews cited previously. For this paper, I will just summarize of several of the features most relevant to the current modeling effort.

Primary data on CPUE in the shrimp fleet has been collected in several observer programs since 1972 (Table 2). Data were available from 3 separate programs for the period between 1972 and 1982. The data were extremely unbalanced, in the sense that work was usually done in different geographic areas in different seasons in different years. Sampling was non-random: convenient vessels were contacted, and those agreeing to host an observer got one.

In 1990, the Gulf Council asked that a panel be assembled to address options for reducing bycatch via season / area closures of the shrimp fishery [Nichols 1990]. The estimates of the extent of closure necessary to accomplish reductions sought by the Council caused great alarm in the shrimping industry. Congress intervened, and required that no bycatch regulations be put in place until a thorough research program was completed. A joint Regional Research Program (RRP) was developed as a partnership among NMFS, the states, and the industry. Several scientific advisory panels were established, including one that gave extensive guidance on sampling and statistical considerations. Unfortunately, many of the recommendations proved impossible to implement. The RRP attained much more balanced coverage than in the 1972-82 period, but attempts to set up random sampling were not successful. Basically, every boat that indicated willingness to take an observer got one. Most of the data were collected under one of two protocols:
> CHAR: "Characterization," in which one net was selected at random, and all species were worked up individually, and
> EVAL: "Evaluation," which paired a net with a trial Bycatch Reduction Device (BRD) with a control net. For EVAL, about 20 key species were worked up individually, with the rest recorded as just fish or invertebrates. Catch rates from the control nets in EVAL were used in estimation of bycatch.

There were a few other protocol variations used occasionally, such as a small number of observations where only red snapper and shrimp were worked up. There are protocol documents available that describe procedures in detail, available from the NMFS Galveston Lab.

In 1998, an additional observer program was mounted to evaluate the effectiveness of new regulations requiring BRDs in a substantial part of the range of the shrimp fishery. This program used a protocol very similar to the EVAL protocol of the RRP, except that for most trawls, only shrimp and red snapper were worked up at the species level. A random sampling of vessel was attempted, but of the first 100 vessels drawn at random from the NMFS list of vessels reporting offshore landings, 99 refused to take an observer. The sampling strategy was switched to a non-random, contract operation, with vessels agreeing to take an observer receiving a cash payment.

In 2001, an observer program was restarted. Plans were based on the recommendations of the 1997 Congressionally mandated peer review [MRAG Americas Inc 1997]. The intent was to cover every spatial and temporal cell sufficiently to make indirect estimation via GLM unnecessary, but full funding was made available mid-year, and only for one year. Many past problems with identifying a sampling universe were eliminated upon the later implementation of the shrimp permit system (although there are still some concerns with completeness), so we are now able for the first time to approach true random sampling of the fleet. NMFS has kept this observer effort alive, but data collection rates and coverage have been similar to the low levels of the mid- 1990s. We still do not have funding for full implementation.

For this paper, I develop estimates only for 1972-1998. (And for convenience, estimates here for 1998 are for a fishery without BRDs; BRD requirements were begun for part of the Gulf of Mexico part way through 1998.) Implementation of successful BRDs on a broad scale would change the seasonal and spatial coefficients considerably from the values established by past data. Without sufficient data to fill every cell, we will still need indirect estimation through modelling, whether those models be the Bayesian techniques of this paper, members of the GLM family used before, or others. All of these modelling approaches will require a sufficient accumulation of data to estimate a post-BRD set of coefficients. Data collected since 2001 are being entered now, and there may be sufficient data for a first cut at modelling post –1998 years in very shortly. It may also be that the unexpectedly low reductions of BRDs under current fishing practices will make separate estimation unnecessary. I will address considerations needed to model 1998 forward in a separate or addendum document once the full data set from 2001-03 becomes available.

Point estimates of shrimping effort are made available by the NMFS Galveston Lab. The level of resolution is that of the shrimp statistical grid system. (See Fig. 2; each of the 21 numbered areas are divided into 5 fm width depth zones; estimates are made and reported for monthly time intervals.) Effort estimation has also controversial over the past 15 years. Several research projects have been funded, and several peer reviews have been held (see Nance 2004) to evaluate the current system, and to suggest improvements. There have been changes in some states with the implementation of trip ticket systems, but in large measure the effort estimation relies on assignment of landings to location (grid) by NMFS and state port agents, and port agent interviews that estimate landings per unit effort in each grid cell. Total landings in each cell are divided by interview CPUE to estimate effort. Landings are considered to be a census. Interviews are a non-random sample, with port agents conducting interviews with available and cooperative personnel during visits to the shrimp dealers. Historically, the shrimp statistical system has never provided an estimate of uncertainty for the shrimp effort estimates, largely due to concern about the non-random sampling. However, the Galveston Lab is now preparing estimates of uncertainty, treating the interview data as if they came from a random sample of trips.

Most observer CPUE data are expressed in numbers per net-hour. Effort data are in vessel-hours, so an estimate of number of nets per vessel is needed. The only data available on this are from the Vessel Operating Units files, which are not on a per trawl or per trip basis (the resolution is vessel.port.year), and which have often lagged behind the current date by several years. In previous bycatch estimates, a constant two nets per vessel was applied, even though it was recognized this caused a bias. (Currently, with the widespread use of quad rigs, the average number of nets per vessel Gulfwide probably exceeds 3). For this paper only, I continue to use only point estimates for effort, and the two nets per vessel convention. These restrictions allow comparison of the new Bayesian approaches with past results, unconfounded by changes

in hours fished and nets per vessel procedures. However, updates are expected incorporating uncertainty in both statistics prior to the next red snapper assessment.

For this paper, I consider data and models for red snapper and king mackerel. Red snapper is the next up on the stock assessment schedule, and is one of the more abundant FMP species that appears in quantity in shrimp trawls as juveniles. Of FMP species, king mackerel has about the lowest abundance in trawls for which one might hope to make meaningful analysis tracking year to year variation. Thus the abundance range covered by these two species should reveal most of the problems that might be encountered in developing these new estimation procedures for use with any species.

The Models:

A sequence of four basic models are developed . The models considered here have structures clearly analogous to the previous GLM work. CPUE (in number) remains the predicted variable in these models. The spatial and temporal stratifications (main effects) in use for last several years are retained (Fig. 2). Terms for years, season, area depth zone, and data set are considered to be fixed, multiplicative effects, thus linear on a log scale. Additional 'Local' terms are considered in the more complex models. The 'main effects' terms, and where appropriate, the 'Local' term, sum to predict the log of the mean catch rate for shrimp fishing in each cell. Around this mean, variation among trawls within any spatial or temporal cell is modelled by a negative binomial distribution, which allows a finite probability for an observation of zero.

The MCMC procedure in BUGS returns posterior distribution of the cell means, conditioned on the individual trawl catch data. The cell means of CPUE are multiplied by appropriate the effort statistics, and summed to give total removals per time interval. For this paper, only annual totals are presented. Previous assessments used 'trimester' (four-month) totals, and estimates at that level of resolution can be made available as data files for the next assessment.

The logical underpinnings of the four models considered are elaborated in the Results section, but in summary, the four models are:

01) Main effects for year, season area depth zone, and data set (observer or research vessel). All variation within cells is modelled by a common negative binomial. There are broad priors assigned to the main effects parameters (also used in the subsequent models). This model is the most analogous to the original, frequentist GLM.

02) A 'Local' or 'Lack of Fit' term is added to the (main effects) prediction for every cell. The prior for this set of terms is lognormal with mean zero on the log scale, and the precision is set up as a hyperprior on a common precision parameter for each lognormal distribution. Thus, the precision of the 'prior' for each local term is actually determined by the data. For cells with data present, the data determine the center and spread of the 'Local' parameter (shrunk toward the prior, of course, depending on the amount of data). For cells without data, the 'Local' values default to the distribution of the prior with the fitted precision. In a certain sense, this makes the 'Local' parameter a fixed effect for cells with data, and a random effect for cells lacking data. There may not be a simple analog to this structure in a frequentist GLM.

03) A 'Local' term is used to model the catch data (where data are present) as in model 02, but to calculate the distribution of every cell mean, only the main effects are used to predict each cell's mean, and a (log)normal random effect with mean zero and precision set by the data and the hyperprior as in model 02 is added to each main effects mean. This structure is probably closest to a mixed model structure that could be simply implemented in a frequentist context (say, via PROC MIXED in SAS). All deviations of cell means from the main effects means are considered to be realizations of a common random effect present in all cells.

04) The general structure of model 02 is retained, but assumptions of a single common negative binomial and a single common precision on the prior for the 'Local' parameters are relaxed. In response to previous discussions of the GLM modelling, 4 terms for each are considered, separating the data by dataset and time period.

A common core of normal priors for the main effects parameters was used in all four models (Table 3 expresses them in BUGS code). The main effects are expressed on a log scale, where they are assumed to be additive. Following BUGS convention, normal distributions are parameterized by their means, and a precision term, which is variance^{-1}. Season, area, depth, and dataset effects are centered, so the prior mean is taken to be zero. The year effect is not centered. In preliminary runs, I found it useful to set the prior mean for year parameters to a convenient value near the global mean of the data for each species. This practice avoided numerical errors that were occasionally encountered in trying to use a prior broad enough as to encompass means for all species in one distribution. The precisions for the priors were chosen by looking at the potential ratios of cpues implied at +/- 1,2, and 3 standard deviations (Table 4), and I believe the final choices should easily span any biological reality. Priors for the additional parameters specific to each model are discussed in the introduction to each model in the Results section.

A standard suite of outputs was examined for each model run. BUGS box plots were used to summarize the posterior distributions for total annual bycatch on both arithmetic and log scales. (In BUGS, the box plots depict the interquartile range, the 2.5% and 97.5% quantiles, and the mean.) BUGS has automatic plotting capabilities for the marginal density distributions, so these were examined for the main effects and common parameters. For parameters specific to each of the 1296 cells in the model, only selected subsets were examined. Usually, I examined all parameters for year 18 (1989) and year 22 (1993). 1989 was chosen because it is a recent year without any observer data, and 1993 was a year with high activity and broad coverage during the Regional Research Program. Goodness of fit was examined graphically, by plotting medians for predicted cell CPUEs vs observed cell means on both arithmetic and log scales. Convergence and mixing were evaluated by examining plots of each parameter value vs iteration number (called 'History' in BUGS), and by examining the density plots for relative 'smoothness.' BUGS has a statistical test for convergence built in (Gelman-Rubin statistic, described in the BUGS Users Manual within the program), but in some preliminary runs, the test appeared to be too liberal, in the sense the GR statistic was stable near 1 before the history showed a convergence pattern satisfactory to the eye. I chose not to rely on the Gelman-Rubin statistic. In general, the results for the models I present in this paper do not have indications of problems with convergence or mixing. (This was not always the case for some other work I have done with BUGS.) For models of the complexity used here, BUGS has a 4000 iteration 'adaptive' phase, where BUGS develops a strategy for sampling the joint distribution. Parameters from this adaptive phase are automatically excluded from the model statistics. In most cases, that 4000 iteration limit was very conservative – most anomalies of intialization and pre-convergence seemed to be over after about 2000 iterations, max. Duration (number of iterations) is also an analytical choice, which I evaluated by looking at the smoothness of the densities, and the stability of the quantiles with increasing number of iterations for a few of the models. For the models examined, the central tendencies in the marginals for predicted cell means appeared to be well established after only a few thousands iterations past the adaptive 4000. The marginal densities for the main effects parameters tended to lose the 'jagged' appearance seen in the shorter chains at about 25000 iterations. 25000 iterations (with 2 chains) also coincided with a computing time of just under 24 hours, so I adopted that as a standard run length. With two chains, and deduction of the adaptive phase, this convention gives 42000 points to characterize the joint distribution, each marginal, and functions thereof. I also ran some of the more complex models out to 45k iterations (providing 82k points), and examined the changes in parameter estimates with increasing iterations, and over shorter segments of iterations within the 45k. There were no indications of problems. The marginal densities looked noticably smoother as number of iterations increased, but based on the consistency of the statistics compared to the distributions' variances, the changes after about 10-15k iterations can be considered largely cosmetic for the models considered here.

Implementation of the negative binomial portion of these models was probably the most difficult part of development. Initial trials with the negative binomial simulation inherent in BUGS (dnegbin) led to serious problems with poor mixing, and excessive computing times per iteration. I switched to a procedure suggested by B Jones (Duke / SAMSI), and used a combination of BUGS' gamma and poisson distributions. A gamma distribution with the r and mu parameters is sampled in the MCMC to produce a lambda parameter for a Poisson distribution, essentially changing lambda for every trawl. The lambda drawn is in catch per hour units, so that lambda is multiplied by the hours fished for each tow to predict the value catch in numbers to compare with the data. The result is a negative binomial distribution for the catch in numbers. Neither gamma parameter is independently related to the cell mean (mean=r/mu). To set

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the mean to the value predicted by the main effects parameters, only r is taken as a free parameter, and mu is set to be r/(predicted mean cpue for each simulation iteration). This two-stage approximation to the negative binomial proved much more satisfactory with respect to speed and mixing, but there were still numerical problems that caused the analyses to crash when using broad priors that allowed the MCMC to explore very low values of r. There appeared to be two sources to the numerical crashes: 1) less frequently, a draw from the gamma with low r would produce a lambda numerically indistinguishable from zero by the computer, which crashed the Poisson portion of the routine, and 2) more frequently, the adapative strategy (first 4000 iterations) for BUGS dropped the trial parameters for r to extremely low levels, and caused a numerical error even when the final posterior might not have been a problem. A solution to both problems was to constrain r with a 'hard-edged' prior that did not allow r below about 0.03. I chose to use a uniform prior on r (or r's, in model 04) on the interval 0.03 to 5. For red snapper, this choice of prior appeared to have little impact on the r distributions ultimately chosen by the data, as the full range of the posteriors tended to be well above the 0.03 minimum. For king mackerel, however, the shapes of the posteriors for the r's are clearly dominated by the lower bound of the prior.

All runs were completed on a Dell computer equipped with Dual 2.6 GHz XEON Processors and 2 GB RAM. The operating system was Windows 2000. The version of BUGS software used was WinBUGS 1.4. As per usual in papers by government scientists, declaration of trade names does not imply a product endorsement by the government. The BUGS code used for the models is collected in the Appendix.

RESULTS:

Model 01

Model 01 is the main effects only model. It was intended to 'convert' the past GLM structure to a Bayesian approach. Results were, predictably, very similar to the GLM results. Figs. 3 & 4 show estimates of the annual totals for bycatch in numbers for red snapper and king mackerel.

Standard errors of the annual totals were generally below 10% of the mean for red snapper, and on the order of 35% for king mackerel, which were comparable to the GLM results using Shah's approximation. A slight skew was evident for most of the annual totals on the arithmetic scale (Figs. 5a & 6a; slight, at least, compared to the results of the more complex models below). The distributions for the annual totals expressed on a log scale were nearly symmetric (Figs 5b & 6b) . On the log scale, and particularly for king mackerel, the years with lower estimates tended to have lower precision. For red snapper, the distribution of the r parameter was nearly symmetric about a centroid (i.e. either mean or median) of about 0.14, and the entire posterior distribution was well away from the bounds of the uniform prior. For king mackerel, the data appear to be drawing the posterior to values below the 0.03 minimum required to avoid numerical error (Fig. 7). The variance of the posterior was so small that one could consider king mackerel r to be effectively 'set' at 0.03.

Model 02

Model 02 adds a 'Local' term to each cell in the model. The Local term uses a lognormal prior with mean zero, and a lognormal hyperprior on the precision parameter with (log)mean zero and precision (log units) of 3.5. (The precision parameter as specified in BUGS is 1/variance.) The prior on Local thus acts as a random effects term, and where data are absent, its uncertainty is carried forward in full into the bycatch estimates. However, in this case, due to the 'hyperprior' status for the precision parameter, the spread of the 'prior' for the Local term is largely determined by the data. This structure takes advantage of a particular strength of the Bayesian approach. A cell mean estimate is dominated by the Local parameter (and its individual variance) for cells where data are plentiful. For cells with smaller numbers of observations, the predicted cell means are still influenced by the Local term, but the means and variances of the Local terms are shrunk toward the prior. Where data are absent, the Local term defaults to the 'fitted' prior, influencing the variances of the bycatch estimates as a fully random effect.

Model 02 returns much broader confidence intervals on the annual totals than model 01 (Figs. 8 & 9; compare to Figs. 3 & 4). The widths of the intervals vary considerably among years, being narrow for data-rich years, and very broad for data poor years. Expressed as CV's, data poor years return CV's for red snapper over 100%, while the most data rich years had CV's ranging down to about 15%. For king mackerel, CV's were generally 200% or greater. However, the skews of the distributions for annual totals are so great that CV is not a very meaningful statistic. (Mean and variance are not sufficient statistics for skewed distributions.) Variation on a log scale is much closer to symmetric, so expressing variation as a factor on the arithmetic scale is more meaningful. For example, the value of plus or minus 0.7 for one standard error on the log scale implies a range from about 0.5x to 2x on the arithmetic scale. This spread is typical of the values returned for red snapper in data poor years. One standard error spreads for data rich years ranged downward from that, to as low as 0.86x to 1.16x for 1993. For king mackerel, a spread of one standard error on the log scale corresponds to factors on the order of 0.3x to 3x for data poor years, improving to factors more like 0.5x to 2x in the most data rich years. However, even on the log scale, the annual totals show some asymmetry for both species, always with an extended tail toward the higher values (Figs. 10 & 11).

For red snapper, the gamma parameter r was centered at 0.167 (Fig. 12a). With the addition of the Local terms, this value was slightly higher (i.e., lower variance) than for model 01. The posterior distribution was still tightly defined compared to the vague prior, with all points from the simulation well above the hard minimum at 0.03 imposed by the prior. For king mackerel, the posterior again obviously collides with the 0.03 of the uniform prior (Fig. 12b), so much so that the posterior can again be considered to be almost fixed at 0.03.

The precision term for Local for red snapper centered at 0.59 (Fig. 13a), implying that +/- one standard deviation of the Local term contributes factors of 0.27x to 3.7x for any cell without data. For king mackerel, the median of the precision parameter was about 0.26 (Fig. 13b), implying one s.d. factors of 0.14x to 7x. For both species, the distribution of this parameter was very narrowed by the data, compared to its lognormal prior. For red snapper, the median of the posterior was about one (prior) standard deviation from the center of the prior, an area where I would expect the prior to have had little influence on the outcome. For king mackerel, however, the median of the posterior was about three (prior) standard deviations from the center of the prior. This is an area where I would expect the prior to have had more influence, perhaps more than one would like, given the absence of substantive knowledge to set the prior. I evaluate an alternative later in the paper.

Model 03

Model 03 also incorporates a Local effect, but its motivation and use are different than for model 02. Suppose that most of the deviation from cell means predicted by main effects was not due to real, cell-wide perturbations, but instead resulted primarily from the non-random sampling within cells. In that case, each Local effect should be used to model the local data, but only the overall variance of the Local effects, and not each central tendency or local variance, should be carried forward into the estimates of the bycatch. I implemented this structure by simulating the Local effects as in model 02, but then adding a term with mean zero and precision equal to the default precision (determined by the data and the hyperprior on the Local precision) to the main effects terms for every cell. This approach seems to be rather non-standard in a Bayesian context, but does resemble fairly closely what one would get with a frequentist model with Local as a random effect.

Modeling non-random sampling as a lognormal random effect is a rather aggressive assumption, but it is probably the most parsimonious approach that could be considered. Effectively, one is saying that the overall distribution of data averages out the non-randomness enough that the main effects estimates may be reasonable, but locally there is considerable uncertainty about the true value of any mean because of the non-random sampling. I should also note that non-random sampling is not the only mechanism that could generate a random effect. However, my motivation here is that I want to consider the impact that the non-

random sampling might have on the estimations, and if it is a dominant mechanism, I would most expect it to act like a fully random effect.

Because the same uncertainty is passed forward for predictions in every cell for Model 03, the confidence intervals for annual bycatch are almost the same every year on a log scale (and thus are nearly constant proportions on an arithmetic scale). All are broader than even the broadest (data poor) years for model 02 (Fig. 14 & 15 compared to Fig. 8 & 9). For red snapper, +/- one standard error on the log scale corresponds to about 0.25x to 4x; For king mackerel; 0.12x to 8x. The skew on the arithmetic scale is even more severe for model 03 than model 02 (Figs. 16a & 17a compared to Figs. 10a & 11a), but this is a consequence of the higher variation on the log scale inherent in the model. The distributions for estimates of annual bycatch on a log scale from model 03 are actually more symmetrical than model 02 (Figs. 16b & 17b compared to Figs 10b and 11b).

Model 03 and model 02 are actually the same model in terms of fitting the main effects and the Local term. The results and comments for r and the (fitted prior) precision of the Local terms are the same as described in the summary of model 02 results. Figs. 12 & 13 apply to model 03 as well.

Model 04

Model 04 incorporates a different type of modification, addressing some of the past criticisms of the GLM approach. There were some fundamental differences in the observer programs between the 1972-1982 and 1992-1998 epochs, and the research survey strategies also were modified over time. These difference were considered by modifying model 02 to allow 4 different precision parameters for distribution of the Local terms, and 4 different r parameters for the within-cell gamma distributions. Separate r and precision parameters were allowed for observer and research data, and for 1972-1986 and 1987-1998. (Within those 4 subdivisions, the parameters are assumed to be in common among all cells.) The main effects parameters remain completely crossed, and applicable over all cells in the model.

I modified the hyperprior for the Local precision parameter for model 04. I was already concerned that the hyperprior might have been overly influential on the king mackerel results in the previous models, and knew that the posterior medians would be lower still for at least some of the four precision components in model 04. I started by dropping both the mean and precision for the lognormal hyperprior to (-1,1). This allowed the potential for very low precision in the MCMC sampling, which caused a numerical crash. I then opted to go the same route I had used with r, and switched to a uniform(0.03,3). This distribution has a slightly higher mean than the original hyperprior, but the prior probability is now flat down to a hard edge well below the smallest values drawn for either species in the MCMC for model 02.

Box plots for annual distributions and examples of annual total marginal posteriors (paralleling most the presentations for the other models) appear in Figs 18-21 for model 04. For red snapper in data poor years, the spreads in the annual bycatch estimates are slightly smaller than for model 03 (+/- one s.d. about 0.27x to 3.7x); the best of the data-rich years match the tightest spreads from model 02. For king mackerel, the spreads are comparable to model 03 on average, but for some data poor years, the spreads became quite extreme, with +/- one s.d. approaching 0.2x to 14x. (For a 95% c.i., several year exceeded a factor of 150x on the high side.) Skew on the arithmetic scale in these situations was very extreme. The median estimates for those several years were also very high compared to expectations derived from previous analyses. However, model 04 appears to be handling the situation correctly, in the sense of telling us through the confidence intervals that we should have little confidence in those particularly high median values. Under this model, the data are not sufficient to exclude extremely high bycatch values, although the highest values are shown to be very unlikely.

For red snapper, the largest difference among the four r parameters turned out to be between the early and late epochs (Fig. 22). The marginal distributions for r between research and observer within each epoch showed substantial separation, but much smaller than the differences for each between the two epochs. None of the posteriors for r seem to be much affected by the hard lower limit of 0.03 imposed by the uniform prior. For king mackerel, the effect of the prior is again evident in all 4 posterior marginals for r,

but the king mackerel results share the pattern with red snapper of higher values for r for both research and observer cells in the 1987-98 epoch (Fig. 23).

For both species, comparing to 02 results, the partitioning the precision term into 4 precision parameters results in a smaller spread for the Local terms for the research vessel cells, a larger spread in the 1992-1998 observer Locals, and an even larger spread for the 1972-86 Local terms (Fig. 24 & 25). The decrease in precision for the observer locals increased the skew of annual totals well beyond that of in models 02 and 03. (The skew was so severe that plots of the marginal posteriors on an arithmetic scale just looked like two perpendicular lines, so these graphs were not included for model 04.) It is also the increased variability in the observer Locals, rather than increased central tendencies for parameter estimates for the main effects, that is responsible for the increase in values for means and medians for the annual totals between models 02 and 04 (Figs. 26 & 27). Those increases seem large when looking just at medians of the annual totals (particularly for king mackerel), but are in fact small compared to width of the 95% confidence intervals.

Sensitivity to the Local precision hyperprior

The comparisons between model 02 and 04 predictions in Figs. 26 and 27 include both the effects of the decision to partition the r and precision parameters and the decision to change the hyperprior used for the spread of the Local effects. To examine this in more detail, I exchanged the hyperpriors, running model 02 with the uniform hyperprior, and model 04 with lognormal hyperprior. I shortened the runs to 10k iterations to save time. I summarized the results with the same types of plots used in Fig. 27.

For red snapper, the change of hyperprior had virtually no effect for models 02 and 03 (Fig. 28 & 29). For model 04, the annual totals are seen to be sensitive to the choice of hyperprior (Fig. 30). The change to the uniform hyperprior increased the annual totals by 23% on average (difference of means on log scale converted to an arithmetic factor). However, the average difference in Fig. 27 was 72%. These two percentages imply that the data are dominating the effects of the structural change between models 02 and 04, but that the choice of hyperprior is having some effect in model 04. The increased sensitivity to the hyperprior in model 04 arises because the data are indicating a much lower fitted precision term for the Local effects for the observer cells, now so far removed from the center of the lognormal hyperprior that shrinkage toward the hyperior center is becoming important. Note, however, that change in medians for total bycatch between models 02 (lognormal version) and 04 (uniform) are small compared to the confidence intervals for either model 02 or model 04.

For king mackerel, the change of hyperprior has virtually no effect on model 03 medians for total bycatch (Fig. 32; as expected -- changes in confidence intervals would be expected for model 03, but not central tendencies). Changing the hyperprior to uniform, but otherwise keeping the model 02 structure raised to total catch medians about 16%, due to the lowering posterior distribution for the precision parameter of the Local effects (barely evident in Fig. 31, but the points are all above the 1:1 line). The change in median of the precision parameter was very small compared to its confidence interval (median changed from 0.26 to 0.23; 95% confidence interval on the 0.26 median was 0.19 to 0.35). This carries over to the posterior distributions of total bycatch, as the changes with change in hyperprior were also very small compared to the confidence intervals (compare Fig. 31 with Fig. 9b). For model 04, the change in bycatch estimates with change in hyperprior was approximately the same magnitude as the change between model 02 with the lognormal hyperprior and the model 04 with the uniform hyperprior. Both were factor near 2.5x for the average of the bycatch medians (compare Figs. 27 & 33). This result arose because the median of the posterior distribution for the precision parameter did not change much between model 02 (lognormal) and 04 (uniform) (0.23 vs 0.20), whereas use of the uniform hyperprior in model 04 dropped the median of the precision parameter to 0.09 for the early years / observer component, implying approximately a doubling of the variance for Local terms in those cells.

The bottom line for both species seems to be that the first choice for hyperprior, the lognormal (0,3.5) had little effect on the results as long as the posterior median came out within 2 standard deviations from the hyperprior mean. As results approached 3 standard deviations, the hyperprior had a stronger influence on

the results than was intended. Therefore, I retained the lognormal hyperprior for further examination of models 02 and 03, and retained the decision to switch to the uniform hyperprior for model 04.

Goodness of fit

Some goodness of fit evaluations are presented graphically in Figs. 34 through 49. The figures show measures of central tendency from the models plotted against cell means of the raw data. Not surprisingly, models 02 and 04 show much tighter fits than models 01 and 03, as the Local terms are used in the calculation of the predicted CPUEs for the cells. In model 01 and 03, Local terms do not have a role in cell predictions. In model 03, they are replaced by a random effect with mean zero in all cells. In model 01, there are no explicit Local terms, and any such effect is subsumed into random variation around the main effects results. Within these structural limits, the different models fit the data well, as in fact did the standard GLM, and many of the alternatives summarized in Fig. 1. The real differences in annual totals among the models come for what the models predict in cells where there are no data, which are consequences of the structural assumptions.

Summary graphs of central tendencies

Figures 50 and 51 summarize the central tendencies of the four models by plotting the annual medians. I have also included the most recent GLM results (the 'ALL" line), and results from combining the delta distribution with the GLM structure available in Ortiz *et al*. 2000 and Ortiz 2002 (the 'delta' line). The same lines are presented on two scales to make a point. If one looks only at the central tendencies, the results may seem quite different, but if one considers the larger, more realistic uncertainties provided by models 02, 03, and 04; and scales the plots accordingly, the differences among the medians are not so impressive. Of course, a plot that summarizes the full distributions for each model would be more appropriate, but a single box plot for the annual totals for all years for all models would be distractingly complex.

DISCUSSION:

Overall, these Bayesian approaches to estimating bycatch seem highly successful. The results look very plausible, in the sense that fits to data (where present) look adequate, and that most medians of the total annual bycatch distributions are similar to what has been seen in the past with other methods. More importantly, the estimates of uncertainty now seem very reasonable. The confidence intervals for model 02, 03, and 04 have sound theoretical bases, building on a structure that incorporates real variation in the data in a manner missing in both in model 01, and in the past application of the GLM approach. The differences among the centroids of the models developed here are comparable to the magnitudes of variations in centroids of figure 1, but the interpretation has changed: the differences among the centroids are almost trivial compared to the uncertainty indicated by the confidence intervals of models 02, 03, and 04. Where data are present, the models fit the data well, with the differences among the models showing a pattern to be expected based on inclusion or exclusion of a fitted 'Local' term. The confidence intervals of models 02, 03, and 04 are very broad – they reflect the true cost of the sparse and the unbalanced data better than any attempts to describe uncertainty used in the past. Model 03 even attempts to include the potential cost of the non-randomness in the data collection programs, but as is generally the case with non-random data, it is impossible to judge whether that cost is over or underestimated by the confidence intervals of model 03. The results of these estimations, expressed as full distributions, should be easy to plug directly into the stock assessment, appear to provide very meaningful solutions to the variance problem of the GLM, and provide a workable but not perfect approach to the zero problem.

My first motivation for exploring a Bayesian approach for bycatch estimation was actually to tap the power of Markov Chain Monte Carlo for dealing with the zero problem. I appreciated the nature of Bayesian probability statements about parameter values, which often seem more natural and useful than frequentist hypothesis testing statements. The ability of a Bayesian approach to operate easily between the extremes of

fixed effects and random effects was something I came to appreciate during the development of these analyses.

The similarity of models 02, 03, and 04 to a frequentist approach using random effects was noted, and thus credit should be given to a previous suggestion to consider random effects. Jay Geaghan (LSU) suggested in the 1990 peer review that incorporating random effects might give a better evaluation of error in the GLM approach. Arvind Shah attempt to implement a version of Geaghan's suggestion at the time, but found it required far more computer memory than was available on any of our machines. Now, after over a decade of improving computer technology, random effects treatments of these data are possible.

With that overall positive introduction, I turn now to a discussion of the factors that may put limits on the effectiveness of this modeling approach.

Prior distributions:

Bayesian approaches have sometimes been criticized, primarily in relation to the use of prior distributions. There is no question that choices of priors do influence the numerical outcomes – it seems impossible that they could not in computers that must deal with finite numbers. Certainly, it is possible to mislead oneself by using priors that put more information into an analysis than is justified. I thought the first (hyper)prior I used on the precision term for Local effects would be broad enough for any situation, but I had to revise my thinking once I realized that my original choice might have too much influence in model 04. That unexpected result emphasized the importance of evaluating whether the priors are unduly influencing the outcomes, at least in undesired ways. However, in model 04 here (which is still a relatively simple model) there are 50 prior distributions. At 24 hours per run, it is not practical to run sensitivity cases around every prior singly, let alone jointly. Generally, I compare the posteriors to the priors. In almost all cases, the priors used were extremely broad compared to spreads of the marginal posteriors. The sole exception was the for the r parameter(s) for king mackerel, where a strong effect from a prior was necessary to prevent numerical crashes.

Prior distributions actually serve multiple functions in the types of analyses being introduced into fisheries. Fundamentally, having a prior allows probability statements of the form: Prob{param value, given the data}, via Bayes theorem. Priors can also be a direct mechanism to incorporate substantive knowledge or subjective belief external to the data at hand into an analysis. (The math is the same for both substantive knowledge and for subjective belief, which seems to be the root of past controversies). A least in fisheries, the philosophy behind the use of priors seems to be tending in a different direction: start with vague priors, and add the assumptions of narrower priors only if data are insufficient in themselves to lead to a realistic solution. (That is basically the approach taken here with the r parameter to generate the negative binomial structure.) An attractive feature of the Bayesian approach is just how explicitly the assumptions must be specified.

Priors have an important additional function – to constrain the potential parameter space to numerical viable values. That turned out to be a primary consideration in setting the precisions on the priors used in this analysis. My first choices for priors on the main effects were even broader than those in Table 3. Individually, they looked acceptable, but applied as sums on a log scale, and moving back and forth between logs and arithmetic scale, the probability of extremely large and small values led to numericial crashes (numbers too near zero or infinity for a computer to deal with). I found it necessary to constrain the priors with narrower precisions than I first considered. Constraints are generally necessary for any technique that searches a parameter space, so these types of adjustments are not unique to Bayesian approaches. I believe it is not necessary to be too concerned with the main effects priors. The choices I settled on seem extremely broad, and if the more extreme posterior predictions for cell means from the main effects have been pulled back toward the prior means, that is not necessarily a bad thing. In model 01, that effect would simply partially discount the extremes relative to a complete uninformative prior; and in models 02, 03, and 04, the Local term would pick up the deviations. I was more concerned with the priors for the Local effects, as changing the posterior variability by changing the prior can impact the magnitudes of the bycatch estimates. In the end, the effect was evident, but the concern turned out to be

more distraction than substance, as the changes in bycatch estimates caused by the changes in the priors turned out to be small compared to the confidence intervals.

Ultimately, I think it best to consider the development of priors as simply an obligatory part of this modeling approach. I feel that many concerns about 'subjectivity' of priors are misplaced, in the sense that most decisions about modeling are have a subjective component under any approach. Why single out on Bayesian approaches in that regard, especially when the 'subjective' decisions must be spelled out so explicitly in the Bayesian format? It is hard to imagine anything more subjective than the considerations that led to Fig. 1.

Negative binomial

I chose to use the negative binomial for within-cell variation simply because it is a common distribution that allows finite probability of an observation of zero, and can describe patchy populations. Certainly the similarity of the medians from model 01 to the estimates from both the GLM and the delta modification to the GLM (Figs. 50 & 51) indicates that the negative binomial is doing its job. (Interestingly, the directions of most differences between model 01 and the GLM are the same directions as between the delta modification and the original GLM, but the magnitudes were not very consistent.) However, the required intervention of the prior for king mackerel shows that the negative binomial is not a perfect solution to the zero problem.

There is something of a dichotomy in the shape of negative binomials, separated by the gamma parameter at $r=1$. For $r>1$, the distribution allows modes greater than zero (although modes of zero are possible for low means). For $r<1$, the distribution has a definite mode at zero, with a monotonic decline in probability for increasing numbers in a sample. This distribution will not describe patterns with a strong mode at zero and a secondary peak at a positive value (patchy patches, if you will), attributing any secondary peak to random noise about the monotonic decline. Particularly for king mackerel, which occur in only a small fraction of the trawls, the mode in any cell will usually be zero, implying low r. It is not clear to me whether the presence of occasional large catches in cells with low means may be part of the numerical instability of low r's, but I suspect that may be part of the problem. I considered allowing r to vary from cell to cell, using a hyperprior structure similar to that used for the precision on the Local parameters, but those attempts also ended in numerical crashes. Without a 'hard edge' at the lower limit of what is numerically possible for r, the analyses failed for king mackerel. I did not explore modifying all the other priors in hopes of allowing lower values of r.

I made several additional runs for king mackerel using the model 02 structure, but setting r to a series of fixed values between 0.03 and 0.9. I kept the runs to 10k iterations to save time. I summarized the results by calculating the average values of the medians of total annual bycatch for each run (Table 5). The results were not monotonic with r, but there does appear to be a downward drift with increasing r. We cannot see below $r=0.03$, but the data seem to be leading that direction, so there may be some chance that bycatch is systematically underestimated for king mackerel due to the constraint on r. However, the magnitude of the drift in the region that can be seen is small (especially when the confidence intervals are considered), so what evidence there is suggests that any bias may not be very serious.

Limitations imposed by the data

Ultimately, all the analytical manipulations cannot completely overcome the limitations imposed by the underlying data. The observer data are still sparse, unbalanced, and non-random. Lack of randomness is a within-cell issue. There are no analytical actions that can make the data more representative, or even evaluate how representative the data are. (Fitting functions within cells could be considered, but it would be essentially equivalent to establishing new cells.) Lack of balance is an among-cell issue. It can be dealt with analytically to a large extent, both by the GLM structure, and by the very similar structures of these Bayesian models. However, one of the biggest faults of the original GLM became clear in developing the models with Local terms. The GLM essentially treats the coefficients as 'partial derivatives' in developing

predictions for sparsely filled or empty cells. This is always dangerous with unbalanced data, as the coefficients are actually dependent on what other terms are in the model, and the distribution of the data. That dependence still holds in the Bayesian models, and the application of the parameters as 'partial derivatives' is still unavoidable. However, models 02, 03, and 04 in this paper incorporate a major advance -- the uncertainties caused by that requirement are now modeled by estimating the uncertainties of the Local terms, and incorporating those uncertainties in the CPUE predictions. With that advance, past debates over the 'best estimates' are shown to have been largely meaningless, as the differences that were debated are now seen to be small compared to the confidence intervals of the new models. Choices remain to be made among models 02, 03, 04, or any further modifications (and the data provide little guidance), but the qualitative differences among them seem small compared to the gap between them and model 01 or the GLM. Possible criteria for choices among 02, 03, and 04 are considered in the Recommendations section.

The absence of data in many cells forces reliance on a model drawing on data from other cells, and relationships among cells are almost certainly dominated by multiplicative factors. Although linearizable with logarithms, this fundamental nonlinearity on the arithmetic scale means that means and variances can never be independent. Increase or decease the variance on the log scale, and the distributions on the arithmetic scale will rise or fall. The can be disconcerting to those conditioned by experience with linear relationships and normal distributions to perceive mean and variance as always separable, but the interdependence is unavoidable unless one can collect enough data to fill every cell and estimate their statistics independently.

Other model structures:

It is easy to think up more elaborate model structures that might be considered. One could partition any of the parameters to apply to only part of the cells to be filled, like I explored in model 04 for the r and the precision of the Local terms. It is more tempting to try to incorporate multiple random effects attributable to different mechanisms. There appear to be 3 mechanisms most likely to contribute to the Local effects. One could consider a full random effect to model impact of the non-random sampling; a Lack of Fit term to describe real perturbations in abundance from the main effects CPUE predictions; and even a third, similar term to model real variations in catchability (q) due to real spatial and temporal changes in fishing effort patterns relative to the fish stocks. Unfortunately, these three potential effects are completely confounded – that is, not identifiable. (Even knowing that, I tried incorporating two terms in the same BUGS model to see what would happen. One term had a vague prior; the other a tight prior. BUGS fitted the term with the vague prior, but essentially just returned the prior as the posterior for the other term.) I also considered fitting separate models in succession. The idea was to use the precision of Local terms for the research cells from model 04 as a tight prior for the precision for a Lack of Fit type term as in model 02. Then, a fully random effect with mean zero and precision determined by the difference in variance between the research and observer Local terms would be added to the CPUE predictions, as in model 03. (This particular strategy would still not model real variations in q appropriately.) I considered several ideas along these lines, but decided they all seemed too contrived, so I never tried to implement them.

Ultimately, I accept the advice we received at the 1997 Congressionally-mandated snapper review: extended exploration of model structures and technique is not really productive, because just like the alternatives of Fig. 1, there is no objective way to chose among them. One could argue forever that certain parameters should be fitted and applied over only restricted parts of the data. Ultimately, what one gains from elaborating structure may be quickly lost in poorer fits for restricted parameters. There is no escaping the fact that the underlying data are sparse and unbalanced. There is no choice but to borrow information from other cells to fill the sparse or empty cells, which implies the 'partial derivative' application of the parameters. Predicting CPUEs with parameters averaged from a wide range in time and space will lose some real variation at smaller scales, but those broad averages might be more safely fit than terms using data from much more restricted ranges of time and space. One can evaluate the precision changes with additional structure, but one cannot protect against biases that the sparse, unbalanced, non-random data could produce. Therefore, simpler seems safer – effects of any hidden, local biases should be minimized by using parameters determined by broad ranges of the available data.

BUGS as a Vehicle

It is not my intent to provide a full evaluation of BUGS software, but I will make some observations about BUGS that I noted in developing these analyses. On the very positive side, BUGS provides automatic set-up of numerical methods to accomplish Markov Chain Monte Carlo estimations, with the user defining the probability distributions and data with some very simple code. This allows users who are not specialists in numerical analysis to take advantage of that expertise in the BUGS development group. Without this automatic set-up and built-in expertise, the development time even for models as simple as I used here might make MCMC approaches impractical for many of us. Specific problems all have their idiosyncrasies, but using BUGS, I usually found ways to make the software work around problems fairly quickly. BUGS has many convenient features built into it. The learning curve is not very steep, beyond getting used to a few annoyances in the notation conventions. Less positively, one of BUGS strengths is also its weakness. The software is written to handle a wide array of problems, and thus is not tuned to the particular problem a user might be addressing. Someone with sufficient expertise in numerical analysis could probably write special purpose routines that were far more efficient. This can be important, as computing time was the most limiting factor in trying alternative analyses and sensitivity cases, and in considering increasingly complex models. When a numerical error is generated (from, say, priors in combination too broad to be numerically possible), BUGS returns very cryptic error messages that are little or no help for correcting the problem. And, if you cannot find a way around a numerical impediment, you are stuck – BUGS puts very little of its internal strategy under user control. I had a particular problem in that regard with implementing the negative binomial. It appeared that the problem was generated by the BUGS adaptive strategy, not impossible parameter combinations per se. The only work-around I could find required trial and error restrictions that excluded seemingly plausible parameter values. BUGS, probably in interaction with Windows, did show some memory management problems. When I tried to store more iterations and parameters than my machine's memory could accommodate, BUGS simply output a nonsense iteration, and crashed. Thus, there are practical limits to number of parameters, number of parameters monitored, and number of iterations that basically had to be learned by trial and error. BUGS also has a built in limit on the length of a chain of dependent variables that it can accommodate (about 40). This had no impact on the work reported here, but did impact some trials I made on surplus production models. There are reports on the BUGS mail list of BUGS code running under Windows 2000 not running on NT. This was not an issue to me – I have used only Windows 2000 and Window 98, and have not seen any compatibility problems. However, my older and several-fold slower Windows 98 machine could not complete the analyses of the models used here in a practical amount of time, tending toward many days per run, rather than 24 hours.

Summary

To summarize the discussion, the Bayesian models presented do offer some real advantages. The negative binomial had some obvious limitations (probably because it does not fit real data all that effectively), but it did accomplish the step to a discrete distribution allowing a finite probability for an observation of zero, and did not appear to be a serious source of bias. The sparse, unbalanced, and non-random nature of the data cannot be completely overcome by analytical techniques. However, the structures of models 02 and 04 allow the uncertainty from the sparse and unbalanced situations to be carried forward into the bycatch estimates. Model 03 even tries to address the non-random aspect of the sampling, but it is not possible to evaluate how successful it truly is in that regard.

RECOMMENDATIONS:

It seems clear that there is predictive power in the 'main effects only' structure; but that model 01, like the GLM after which it was patterned, does not provide a realistic description of the uncertainty for the estimates of bycatch. With the alternatives of models 02, 03, and 04 available, I no longer recommend the GLM results.

There is nothing inherent in the data or the analyses to help make a choice between model 02 and 03. The only basis for a choice really depends on your opinion about dominant source of deviation from the main effects prediction. If you believe the variation is dominated by real, local perturbations of abundance or catchability captured by the field sampling, model 02 makes the most sense. If you believe the variation is dominated by a varying bias from the non-random sampling, model 03 would be the logical choice. Of course, there is no guarantee that one source of variation dominates in all cells, thus the truth might be somewhere between models 02 and 03, or the truth could be closer to one model at some times and places, and closer to the other elsewhere. Unfortunately, there is no objective way to identify when and where one model or the other might be more appropriate.

The dependence between mean and variance in the Local terms clearly led to median predicted values of total bycatch from model 04 for some years to be surprisingly large, and much greater than the predictions from model 02 for the same years. However, the broader confidence intervals around those anomalous predictions in models 02 and 04 already instruct us to put little credence in their central tendencies. Alternatively, if we accept the philosophy of model 03, the Local terms are disregarded in calculation of the cell medians, at the cost of much broader confidence intervals for all the estimates.

Given the intensity and breadth of coverage during the 1992-1997 Regional Research Program and the 1998 BRD evaluation project, I am reluctant to dismiss the perturbations from the main-effects-only predictions as consequences of non-random sampling. However, one can never be sure, and that is the real cost of living with non-random sampling. If you do trust the non-random sampling to be representative, at least most of the time, then the power of model 02 to use data where present, and default to an average variability where data are not present, is extremely attractive. I recommend model 02 over 03.

If you accept the general structure of model 02, then a choice between model 02 and model 04 remains to be made, and must also be largely subjective. Certainly there were clear indications in the posterior distributions that the parameters for r and precision of the Local effect are distinguishable among the subsets of the data investigated. However, lingering doubts about the non-random sampling leads me to think that the more subdivisions made, the more risk that at least some of the parameters will have important systematic error. For that reason, I recommend model 02 over model 04, but again there is no objective evidence strongly favoring that choice.

In principle, much of the detail of simulated posterior distributions for the bycatch totals could be carried forward into the stock assessment, but in practice it may be much simpler to parameterize the posterior distributions and ignore some detail. The skew evident even on the log scale may complicate the search for sufficient statistics. The highest values in some of the distributions, although supported by the model and data at low likelihood, seem biologically unlikely. We might therefore consider a simplification to a lognormal distribution. I calculated lognormal parameters based on the median, and an averaging of the 2.5 and 97.5 percentile statistics tabulated by BUGS. This procedure shifts the confidence intervals, but still retains the central tendency and general magnitude of the uncertainty of the direct simulation results. I would postpone the choice of whether to use this simplification until we see how difficult it would be to incorporate the original, skewed distribution into the stock assessment model.

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{BUGS stands for **B**ayesian inference **U**sing **G**ibbs **S**ampling, and there is now a fairly sizeable literature on its use. The Gilks *et al.* book containing the Spiegelhalter *et al.* citation has several other references to BUGS as well. The BUGS software is available at www.mrc-bsu.cam.ac.uk/bugs/ }

FIGURES AND TABLES

Table 1. Summary of the major families of suggestions by reviewers for alternative estimations that contributed to Figure 1. This table was originally a slide in a presentation to the Reeffish Stock Assessment Panel in 1997.

Theme Areas for Alternative Analyses

Reconsider Cells

Try Fish:Shrimp Ratios

Try 'By Trip' Analyses

Try Epoch Effects

Explore Interactions.

Figure 1. Distribution of estimates from the many alternative analyses suggested by reviewers. Values are derived from means over all years, expressed as a deviation from the standard GLM results on a log scale. Approximate factors on an arithmetic scale are given below the log axis. Over 70 alternatives were considered, but this is clearly not a random sample of 'all possible analyses.' There also was no feedback to the suggestors, i.e. no opportunity to see the results and modify or withdraw their advice. There has been some investigation of properties of some estimation approaches suggest here since. For example, Diamond has shown how fish:shrimp ratios can give very misleading results in some circumstances. Most of the highest estimates is this figure were based on fish:shrimp ratios.

Red Snapper

17
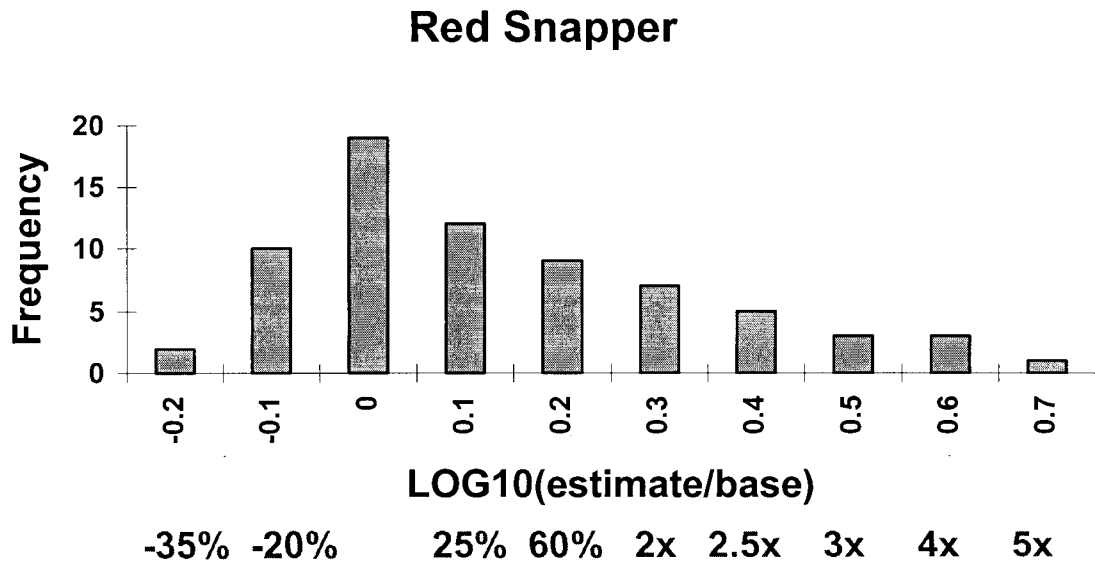
Table 2. Summary of past observer programs in the Gulf of Mexico Shrimp fishery.

Historical   1972-1982

     Bycatch Studies

     Turtle Capture Study

     Ted Evaluations

Regional Research Program   1992-1997   (TSA, GSAFDF, & NMFS)

     Characterization

     Evaluation

     Snapper / Shrimp only

BRD effectiveness evaluations   1998

     Evaluation

     Snapper / Shrimp only

Figure 2. Strata used in bycatch estimation. Georgraphically, strata are based on the shrimp statistical areas (pictured).
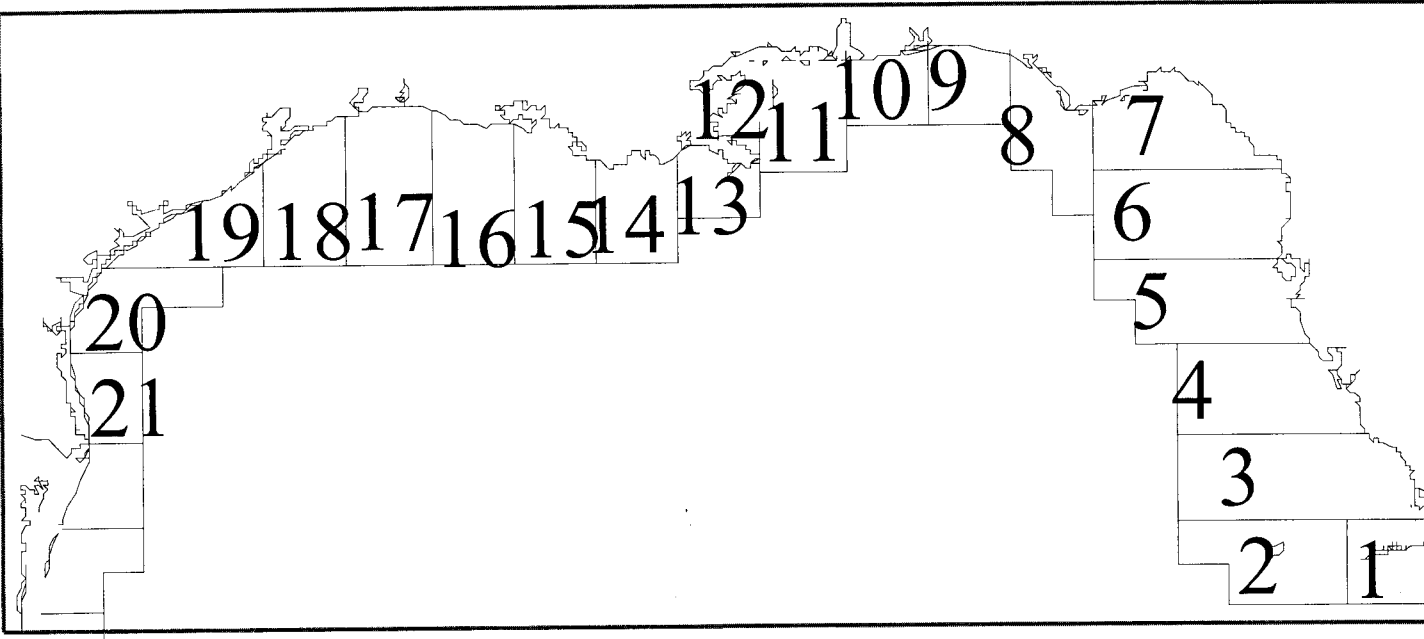
Seasonal

       Jan – Apr   May – Aug Sep – Dec

Area   (alongshore statistical areas)

        1 – 9   10 – 12   13 – 17   18 – 21

Depth

       Inside 10 fm   Outside 10 fm

Strata 'boundaries' are set by the combinations shown in the text under the diagrams, and also established by year and dataset (shrimp fishery or research trawl). Individual strata or 'cells' are established by the complete crossing of the five 'main effects:' year, season, area, depth, and dataset.

Table 3. BUGS code used for the priors in these analyses. This code shown is part of model 02 and 03 for red snapper. The first 3 parameters are: r – gamma parameter, tau – precision parameter for the Local variable, center – the fully random effect term used in model 03. For model 04 there are four separate parameters for r and tau, and the prior for tau was switched to uniform (0.03,3). For model 01, there is no tau parameter. The main effects parameters are: yx (year, indexed by i), sx (season, indexed by j), ax (alongshore area, indexd by k), zx (depth zone, indexed by l), and dx (data set, observer or research, indexed by m). Refer to Fig. 2 for the stratum (main effects) definitions. All main effects except year are centered. For king mackerel the prior mean of 1 for each year effects was replaced by –2.

```
r~dunif(0.03,5)
tau~dlnorm(0,3.5)
center~dnorm(0,tau)

for (i in 1:27) {
  yx[i]~dnorm(1,0.7)
  }
for (j in 1:3) {
  sraw[j]~dnorm(0,1)
  sx[j]<-sraw[j]-mean(sraw[])
  }
for (k in 1:4) {
  araw[k]~dnorm(0,0.2)
  ax[k]<-araw[k]-mean(araw[])
  }
for (l in 1:2) {
  zraw[l]~dnorm(0,0.2)
  zx[l]<-zraw[l]-mean(zraw[])
  }
for (m in 1:2) {
  draw[m]~dnorm(0,1)
  dx[m]<-draw[m]-mean(draw[])
  }
```

Table 4. Ranges allowed by the priors coded in Table 3. For one, two, and three standard deviations on the log scale, the corresponding range on an arithmetic scale (max: min) is tabled as a factor. For example, from the prior on depthzone (zx in Table 3), two standard deviations corresponds to one depth zone having over 7000 times the abundance (CPUE) of the other. The ranges out three standard deviations seem far larger than ranges that could be reasonably expected. There are around 30,000 data points available, so the posterior distributions are dominated by the data, not the priors.

| | Range implied by +/- N std dev's: | | |
	1 std dev	2 std dev	3 std dev
Year	11x	119x	1302x
Season	7x	55x	403x
Area	88x	7664x	670922x
Depth	88x	7664x	670922x
Dataset	7x	55x	403x

Figure 3. Box plots of annual bycatch estimates by model 01 for red snapper, on arithmetic (a) and log (b) scales. Vertical axes are millions of fish, or the log thereof.

3a. Red snapper on an arithmetic scale, model 01
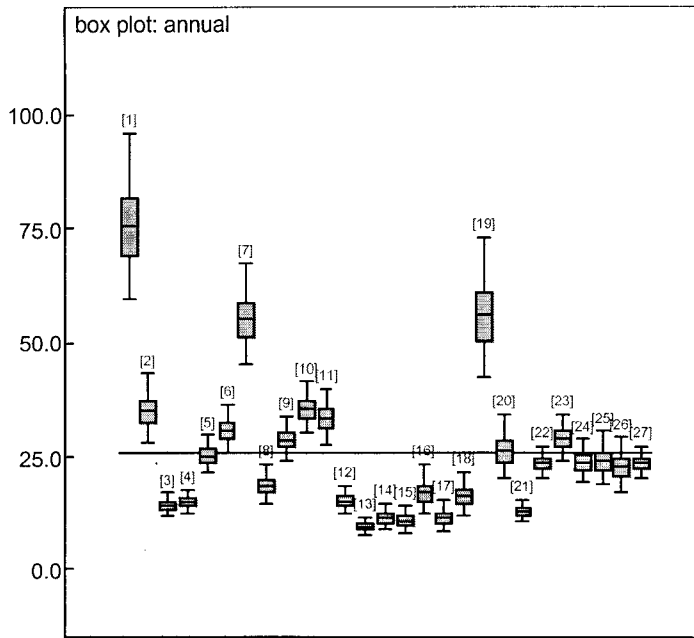
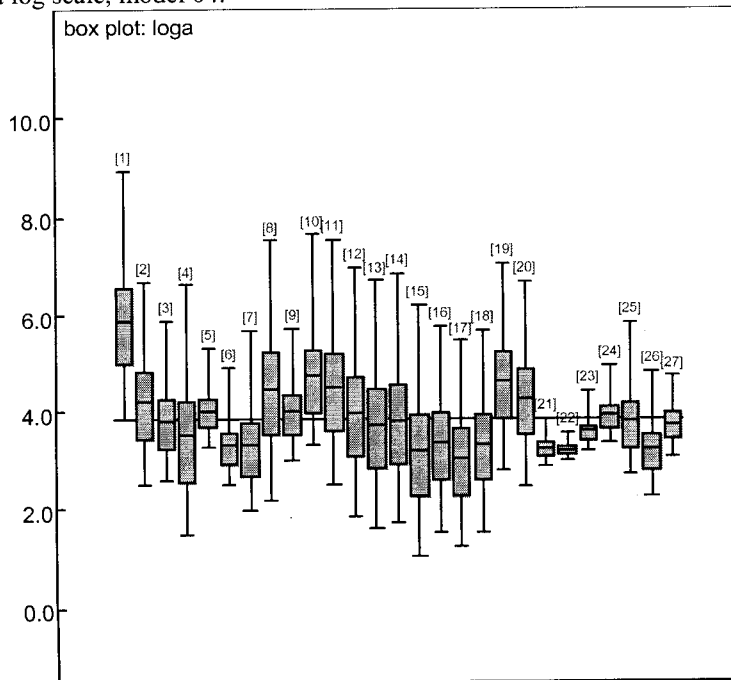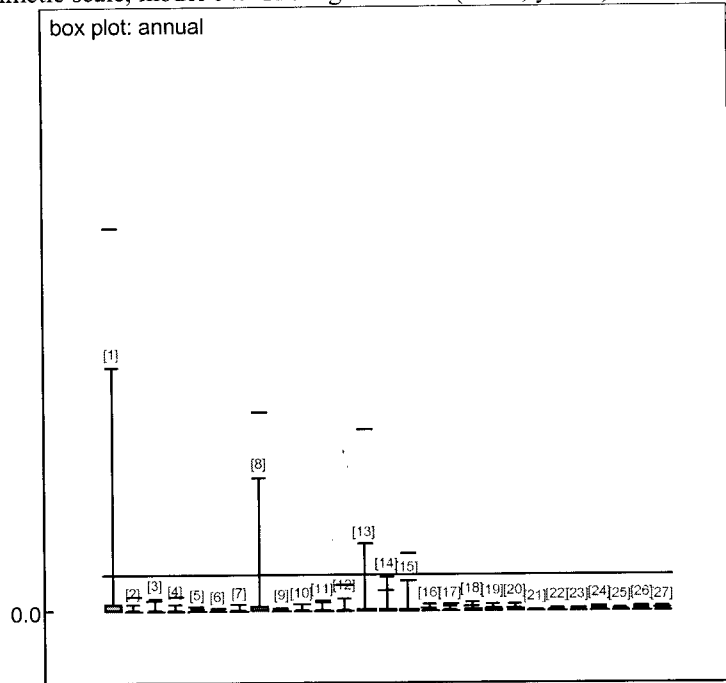**3b.** Red snapper on a log scale, model 01
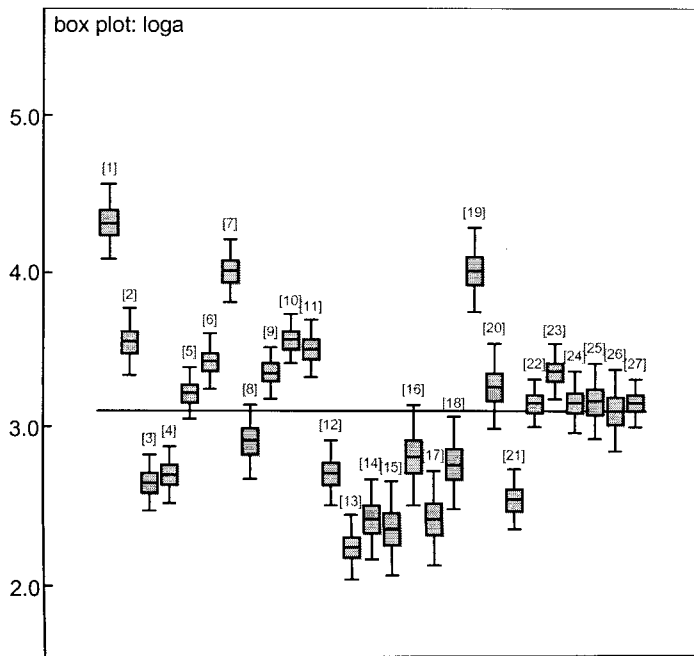
Figure 4. Box plots of annual bycatch estimates by model 01 for king mackerel, on arithmetic (a) and log (b) scales. Vertical axes are millions of fish, or the log of thereof.

4a. King mackerel on an arithmetic scale, model 01
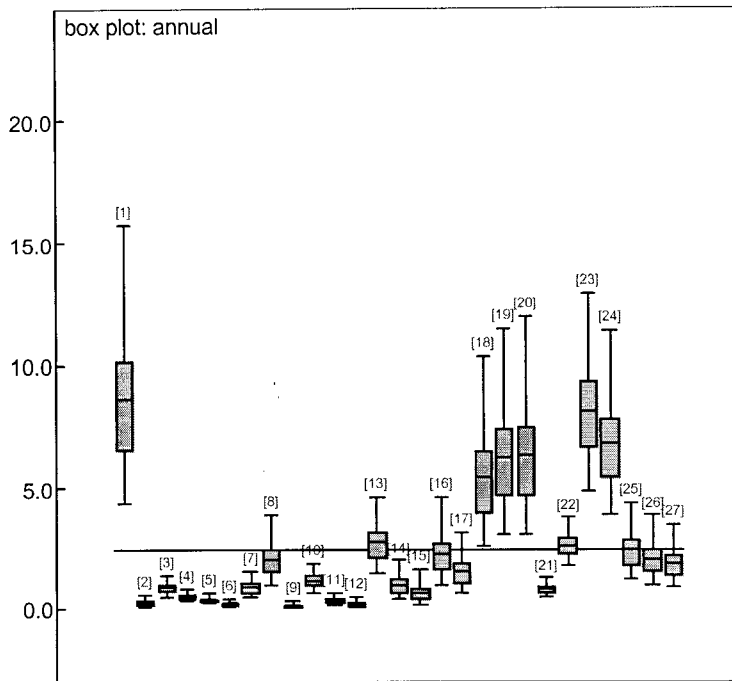
4b. King mackerel on a log scale, model 01
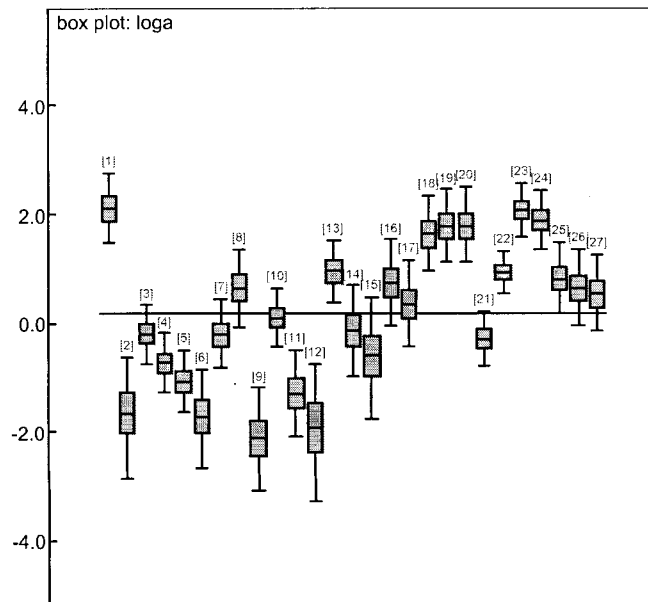
Figure 5. Examples of marginal posteriors for total annual bycatch for red snapper estimated via model 01. (a) on an arithemetic scale, and (b) on a log scale. The two years shown are 1973 and 1993, which were among the most skewed and least skewed, respectively, on the arithmetic scale.

5a. Red snapper, arithmetic scale, model 01. Marginal posterior distributions for 1973 and 1993.
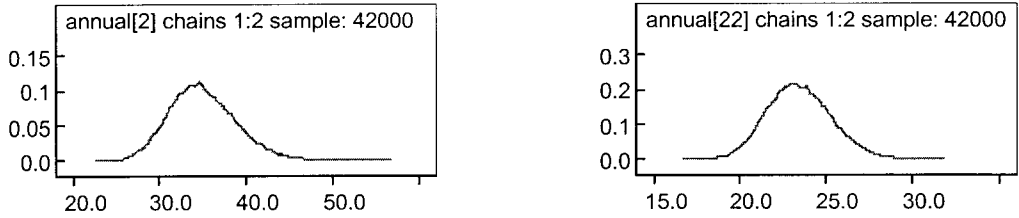
5b. Red snapper, log scale, model 01. Marginal posterior distributions for 1973 and 1993.
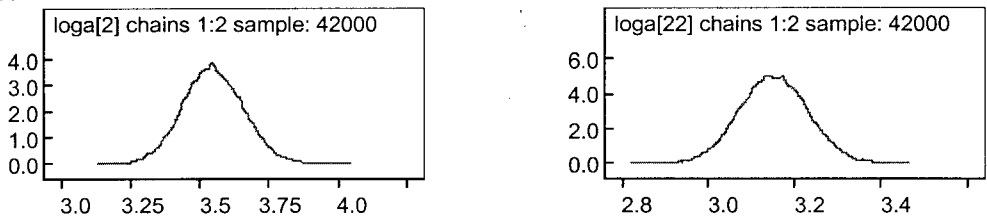
Figure 6. Examples of marginal posteriors for total annual bycatch for king mackerel estimated via model 01. (a) on an arithmetic scale, and (b) on a log scale. The two years shown are 1983 and 1993, which were among the most skewed and least skewed, respectively, on the arithmetic scale.

6a. King mackerel, arithmetic scale, model 01. Marginal posterior distributions for 1983 and 1993.
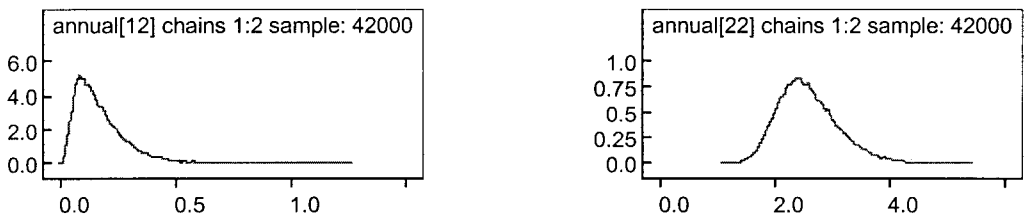
6b. King mackerel, log scale, model 01. Marginal posterior distributions for 1983 and 1993.
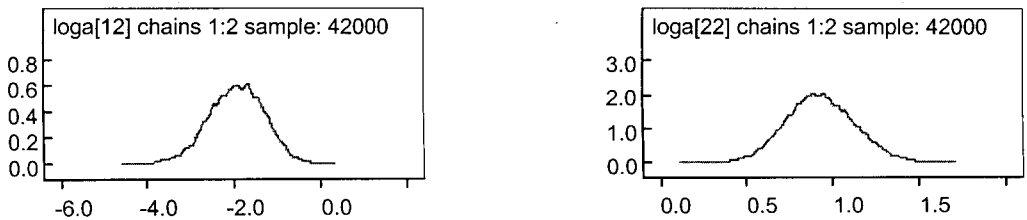
Figure 7. Posterior marginals for the gamma parameter r. (a) red snapper. (b) king mackerel.

7a. Red snapper, model 01.
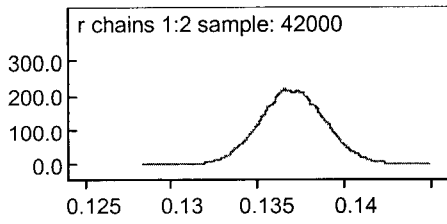
7b. King mackerel, model 01.
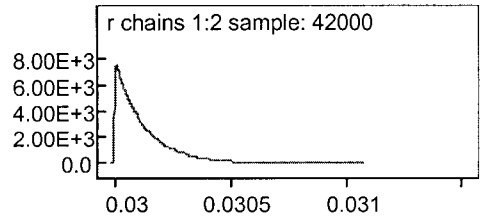
Figure 8. Box plots of annual bycatch estimates by model 02 for red snapper, on arithmetic (a) and log (b) scales. Vertical axes are millions of fish, or the log thereof.

8a. Red snapper on an arithmetic scale, model 02
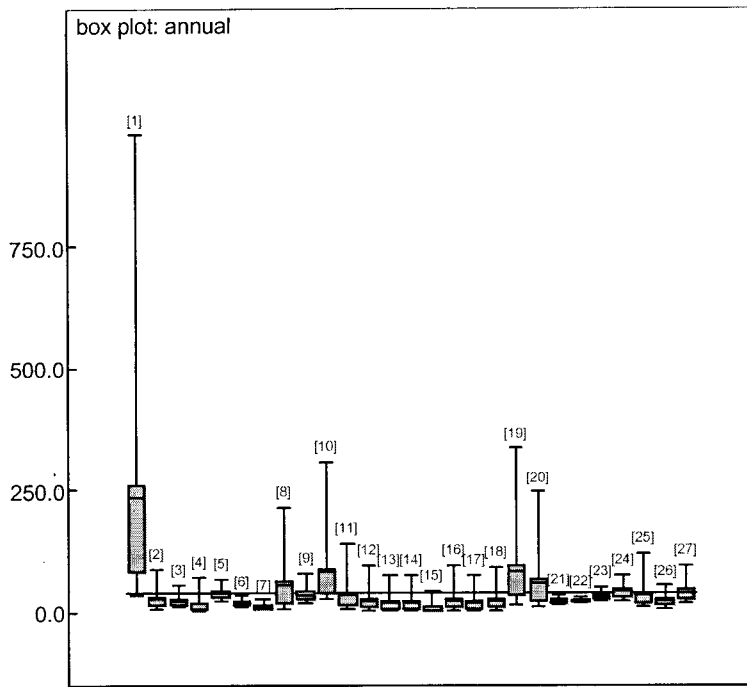
8b. Red snapper on a log scale, model 02
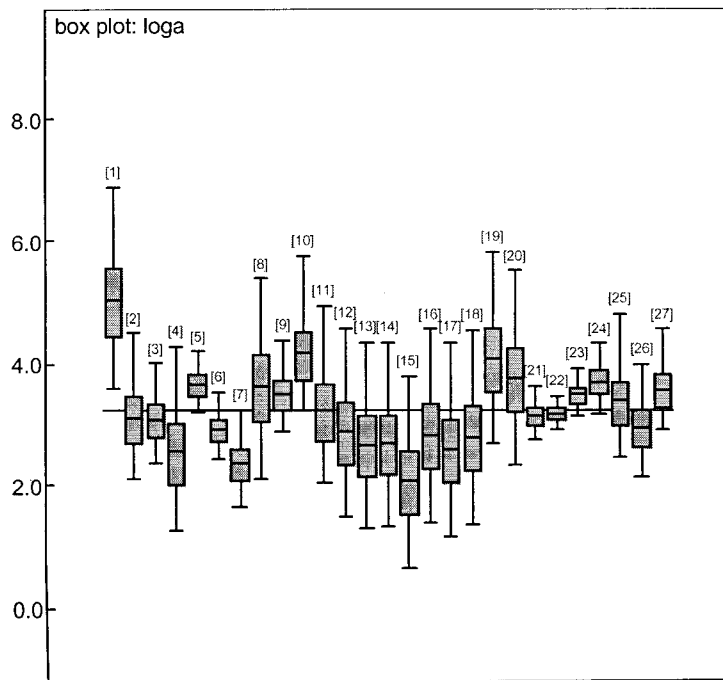
Figure 9. Box plots of annual bycatch estimates by model 02 for king mackerel, on arithmetic (a) and log (b) scales. Vertical axes are millions of fish, or the log thereof.

9a. King mackerel on an arithmetic scale, model 02

box plot: annual

9b. King mackerel on a log scale, model 02.

box plot: loga
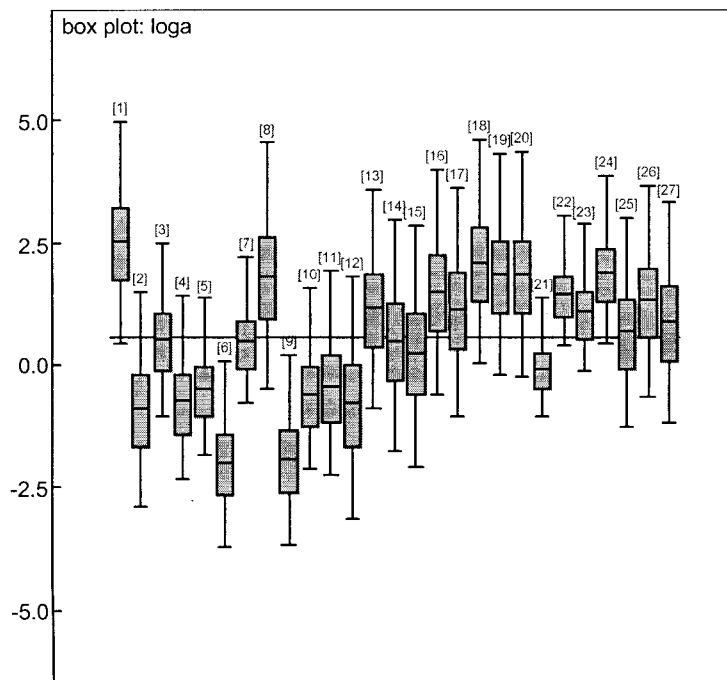
Figure 10. Examples of marginal posteriors for total annual bycatch for red snapper estimated via model 02. (a) on an arithmetic scale, and (b) on a log scale. The two years shown are 1975 and 1993, which were among the most skewed and least skewed, respectively, on the arithmetic scale.

10a. Red snapper, arithmetic scale, model 02. Marginal posterior distributions for 1975 and 1993.
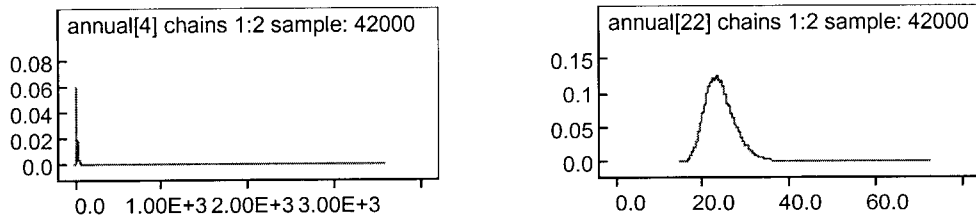
10b. Red snapper, log scale, model 02. Marginal posterior distributions for 1975 and 1993.
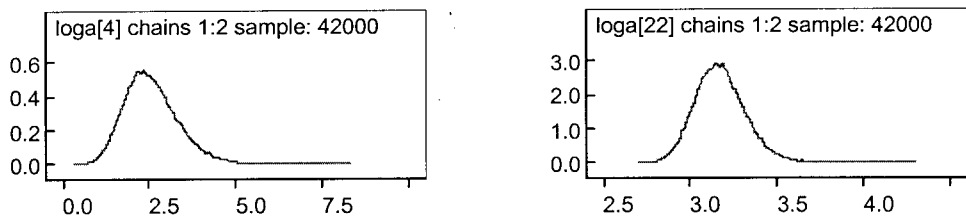
Figure 11. Examples of marginal posteriors for total annual bycatch for king mackerel estimated via model 02. (a) on an arithmetic scale, and (b) on a log scale. The two years shown are 1979 and 1992, which were among the most skewed and least skewed, respectively, on the arithmetic scale.

11a. King mackerel, arithmetic scale, model 02. Marginal posterior distributions for 1979 and 1992.
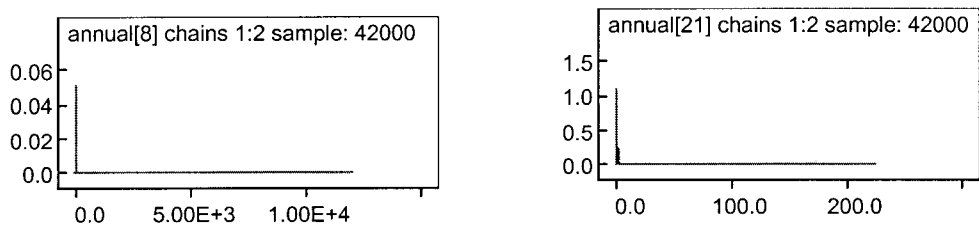
11b. King mackerel, log scale, model 02. Marginal posterior distributions for 1979 and 1992.
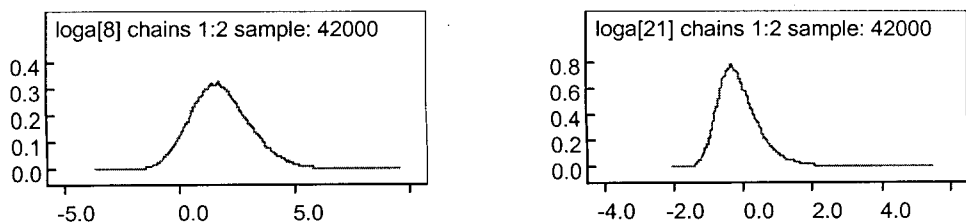
Figure 12. Posterior marginals for the gamma parameter r. (a) red snapper. (b) king mackerel.

12a. Red snapper, model 02.
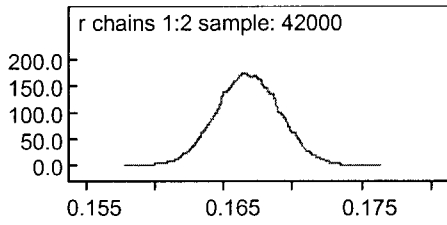
12b. King mackerel, model 02.
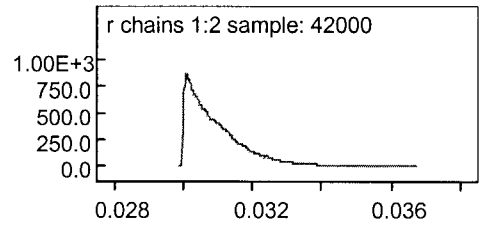
Figure 13. Posterior marginals for the precision parameter for the Local terms. (a) red snapper. (b) king mackerel.

13a. Red snapper, model 02
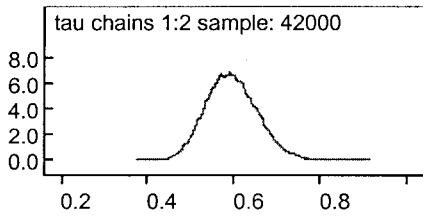
13b. King mackerel, model 02
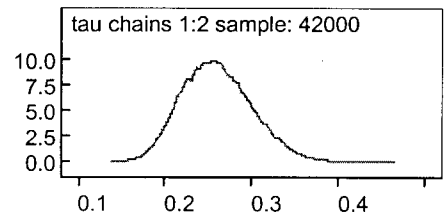
Figure 14. Box plots of annual bycatch estimates by model 03 for red snapper, on arithmetic (a) and log (b) scales. Vertical axes are millions of fish, or the log thereof.

14a. Red snapper on an arithmetic scale, model 03

box plot: annupred
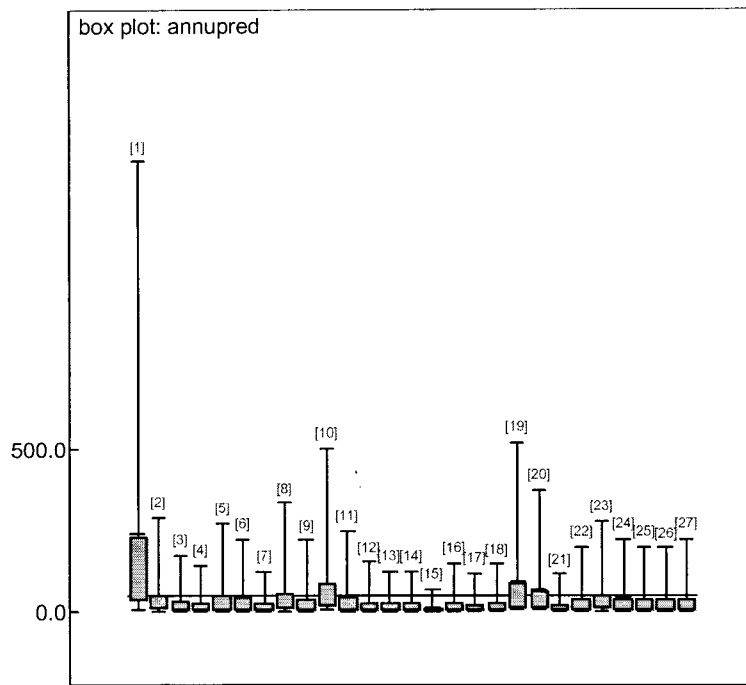
14b. Red snapper on a log scale, model 03

box plot: logp
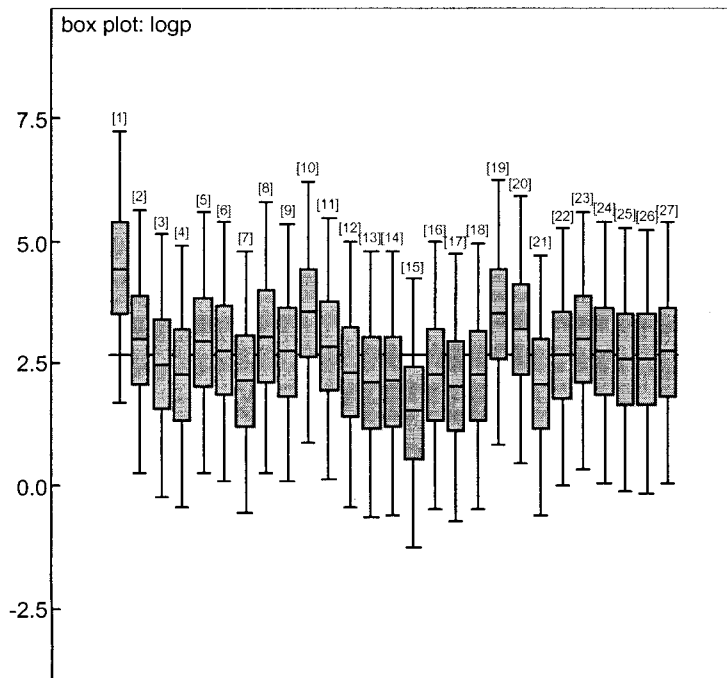
Figure 15. Box plots of annual bycatch estimates by model 03 for king mackerel, on arithmetic (a) and log (b) scales. Vertical axes are millions of fish, or the log thereof.

15a. King mackerel on an arithmetic scale, model 03
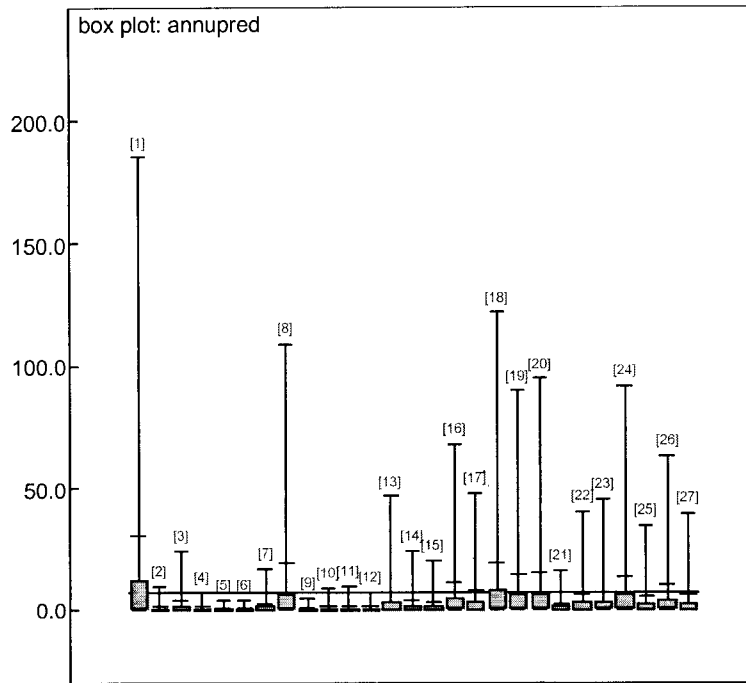
15b. King mackerel on a log scale, model 03.
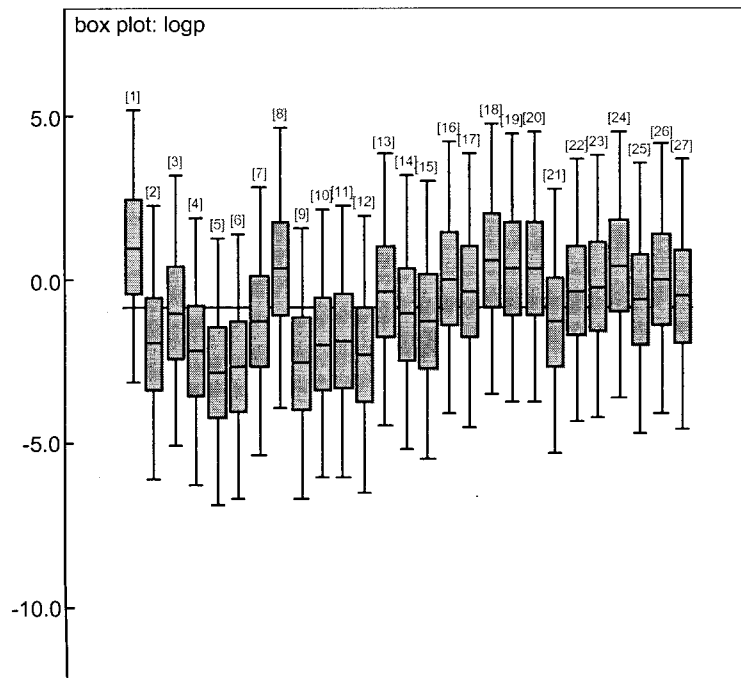
Figure 16. Examples of marginal posteriors for total annual bycatch for red snapper estimated via model 03. (a) on an arithmetic scale, and (b) on a log scale. The two years shown are 1972 and 1992.

16a. Red snapper, arithmetic scale, model 03. Marginal posterior distributions for 1972 and 1992.
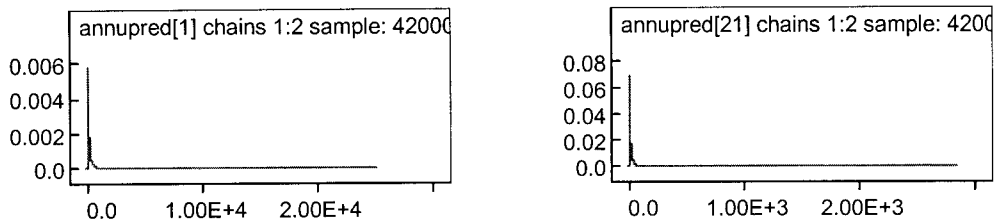
16b. Red snapper, log scale, model 03. Marginal posterior distributions for 1972 and 1992.
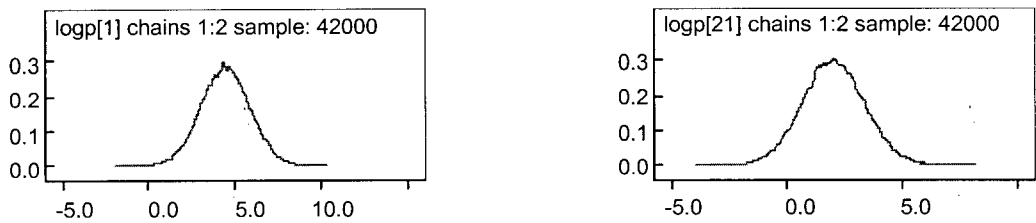
Figure 17. Examples of marginal posteriors for total annual bycatch for king mackerel estimated via model 03. (a) on an arithmetic scale, and (b) on a log scale. The two years shown are 1979 and 1993.

16a. King mackerel, arithmetic scale, model 03. Marginal posterior distributions for 1979 and 1993.
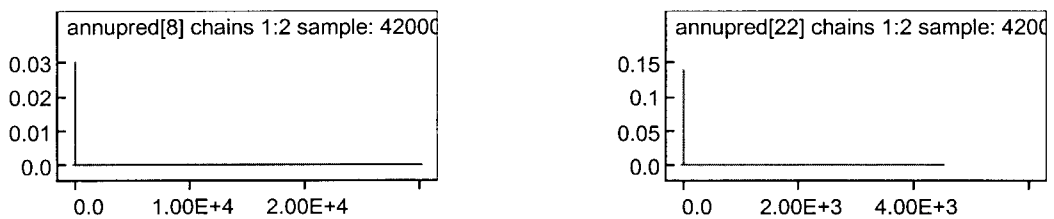
17b. King mackerel, log scale, model 03. Marginal posterior distributions for 1979 and 1993.
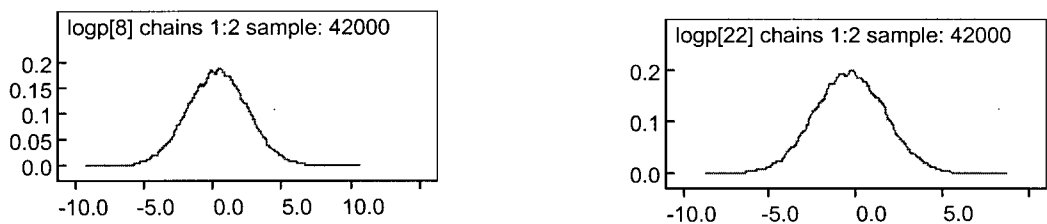
Figure 18. Box plots of annual bycatch estimates by model 04 for red snapper, on arithmetic (a) and log (b) scales. Vertical axes are millions of fish, or the log thereof.

18a. Red snapper on an arithmetic scale, model 04. The value of the highest mark (1st year) is 7403.
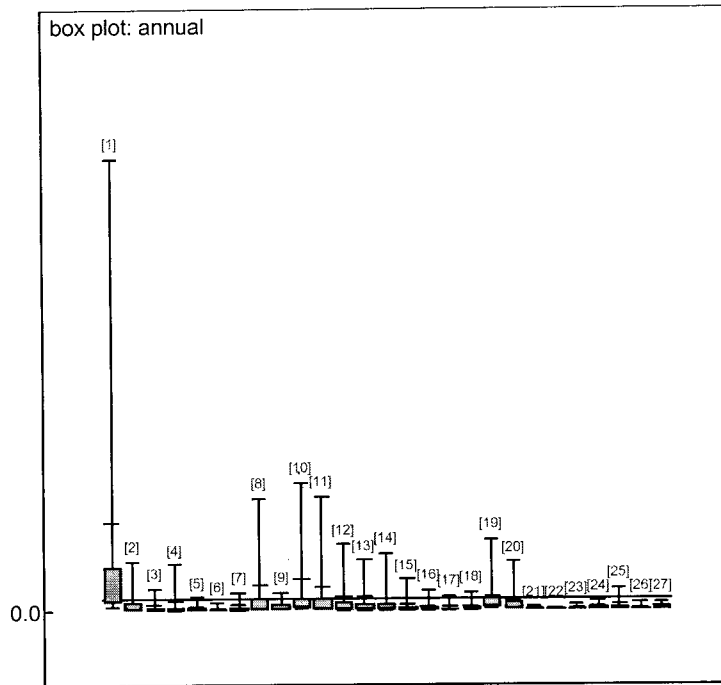
18b. Red snapper on a log scale, model 04.

Figure 19. Box plots of annual bycatch estimates by model 04 for king mackerel, on arithmetic (a) and log (b) scales. Vertical axes are millions of fish, or the log thereof.

19a. King mackerel on an arithmetic scale, model 04. The highest mark (mean, year 1) is 15630.

19b. King mackerel on a log scale, model 04.
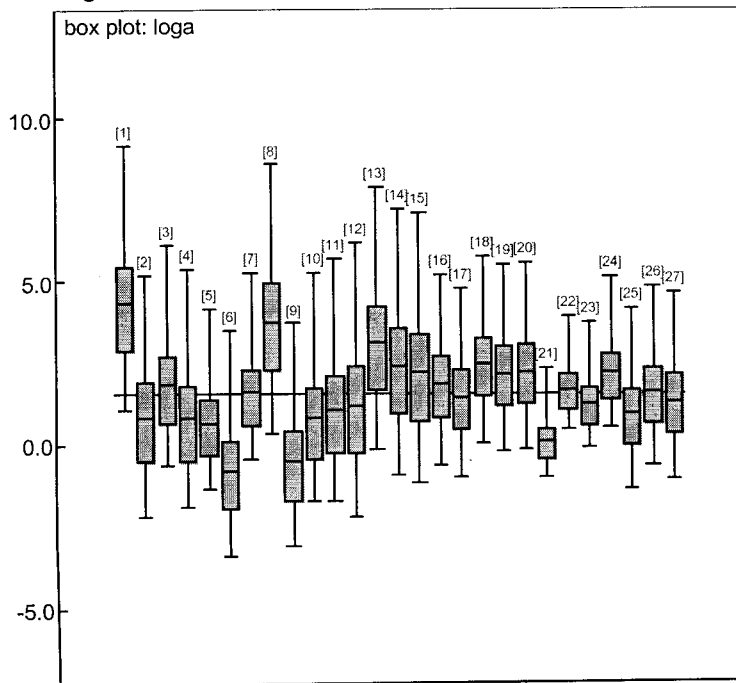
Figure 20. Examples of marginal posteriors for total annual bycatch for red snapper estimated via model 04, plotted on a log scale. The two years shown are 1984 and 1993
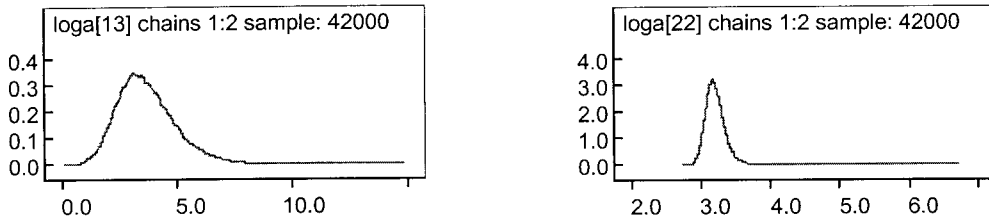
Figure 21. Examples of marginal posteriors for total annual bycatch for king mackerel estimated via model 04, plotted on a log scale. The two years shown are 1984 and 1993.
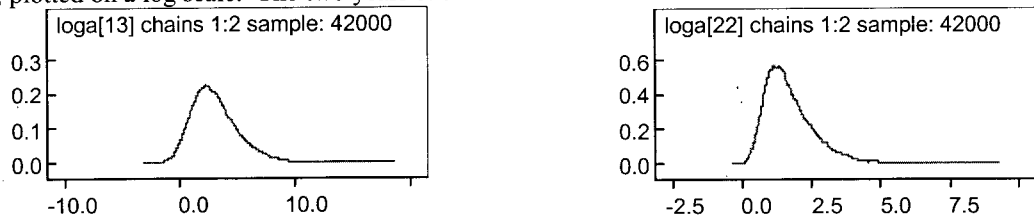
Figure 22. Marginal posterior distribution for the four gamma r parameters for red snapper under model 04. [1,1] is for 1972-1986 observer data. [1,2] is for 1972-1986 research vessel data. [2,1] is for 1987-1998 observer data. [2,2] is 1987-1998 research vessel data.
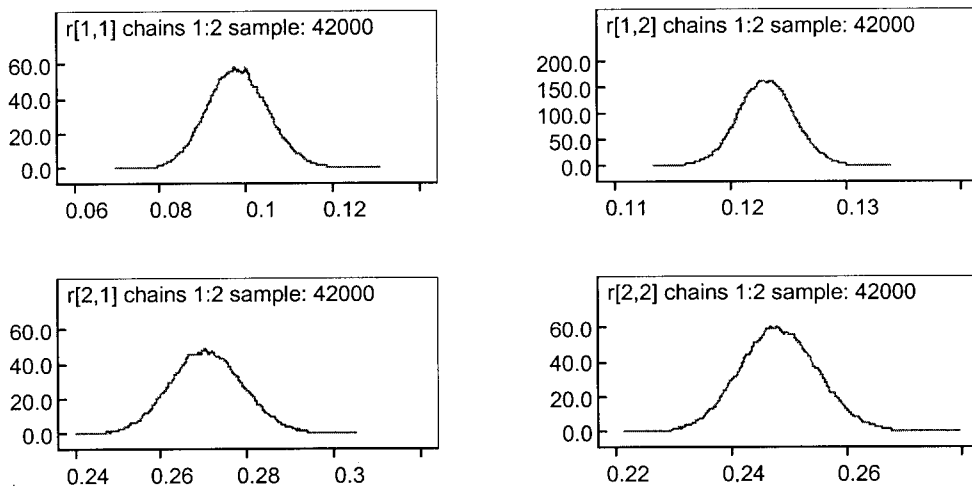
Figure 23. Marginal posterior distribution for the four gamma r parameters for king mackerel under model 04. [1,1] is for 1972-1986 observer data. [1,2] is for 1972-1986 research vessel data. [2,1] is for 1987-1998 observer data. [2,2] is 1987-1998 research vessel data
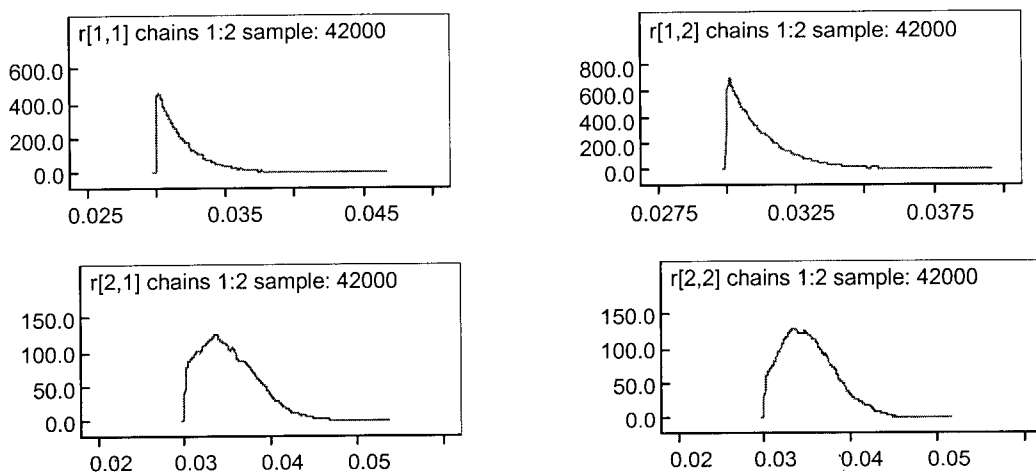
Figure 24. Marginal posterior distribution for the four Local precision parameters for red snapper under model 04. [1,1] is for 1972-1986 observer data. [1,2] is for 1972-1986 research vessel data. [2,1] is for 1987-1998 observer data. [2,2] is 1987-1998 research vessel data.
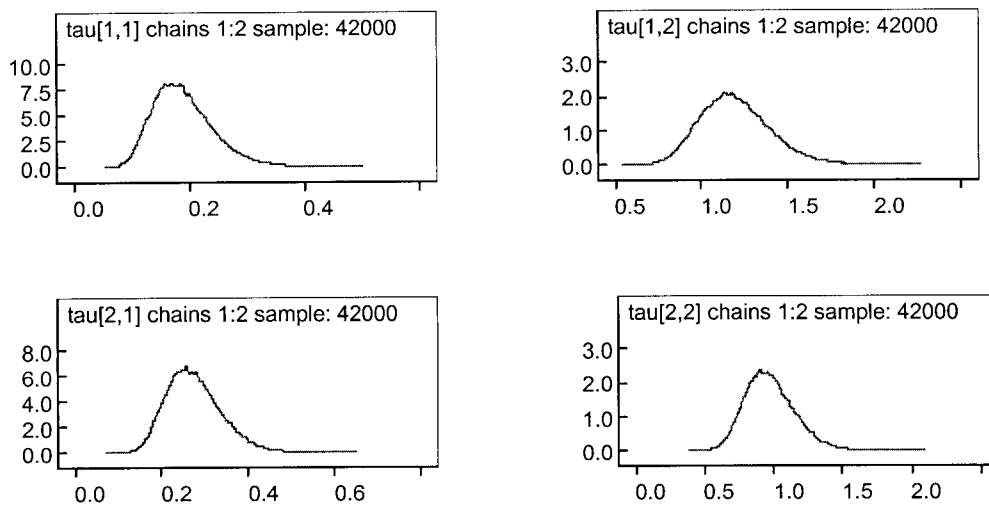
Figure 25. Marginal posterior distribution for the four Local precision parameters for king mackerel under model 04. [1,1] is for 1972-1986 observer data. [1,2] is for 1972-1986 research vessel data. [2,1] is for 1987-1998 observer data. [2,2] is 1987-1998 research vessel data.
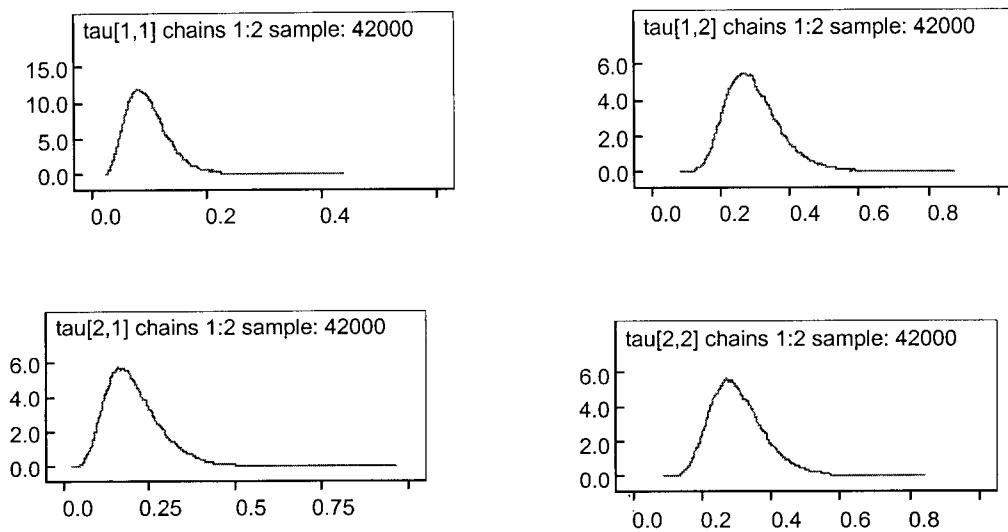
Figure 26. Graph of medians of log CPUE predictions for all cells from model 04 plotted against same values for model 02. (a) Red snapper. (b) King mackerel. Graphs for both species appear to bracket a 1:1 relationship fairly closely.

26a.

RED SNAPPER

26b.
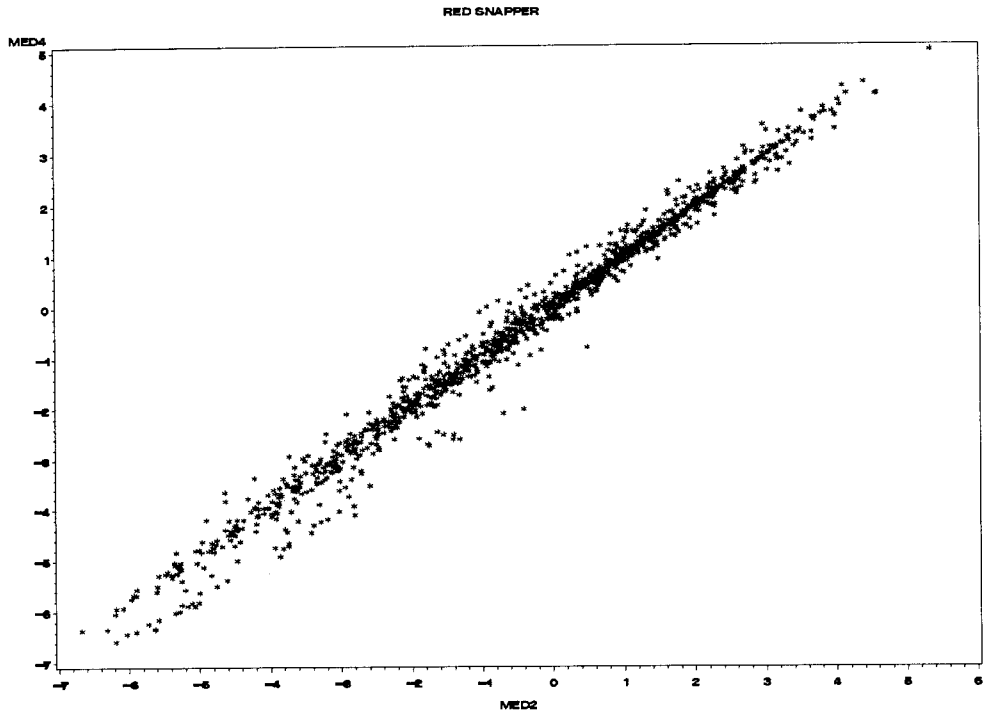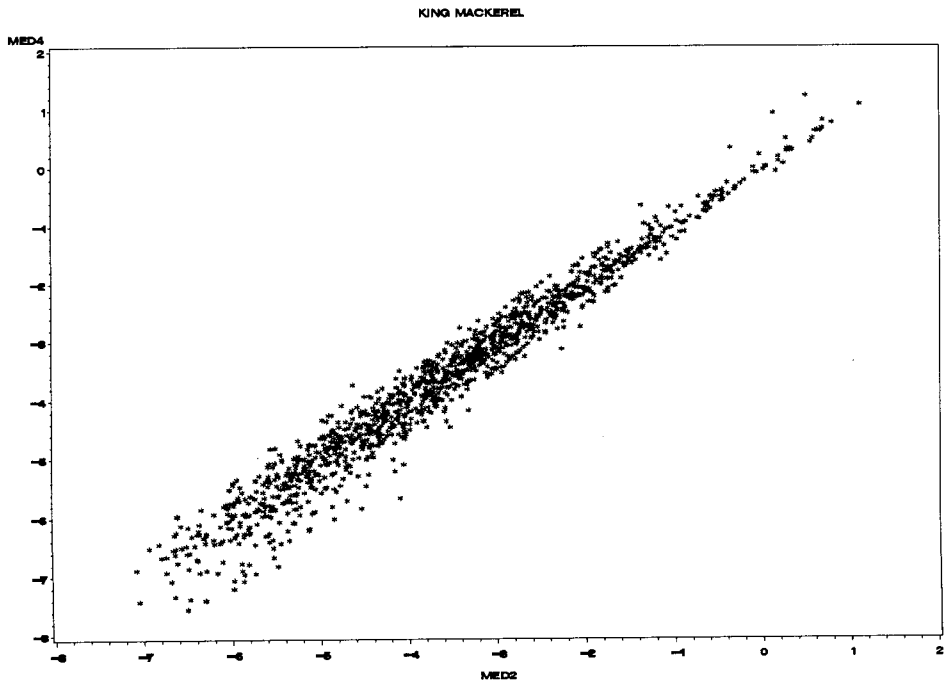
KING MACKEREL

Figure 27. Graphs of medians of annual totals from model 04 plotted against medians of annual totals for model 02. Log scale. (a) Red snapper. (b) King mackerel. All points for both species are above the 1:1 relationship.

27a.
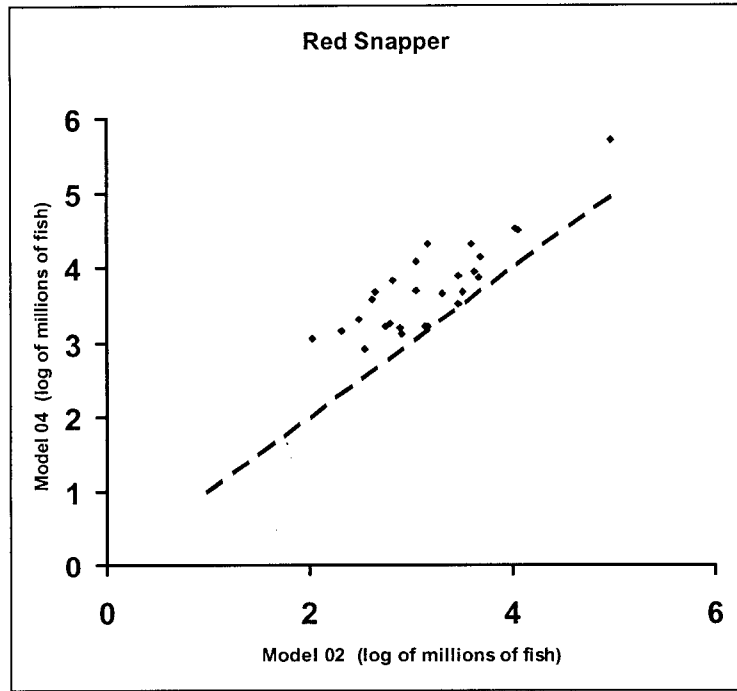
27b.
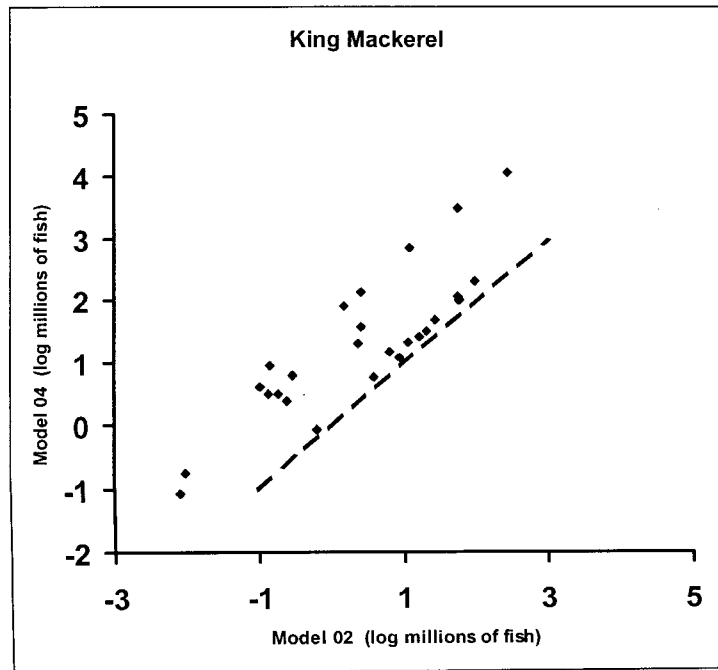
Figure 28. Graph of medians of annual totals from model 02 with the uniform hyperprior plotted against medians of annual totals for model 02 with the lognormal hyperprior. Red snapper, log scale. The dotted line is 1:1.
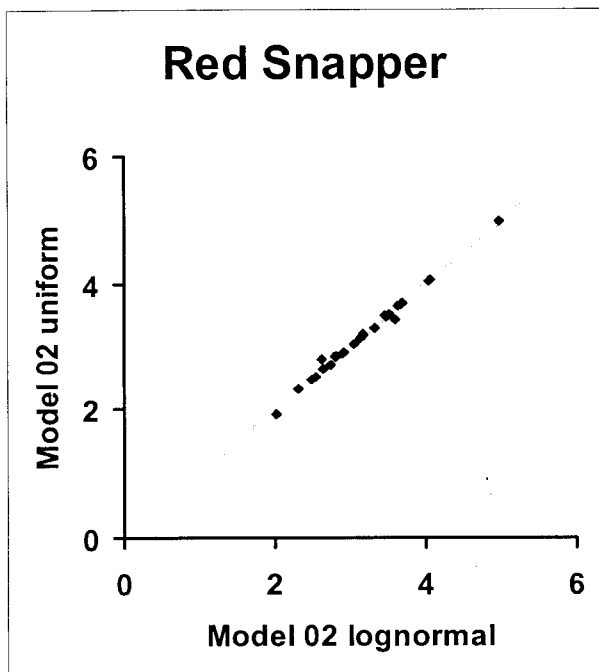
Figure 29. Graph of medians of annual totals from model 03 with the uniform hyperprior plotted against medians of annual totals for model 03 with the lognormal hyperprior. Red snapper, log scale. The dotted line is 1:1.
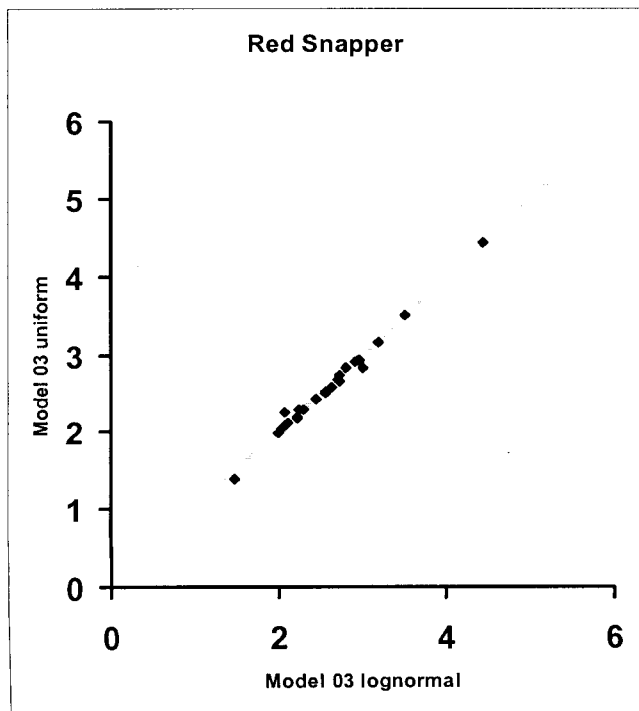
Figure 30. Graph of medians of annual totals from model 04 with the lognormal hyperprior plotted against medians of annual totals for model 04 with the uniform hyperprior. Red snapper, log scale. The dotted line is 1:1.

Red Snapper
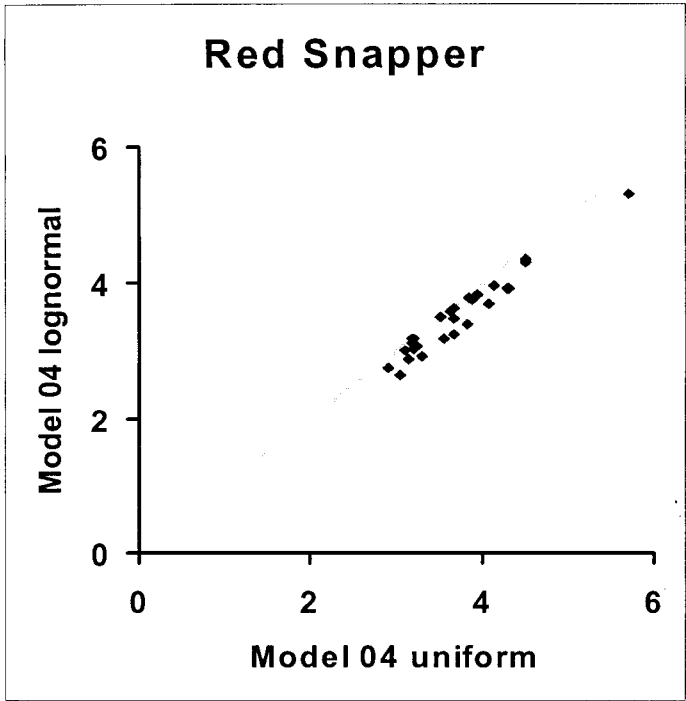
Figure 31. Graph of medians of annual totals from model 02 with the uniform hyperprior plotted against medians of annual totals for model 02 with the lognormal hyperprior. King mackerel, log scale. The dotted line is 1:1.
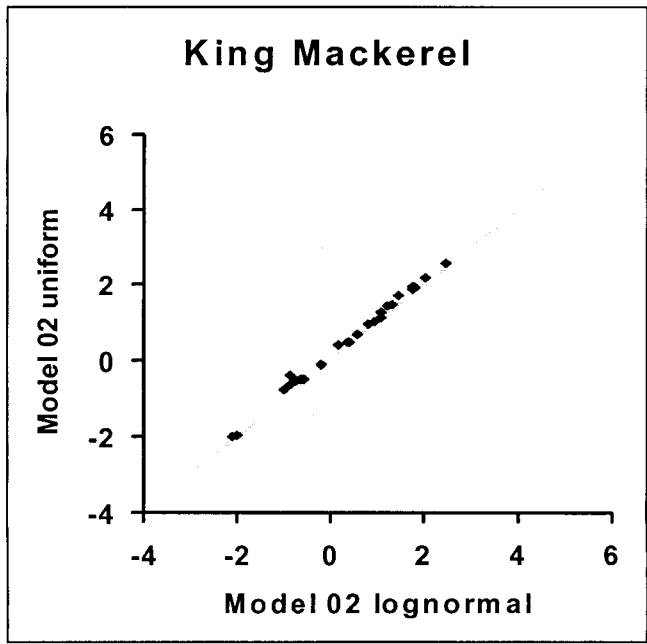
King Mackerel

Figure 32. Graph of medians of annual totals from model 03 with the uniform hyperprior plotted against medians of annual totals for model 03 with the lognormal hyperprior. King mackerel, log scale. The dotted line is 1:1.
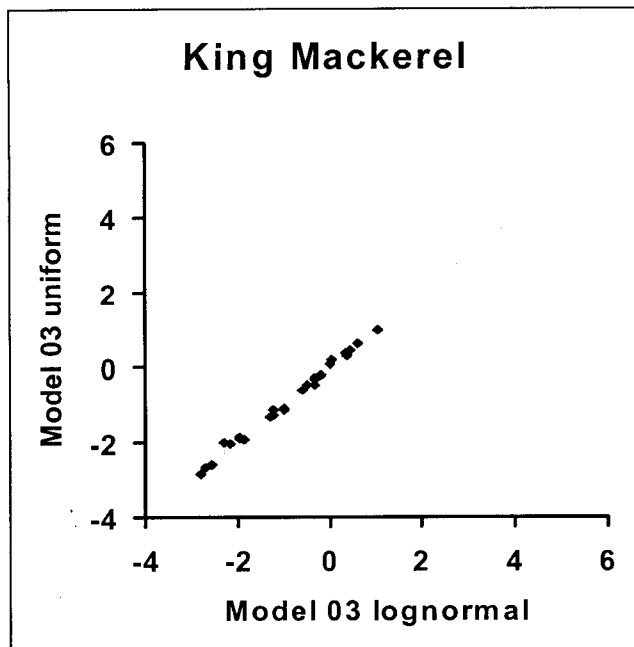
Figure 33. Graph of medians of annual totals from model 04 with the lognormal hyperprior plotted against medians of annual totals for model 04 with the uniform hyperprior. King mackerel, log scale. The dotted line is 1:1.
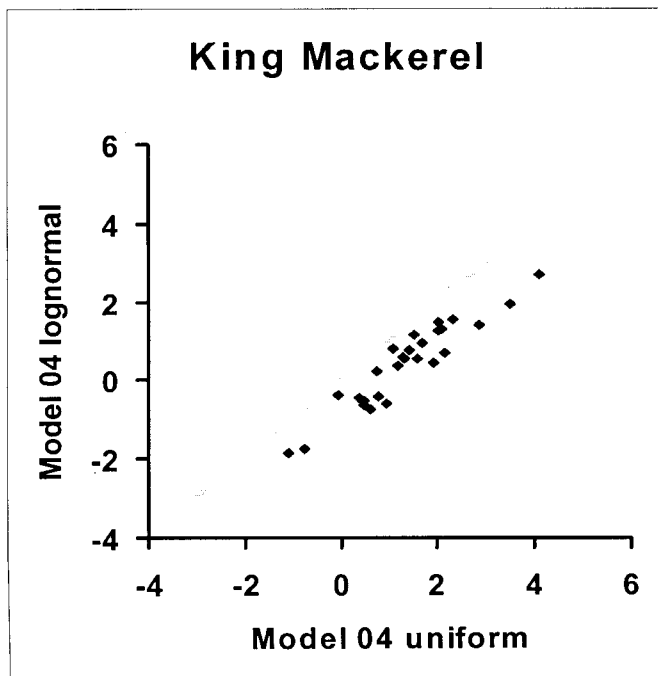
Figure 34. Medians of predicted values for log(CPUE) vs observed log (mean CPUE) in cells with observed means > 0. Red snapper results for model 01.

RS01ALOG
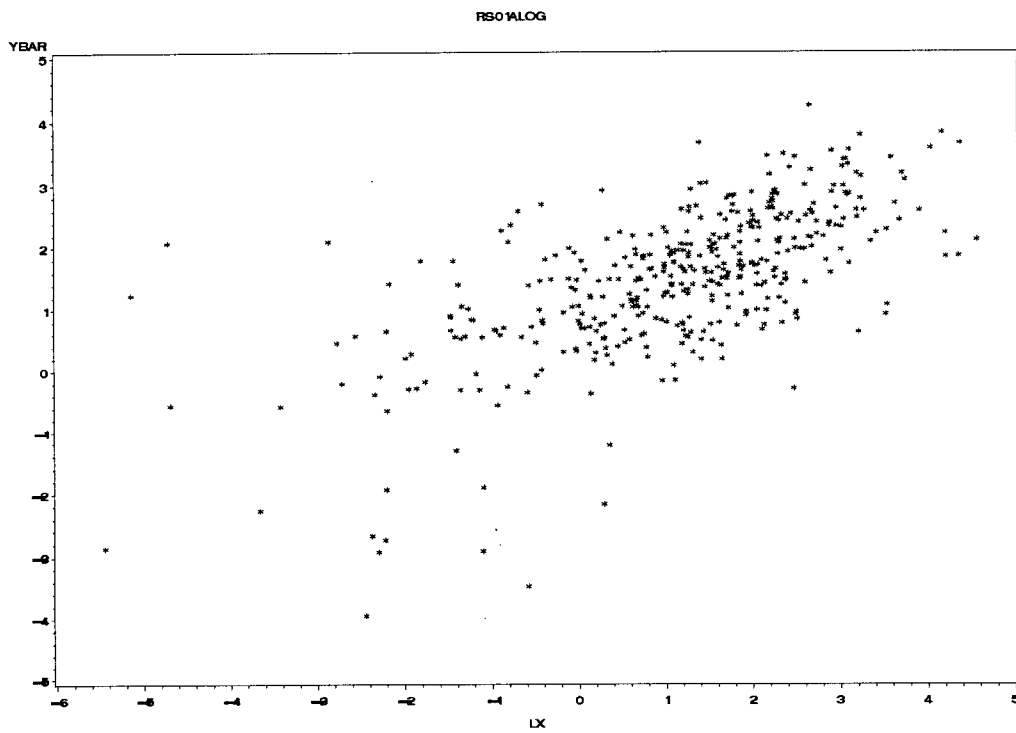
Figure 35. Medians of predicted values for CPUE vs observed mean CPUE for cells having data. Red snapper results for model 01.
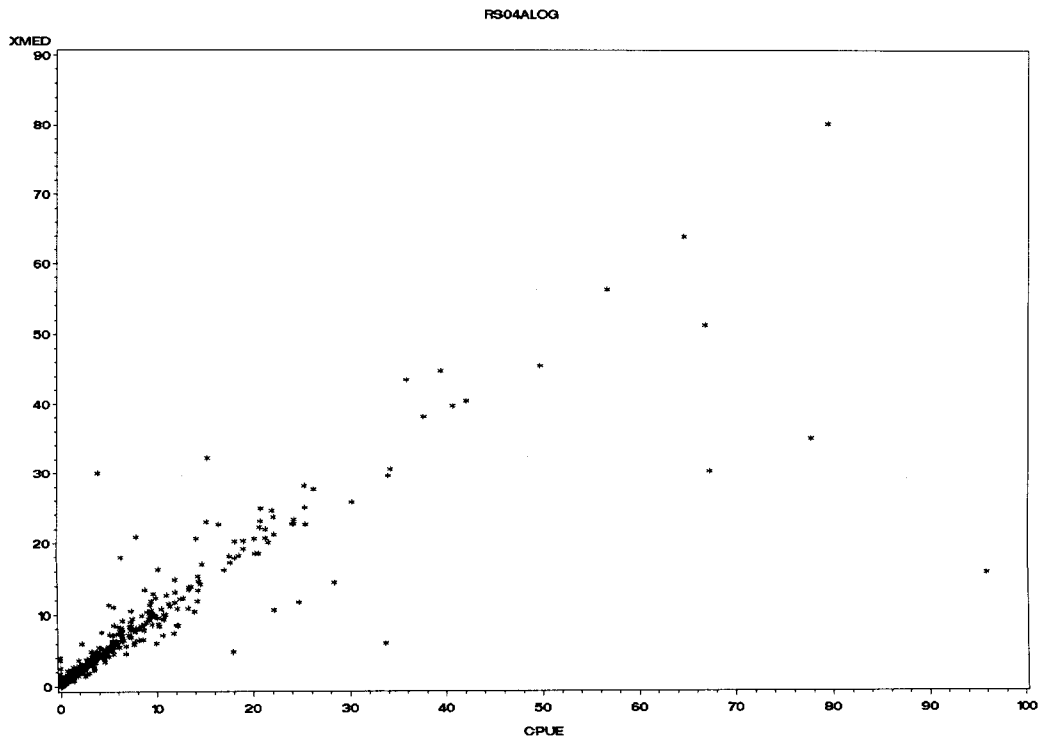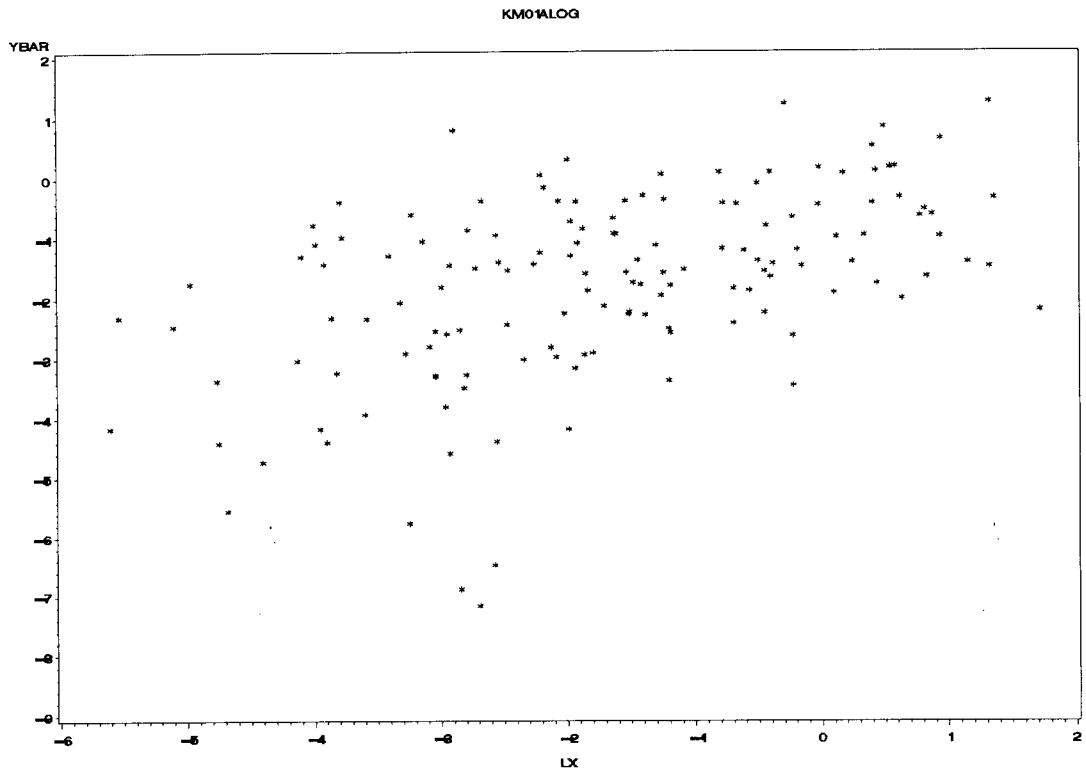

RS01ALOG

43
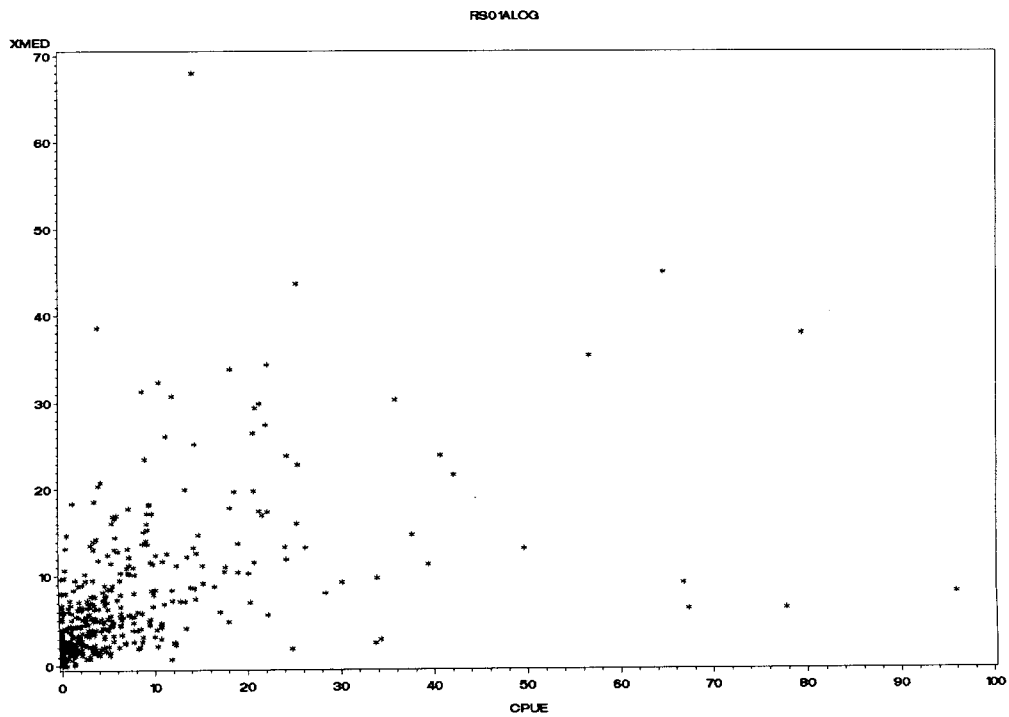
Figure 36. Medians of predicted values for log(CPUE) vs observed log (mean CPUE) in cells with observed means > 0. Red snapper results for model 02.
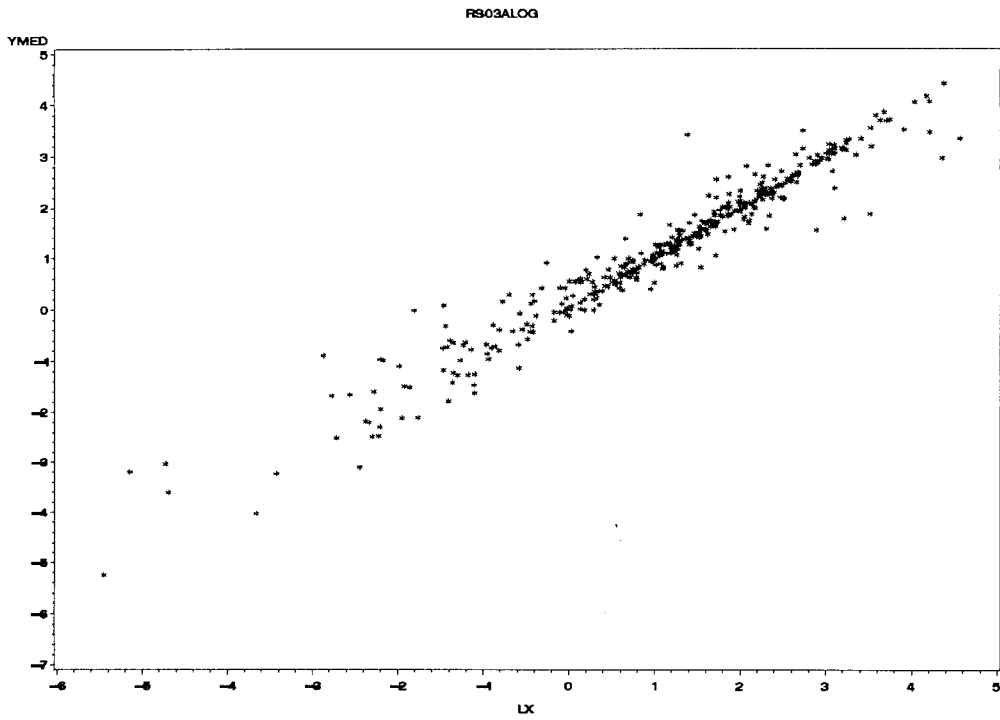
Figure 37. Medians of predicted values for CPUE vs observed mean CPUE for cells having data. Red snapper results for model 02.
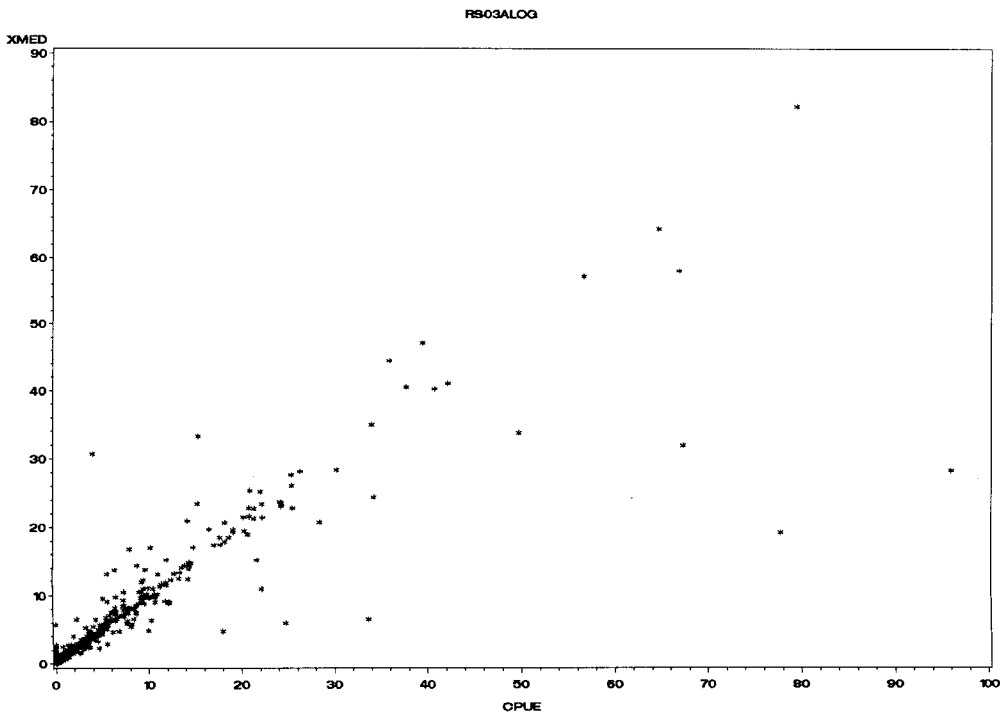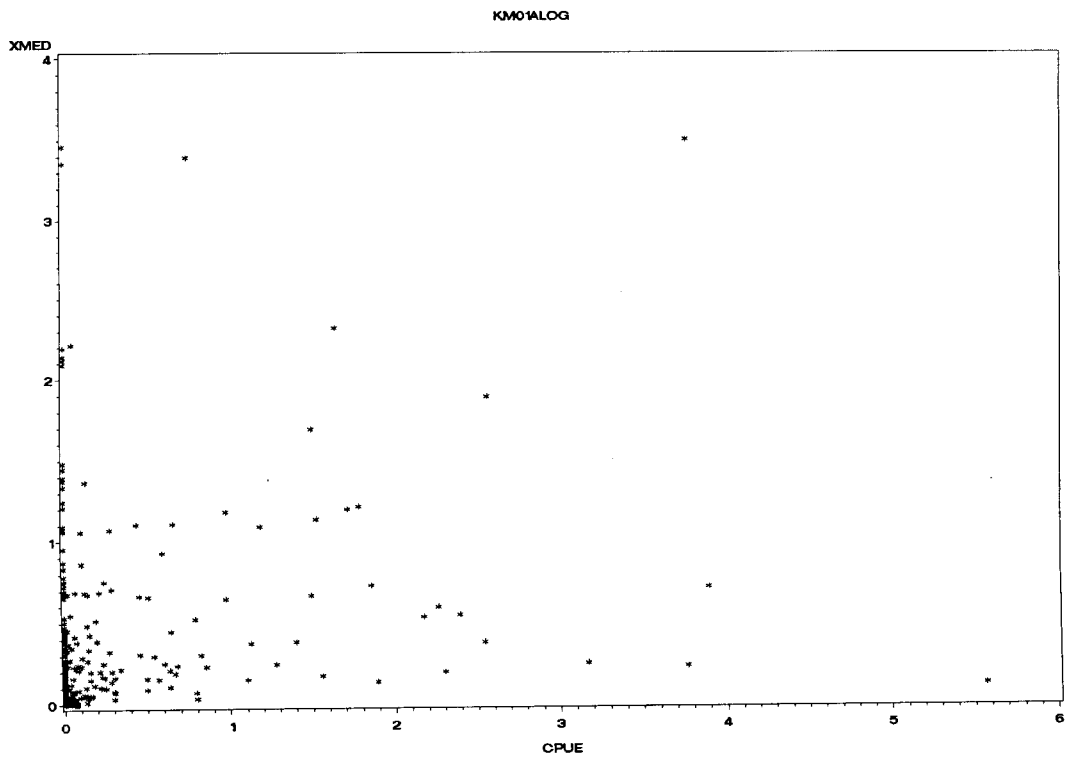
Figure 38. Medians of predicted values for log(CPUE) vs observed log (mean CPUE) in cells with observed means > 0. Red snapper results for model 03.

RS03APLG
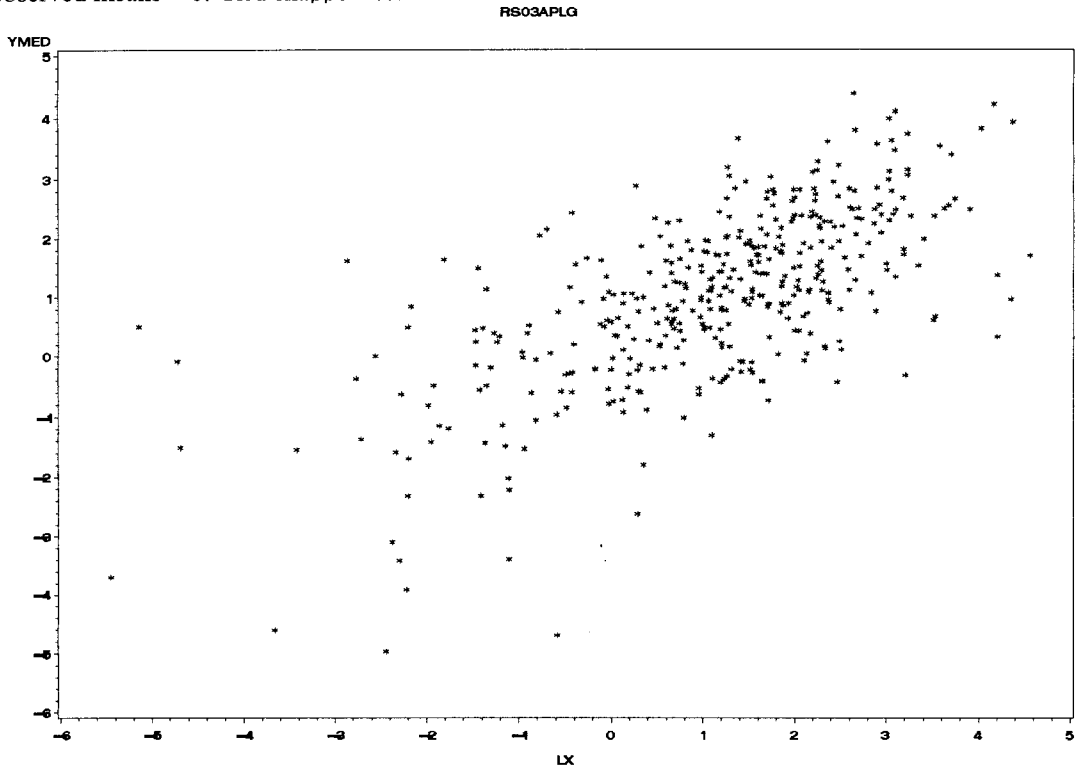
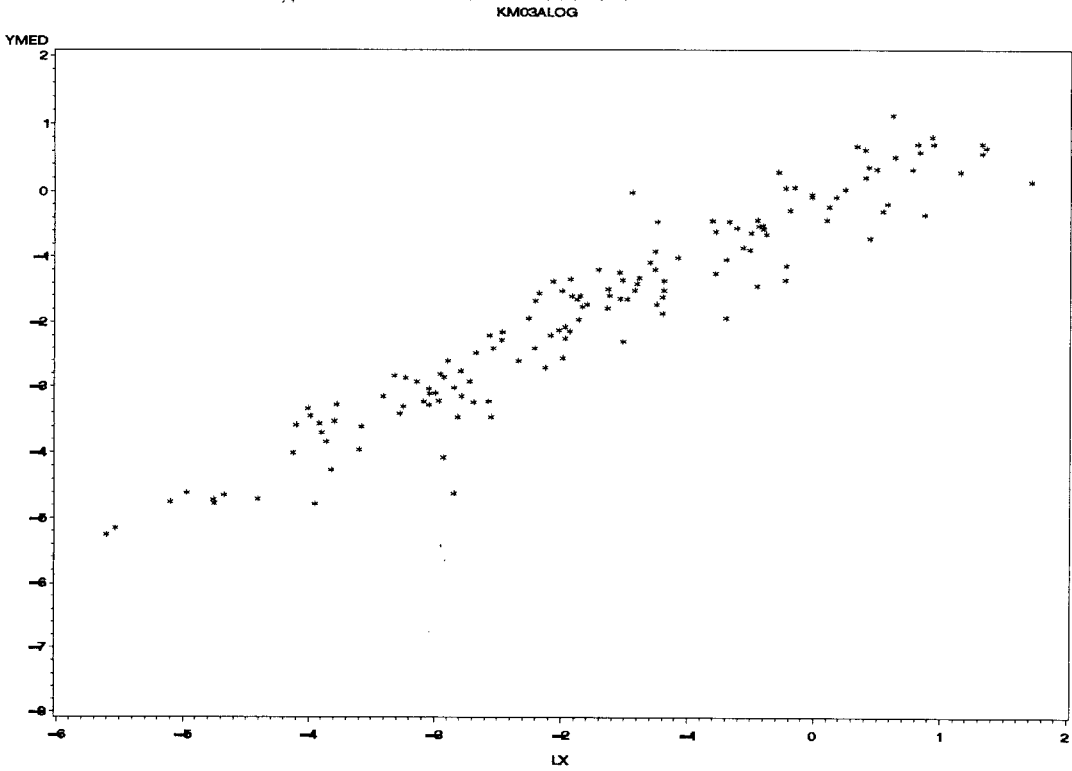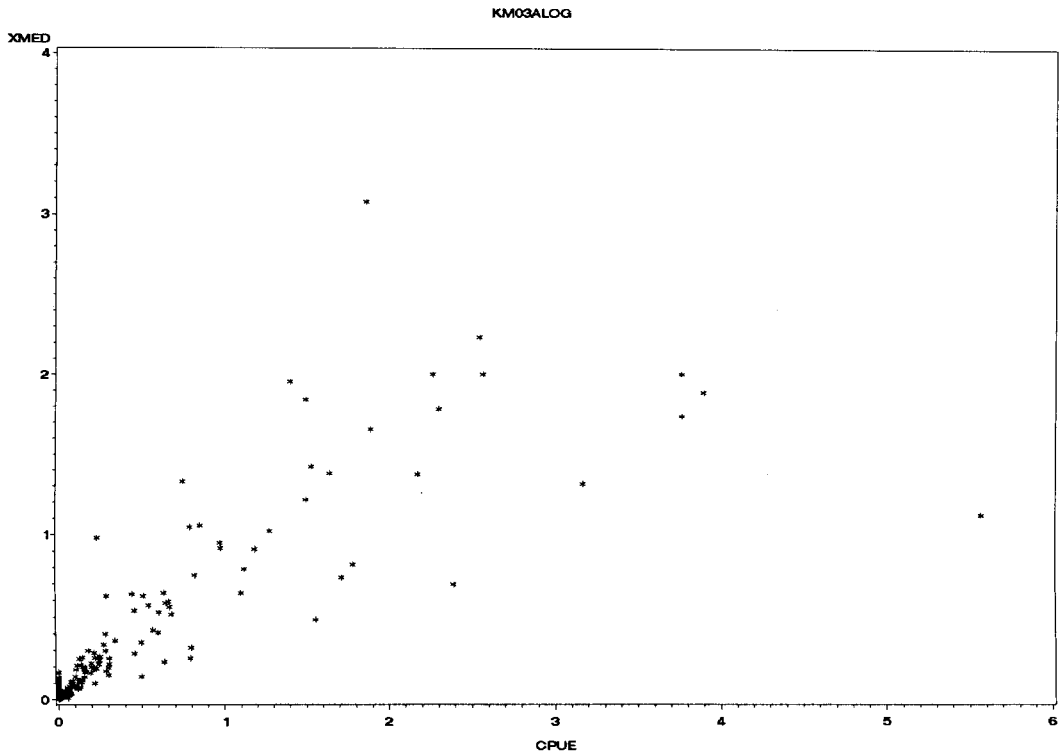**Figure 39.** Medians of predicted values for CPUE vs observed mean CPUE for cells having data. Red snapper results for model 03.

RS03APLG
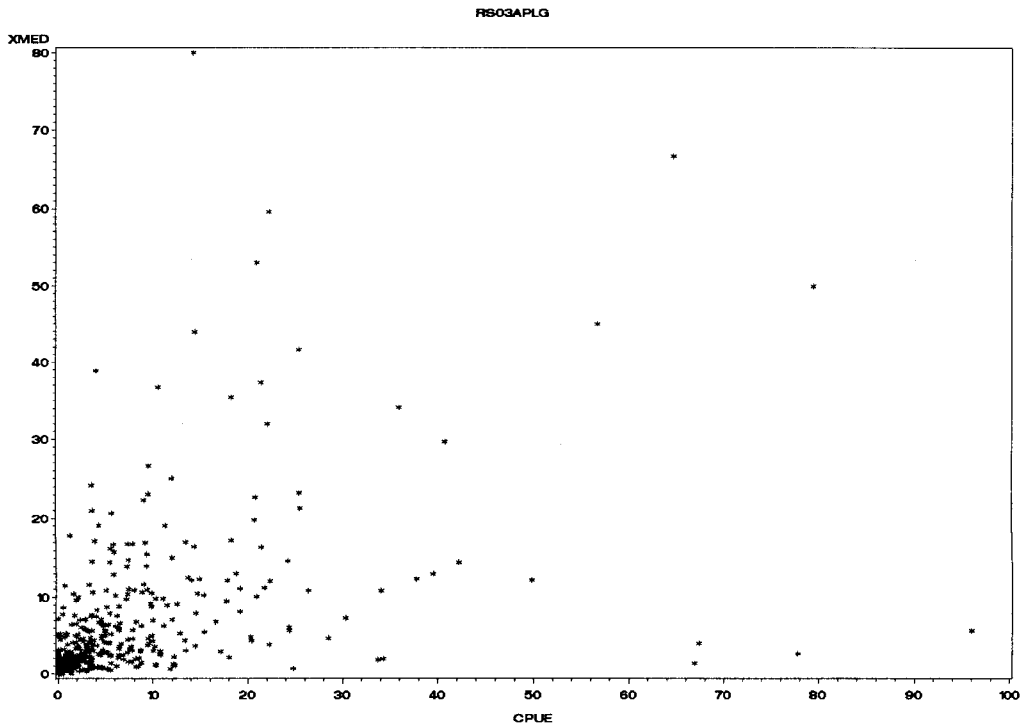
Figure 40. Medians of predicted values for log(CPUE) vs observed log (mean CPUE) in cells with observed means > 0. Red snapper results for model 04

RS04ALOG
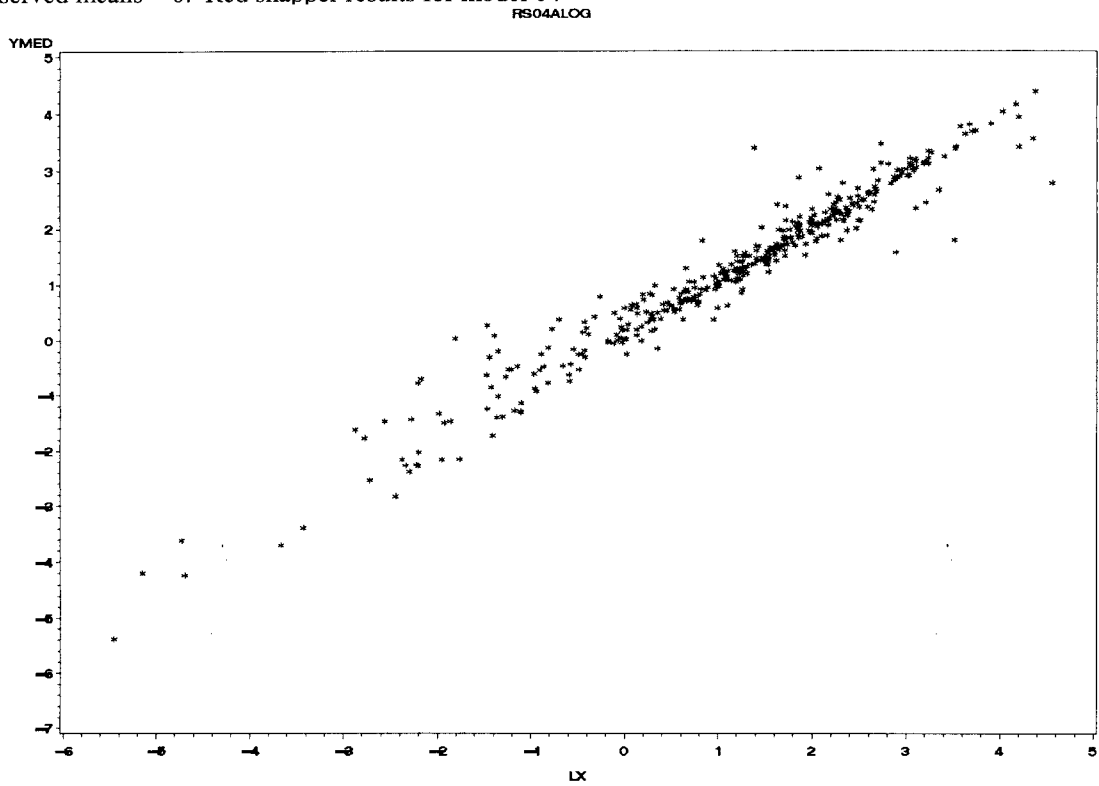
Figure 41. Medians of predicted values for CPUE vs observed mean CPUE for cells having data. Red snapper results for model 04.

RS04ALOG

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Figure 42. Medians of predicted values for log(CPUE) vs observed log (mean CPUE) in cells with observed means > 0. King mackerel results for model 01.
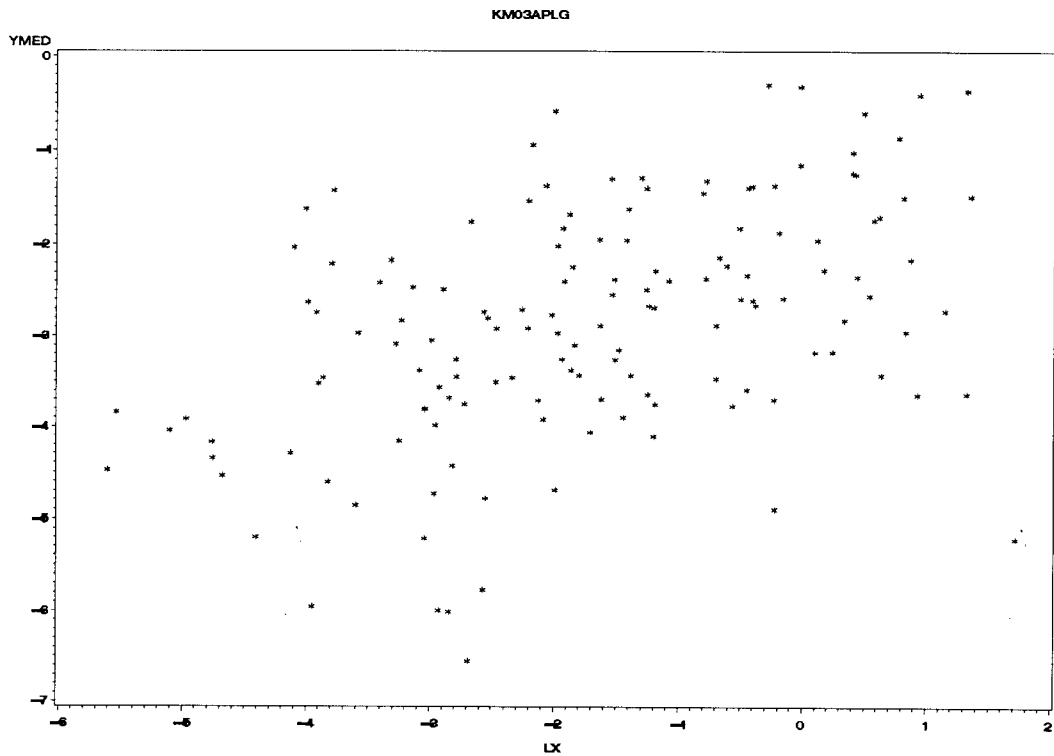

Figure 43. Medians of predicted values for CPUE vs observed mean CPUE for cells having data. King mackerel results for model 01.
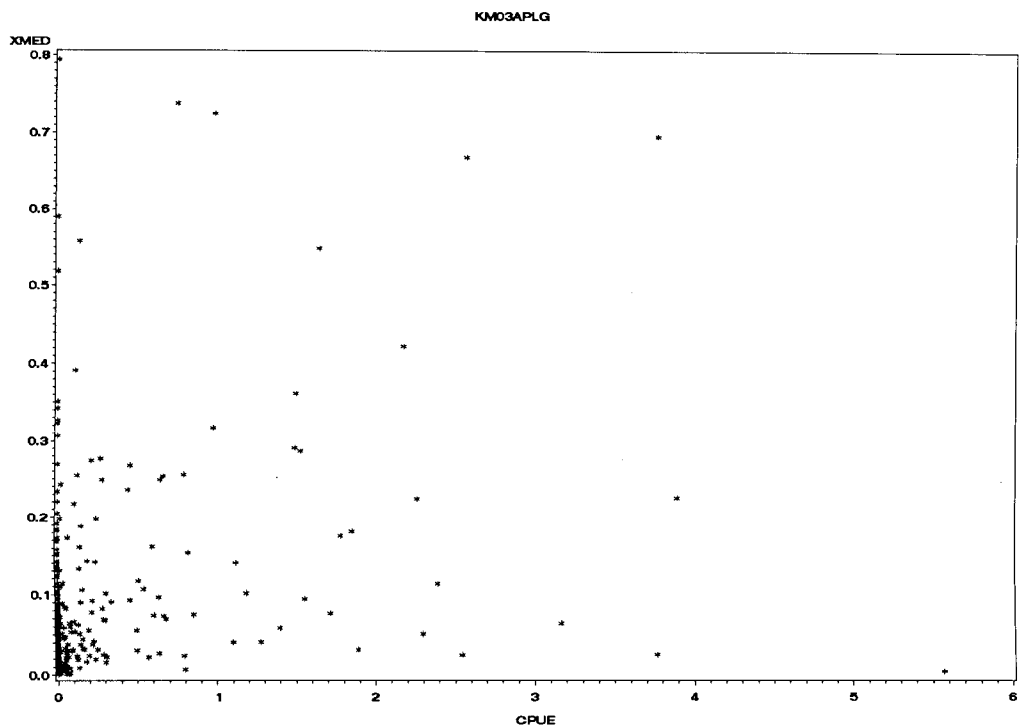
Figure 44. Medians of predicted values for log(CPUE) vs observed log (mean CPUE) in cells with observed means > 0. King mackerel results for model 02.

KM03ALOG

Figure 45. Medians of predicted values for CPUE vs observed mean CPUE for cells having data. King mackerel results for model 02.

KM03ALOG

Figure 46. Medians of predicted values for log(CPUE) vs observed log (mean CPUE) in cells with observed means > 0. King mackerel results for model 03.
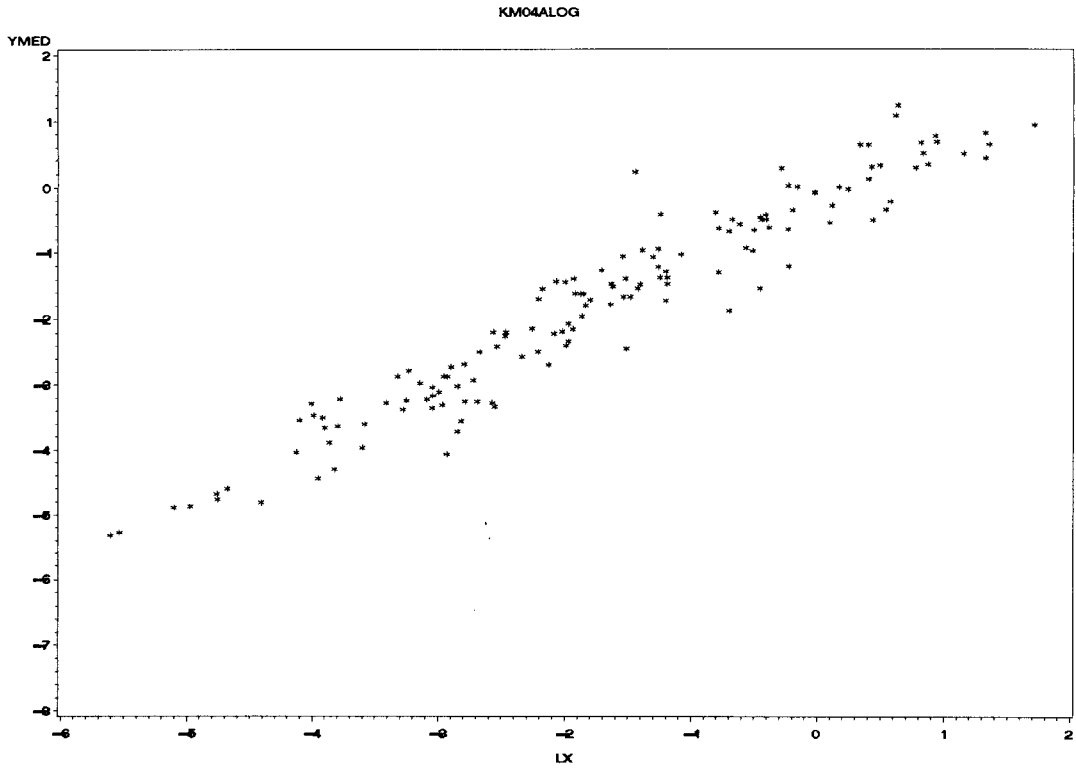

KM03APLG

Figure 47. Medians of predicted values for CPUE vs observed mean CPUE for cells having data. King mackerel results for model 03.

KM03APLG

Figure 48. Medians of predicted values for log(CPUE) vs observed log (mean CPUE) in cells with observed means > 0. King mackerel results for model 04.

KM04ALOG

Figure 49. Medians of predicted values for CPUE vs observed mean CPUE for cells having data. King mackerel results for model 04.
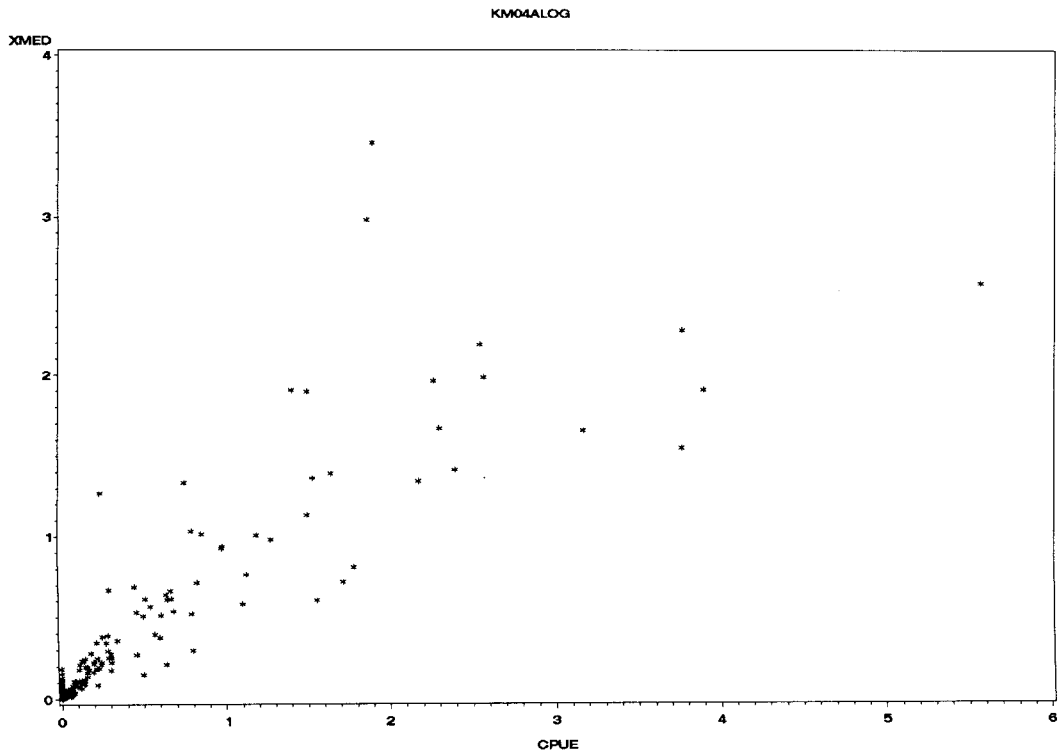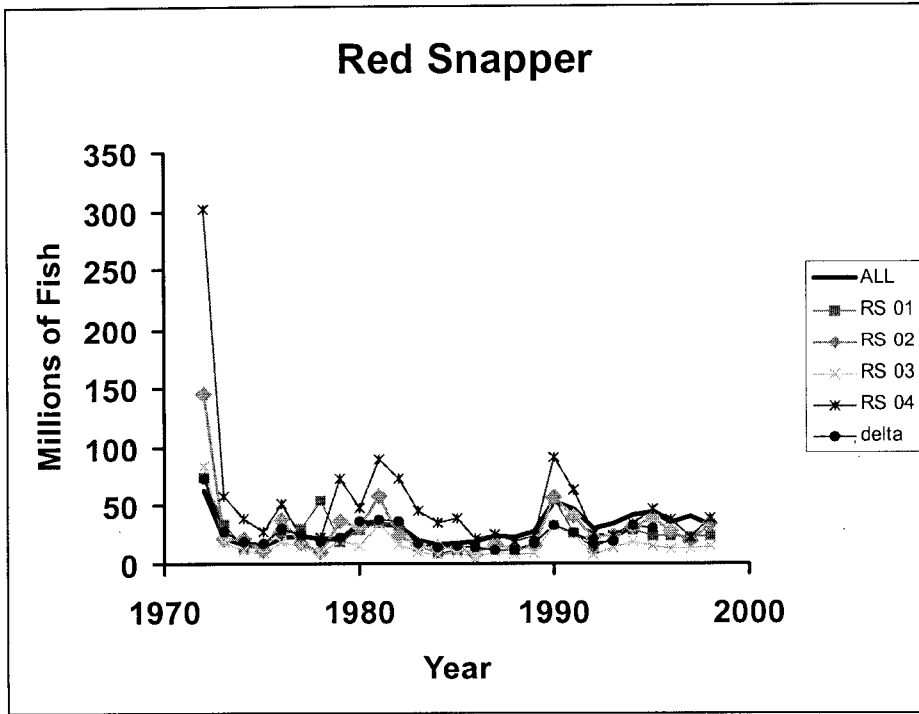

KM04ALOG

Figure 50. Medians for annual totals for red snapper from the four models, and from the last GLM. (a) scaled to fit all medians. (b) scaled appropriately to fit the average of the upper 95% confidence intervals from model 04.
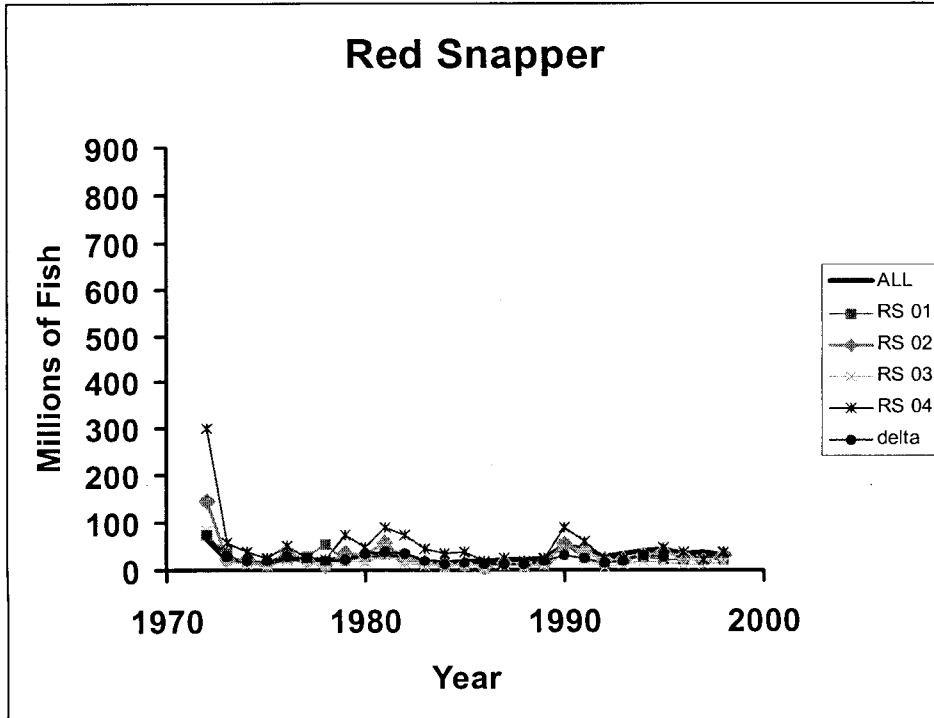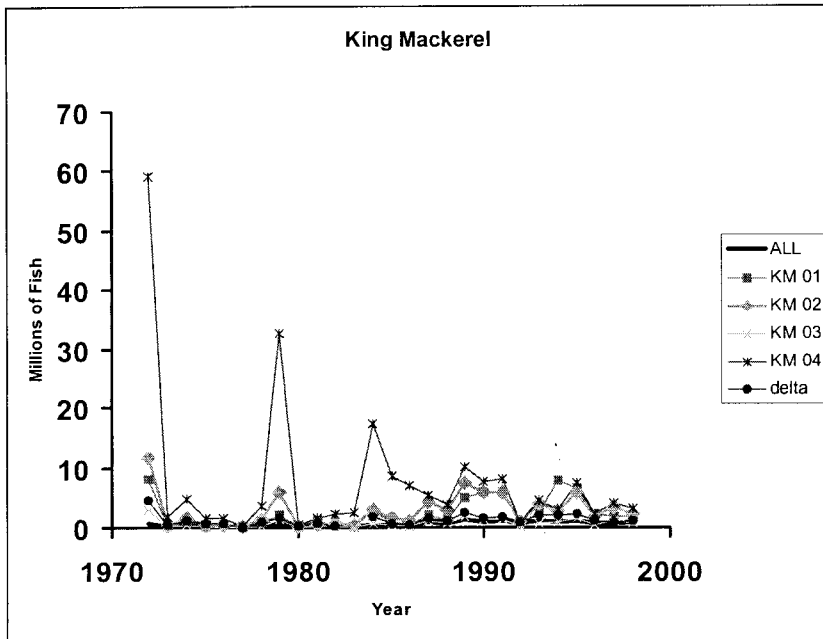
50a.

50b.

Figure 51. Medians for annual totals for king mackerel from the four models, and from the last GLM. (a) scaled to fit all medians. (b) scaled appropriately to fit the average of the upper 95% confidence intervals from model 04.
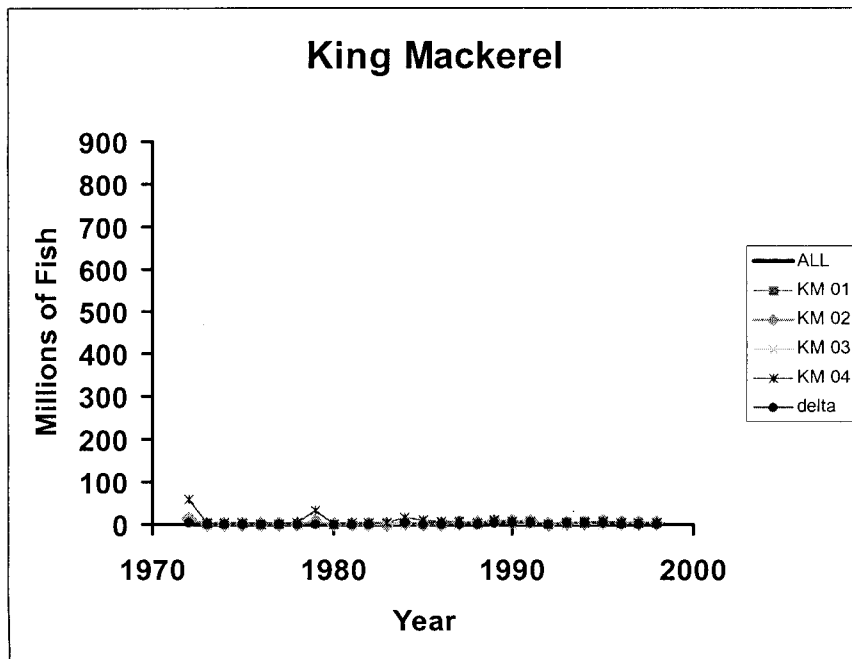
51a.

51b.

Table 5. Average of medians of annual totals for several choices of (fixed) values for the r parameter, using model 02. Average medians are millions of fish.

r	avg med
0.03	2.812715
0.05	2.418307
0.07	2.14986
0.09	2.329909
0.3	2.057633
0.9	1.793532

APPENDIX.

BUGS code for the models. Code for red snapper models are presented. King mackerel models differ only in using −2 instead of 1 as the mean for the year effects priors. Models 02 and 03 use the same code.

Model 01:

```
model rsbcpue01A {

r~dunif(0.03,5)

for (i in 1:27) {
  yx[i]~dnorm(1,0.7)
  }
for (j in 1:3) {
  sraw[j]~dnorm(0,1)
  sx[j]<-sraw[j]-mean(sraw[])
  }
for (k in 1:4) {
  araw[k]~dnorm(0,0.2)
  ax[k]<-araw[k]-mean(araw[])
  }
for (l in 1:2) {
  zraw[l]~dnorm(0,0.2)
  zx[l]<-zraw[l]-mean(zraw[])
  }
for (m in 1:2) {
  draw[m]~dnorm(0,1)
  dx[m]<-draw[m]-mean(draw[])
  }
for (i in 1:27) {
  for (j in 1:3)  {
    for (k in 1:4) {
      for (l in 1:2) {
        for (m in 1:2) {
          logy[i,j,k,l,m]<-yx[i]+sx[j]+ax[k]+zx[l]+dx[m]
          y[i,j,k,l,m]<-exp(logy[i,j,k,l,m])
          mu[i,j,k,l,m]<-r/y[i,j,k,l,m]
          }
        }
      }
    }
  }
for (h in 1:29617) {
  lamb[h]~dgamma(r,mu[yr[h],seas[h],ar[h],dp[h],ds[h]])
  lambda[h]<-lamb[h]*hrsfishd[h]
  catch[h]~dpois(lambda[h])
  }
for (i in 1:27) {
  for (j in 1:3)  {
    for (k in 1:4) {
      for (l in 1:2) {
        take[i,j,k,l]<-y[i,j,k,l,1]*2*effort[i,j,k,l]*24/1000000
        }
      }
    }
  }
for (i in 1:27) {
  annual[i]<-sum(take[i,,,])
  loga[i]<-log(annual[i])
  }
}
```

Model 02 and 03:

```
model rsbcpue03A {

r~dunif(0.03,5)
tau~dlnorm(0,3.5)
center~dnorm(0,tau)

for (i in 1:27) {
 yx[i]~dnorm(1,0.7)
 }
for (j in 1:3) {
 sraw[j]~dnorm(0,1)
 sx[j]<-sraw[j]-mean(sraw[])
 }
for (k in 1:4) {
 araw[k]~dnorm(0,0.2)
 ax[k]<-araw[k]-mean(araw[])
 }
for (l in 1:2) {
 zraw[l]~dnorm(0,0.2)
 zx[l]<-zraw[l]-mean(zraw[])
 }
for (m in 1:2) {
 draw[m]~dnorm(0,1)
 dx[m]<-draw[m]-mean(draw[])
 }
for (i in 1:27) {
 for (j in 1:3)  {
   for (k in 1:4) {
     for (l in 1:2) {
       for (m in 1:2) {
         local[i,j,k,l,m]~dnorm(0,tau)
         logy[i,j,k,l,m]<-yx[i]+sx[j]+ax[k]+zx[l]+dx[m]+local[i,j,k,l,m]
         predlogy[i,j,k,l,m]<-yx[i]+sx[j]+ax[k]+zx[l]+dx[m]+center
         predy[i,j,k,l,m]<-exp(predlogy[i,j,k,l,m])
         y[i,j,k,l,m]<-exp(logy[i,j,k,l,m])
         mu[i,j,k,l,m]<-r/y[i,j,k,l,m]
         }
       }
     }
   }
 }
for (h in 1:29617) {
 lamb[h]~dgamma(r,mu[yr[h],seas[h],ar[h],dp[h],ds[h]])
 lambda[h]<-lamb[h]*hrsfishd[h]
 catch[h]~dpois(lambda[h])
 }
for (i in 1:27) {
 for (j in 1:3)  {
   for (k in 1:4) {
     for (l in 1:2) {
       take[i,j,k,l]<-y[i,j,k,l,1]*2*effort[i,j,k,l]*24/1000000
       taketwo[i,j,k,l]<-predy[i,j,k,l,1]*2*effort[i,j,k,l]*24/1000000
       }
     }
   }
 }
for (i in 1:27) {
 annual[i]<-sum(take[i,,,])
 loga[i]<-log(annual[i])
 annupred[i]<-sum(taketwo[i,,,])
 logp[i]<-log(annupred[i])
 }
}
list(tau=0.1)
list(tau=1.2)
```

Model 04:

```
model rsbpue04A {

for (i in 1:15) { g[i]<-1}
for (i in 16:27) { g[i]<-2 }

for (gg in 1:2) {
  for (m in 1:2) {
    r[gg,m]~dunif(0.03,5)
    tau[gg,m]~dunif(0.03,3)
    center[gg,m]~dnorm(0,tau[gg,m])
  }
}

for (i in 1:27) {
  yx[i]~dnorm(1,0.7)
}
for (j in 1:3) {
  sraw[j]~dnorm(0,1)
  sx[j]<-sraw[j]-mean(sraw[])
}
for (k in 1:4) {
  araw[k]~dnorm(0,0.2)
  ax[k]<-araw[k]-mean(araw[])
}
for (l in 1:2) {
  zraw[l]~dnorm(0,0.2)
  zx[l]<-zraw[l]-mean(zraw[])
}
for (m in 1:2) {
  draw[m]~dnorm(0,1)
  dx[m]<-draw[m]-mean(draw[])
}
for (i in 1:27) {
  for (j in 1:3) {
    for (k in 1:4) {
      for (l in 1:2) {
        for (m in 1:2) {
          local[i,j,k,l,m]~dnorm(0,tau[g[i],m])
          logy[i,j,k,l,m]<-yx[i]+sx[j]+ax[k]+zx[l]+dx[m]+local[i,j,k,l,m]
          predlogy[i,j,k,l,m]<-yx[i]+sx[j]+ax[k]+zx[l]+dx[m]+center[g[i],m]
          predy[i,j,k,l,m]<-exp(predlogy[i,j,k,l,m])
          y[i,j,k,l,m]<-exp(logy[i,j,k,l,m])
          mu[i,j,k,l,m]<-r[g[i],m]/y[i,j,k,l,m]
        }
      }
    }
  }
}
for (h in 1:29617) {
  lamb[h]~dgamma(r[g[yr[h]],ds[h]],mu[yr[h],seas[h],ar[h],dp[h],ds[h]])
  lambda[h]<-lamb[h]*hrsfishd[h]
  catch[h]~dpois(lambda[h])
}
for (i in 1:27) {
  for (j in 1:3) {
    for (k in 1:4) {
      for (l in 1:2) {
        take[i,j,k,l]<-y[i,j,k,l,1]*2*effort[i,j,k,l]*24/1000000
        predtake[i,j,k,l]<-predy[i,j,k,l,1]*2*effort[i,j,k,l]*24/1000000
      }
    }
  }
}
for (i in 1:27) {
  annual[i]<-sum(take[i,,,])
  loga[i]<-log(annual[i])
  annupred[i]<-sum(predtake[i,,,])
  logp[i]<-log(annupred[i])
```

```
  }
for (i in 1:27) {
  for (j in 1:3)    {
    trimester[i,j]<-sum(take[i,j,,])
    logt[i,j]<-log(trimester[i,j])
    tripred[i,j]<-sum(predtake[i,j,,])
    logtp[i,j]<-log(tripred[i,j])
    }
  }
}

list(tau=structure(.Data=c(0.5,0.5,0.5,0.5),.Dim=c(2,2)))
list(tau=structure(.Data=c(1,1,1,1),.Dim=c(2,2)))
list(r=structure(.Data=c(0.8,0.8,0.8,0.8),.Dim=c(2,2)))
```