Population Dynamics

Development of a Three-stage Catch-Survey Analysis

Report to the Alaska Department of Fish and Game

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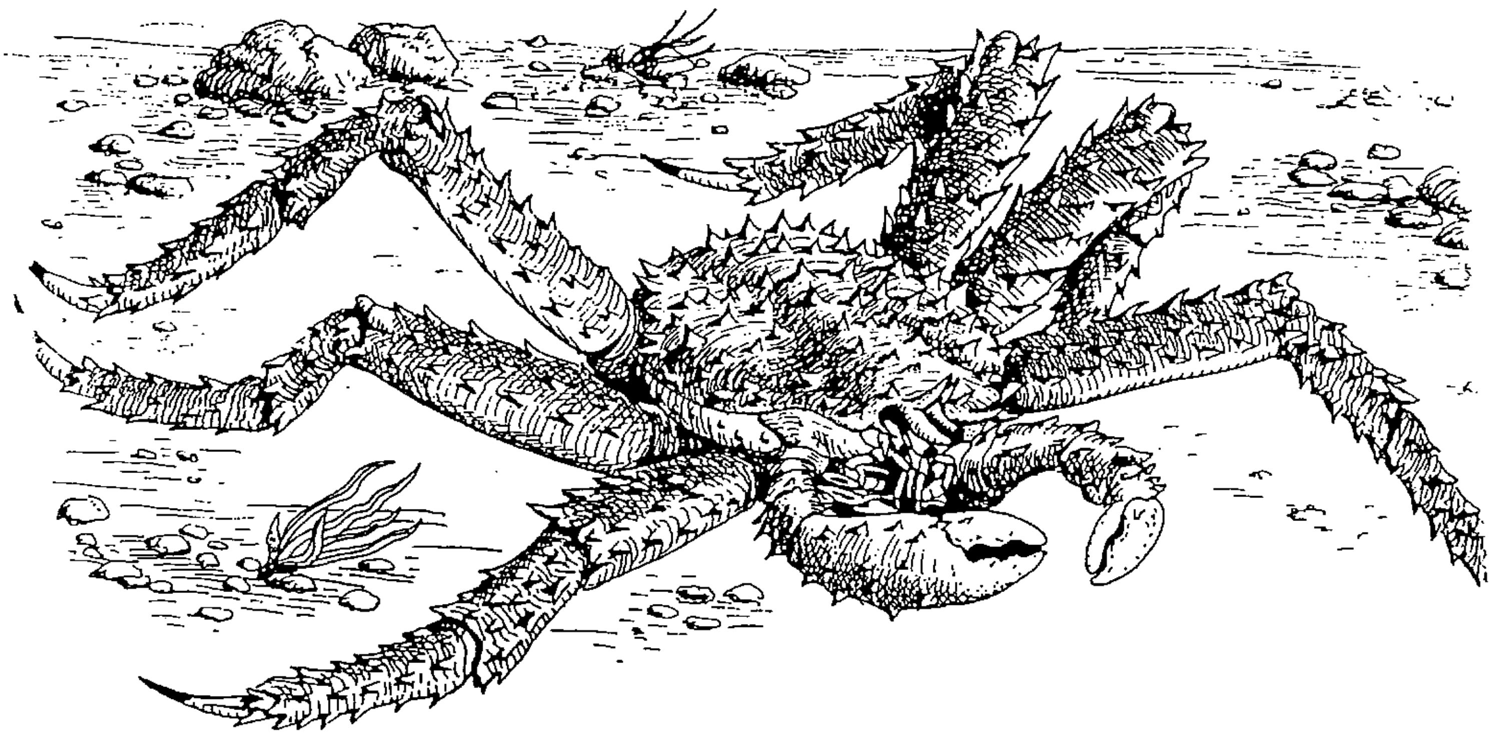

Drawing by
Dennis L. Kuklok
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this program is in Appendix B. The output files from this program are CSA33.out and qtheta.out. The first file provides summary output information and the second contains the fitted q and θ values from each Monte Carlo replicate.

METHODS

Model Formulation

The three-stage catch-survey analysis uses a simple population model, research survey relative abundance indices and the commercial catch to estimate a time series of mature and legal-sized crab population abundance. The stages are defined as pre-recruit, recruit and post-recruit. The pre-recruit class is set to include those crabs whose carapace length ranks them as sexually mature and one molt increment shy of recruitment into the commercial fishery. The recruit class is defined to include crabs that enter the commercial fishery in that year; i.e. the crabs that have recently molted (new shell) and are within one molt increment greater than the legal size cutoff. The post-recruit size class includes all crabs greater than legal size that are not new recruits. The size classes are different for each of the stocks. The modified version approximates post-recruit abundance in the same manner as the two-stage model (Collie and Kruse 1998); however, recruit abundance is a function of pre-recruit abundance in the previous year. The population model is as follows:

$$POST_{t+1} = (REC_t + POST_t)e^{-M_t} - C_t e^{-M_t(1-T_t)}$$

$$REC_{t+1} = molt_t PRE_t e^{-M_t},$$

where $POST_t$, REC_t and PRE_t are the respective post-recruit, recruit and pre-recruit absolute abundances at time t, C_t is the commercial catch in year t, M_t is the instantaneous natural mortality rate in year t, $molt_t$ is the probability a pre-recruit will molt, and T_t is the time lag from the survey to the midpoint of the fishery in year t. As in the two-stage CSA, population with a lognormally distributed measurement error. Therefore, the observed relative abundances can be written as

$$\tilde{pre}_t = pre_t \cdot e^{\gamma_t},$$

$$\tilde{rec}_t = rec_t \cdot e^{\kappa_t}, \text{ and}$$

$$\tilde{post}_t = post_t \cdot e^{\varepsilon_t},$$

where γ_t, κ_t, and ε_t are correlated or uncorrelated normal deviates. The objective function minimized to approximate the parameters is

$$SSQ = \sum_{t=1}^{n-1} w_{pre}^2 (\ln(\tilde{pre}_t + \delta) - \ln(\hat{pre}_t + \delta))^2 + \sum_{t=1}^{n} w_{rec}^2 (\ln(\tilde{rec}_t + \delta) - \ln(\hat{rec}_t + \delta))^2$$
$$+ \sum_{t=1}^{n} (\ln(\tilde{post}_t + \delta) - \ln(\hat{post}_t + \delta))^2,$$

where $\hat{pre}_t$, $\hat{rec}_t$ and $\hat{post}_t$ are the fitted pre-recruit, recruit and post-recruit relative abundances respectively, $\tilde{pre}_t$, $\tilde{rec}_t$ and $\tilde{post}_t$ are the respective observed pre-recruit, recruit and post-recruit relative abundances at time t, δ is a constant added to ensure the equation remains defined, w_{pre} and w_{rec} are the weights of pre-recruits and recruit errors relative to post-recruit errors, and n is the number of years. Relative abundance indices are converted to absolute population estimates using

$$\hat{PRE}_t = \hat{pre}_t / \hat{q}\hat{\theta}, \quad \hat{REC}_t = \hat{rec}_t / \hat{q}\hat{\phi}, \text{ and } \hat{POST}_t = \hat{post}_t / \hat{q}.$$

The number of mature crabs each year is estimated as $\hat{PRE}_t + \hat{REC}_t + \hat{POST}_t$, and the number of legal crabs each year is estimated as $\hat{REC}_t + \hat{POST}_t$. The three-stage formulation allows legal crab abundance to be estimated in all years and mature crab where $P(L)$ is the probability a crab of length L will molt in any given year and a and b are parameters to estimate. We estimated the pre-recruit molt probability by averaging the fitted equation over the length of the pre-recruit size-class, which is 120-134 mm for the Pribilof Islands stock and 105-119 mm for the St. Matthew Island stock.

For the Pribilof Islands stock, we followed the procedure put forth in Otto and Cummiskey (1990); we used crabs that were at large between 1 and 1.5 years, which ensures the crabs had the opportunity to molt once and only once. There were 188 such recaptures. A crab was presumed to have molted if the carapace length increased more than 7 mm and to have not molted if the recapture carapace length was within 3 mm of the release length. In accordance with the methodology of Otto and Cummiskey (1990), the four crabs with growth increments between 4 and 7 mm inclusive were excluded from the analysis as it can not be determined whether these crabs molted or their shells were measured with error. We explored several alternate fitting methodologies to those of Otto and Cummiskey (1990), such as weighted and unweighted nonlinear regression and the use of the logit transformation of the logistic equation to fit a generalized linear model (GLM) assuming binomially distributed data (Figure 1a). The logit transformation of the logistic molt probability function written above is

$$\ln\left(\frac{P_L}{1 - P_L}\right) = \ln\left(\frac{1}{a}\right) - b \cdot L.$$

Theoretically, the logistic regression (GLM) methodology is the most appropriate method for these recapture data as each data point is weighted equally and the molt probability is a binomially distributed random variable (the crab molted or it didn't), with an expected molt probability associated with the crab's release length. The GLM fit resulted in a pre-recruit molt probability of 0.75. Both chi-square and deviance goodness of fit tests indicate that these data do not significantly differ from the logistic model (Netter et al. 1996). Using Otto and Cummiskey's (1990) parameters, with the exponent on the parameter a decreased from -5 to -6 (personal communication of Gordon Kruse with Bob

Preliminary Analysis:

We performed some preliminary analyses on the baseline runs of the model. For the baseline runs the offset parameter in the sum of squared residuals term, δ, was set to 0.001. Results from the baseline runs are provided in Tables 2a, 2b, and 2c.

Jie Zheng pointed out that pre-recruits that don't molt can survive as pre-recruits the following year. This could add additional structure to the three-stage model, especially if the shell age were known for the pre-recruit size class. Even without observations of shell age, the predicted number of old shell pre-recruits (surviving pre-recruits that didn't molt the previous year) should be less than or equal to the predicted number of total pre-recruits for each year.

We examined the output from the baseline runs of the three-stage model to see if this constraint was met. In every case but one the total pre-recruit estimate exceeded the prediction of old-shell pre-recruits. The exception occurred in 1988 for the Pribilof Islands stock, for which the pre-recruit index was 0.0 and the predicted old-shell pre-recruits was 0.0075, a very small difference. For these king crab stocks, the proportion of pre-recruits not molting and surviving is small, around 0.2. Thus the extra constraint is unlikely to be binding.

We examined the residuals from the baseline runs (Table 3). The distribution of residuals was examined with histograms and quantile-quantile plots. The residual distributions were skewed but were not significantly different from a normal distribution based upon results of chi-square tests. The Pribilof stock had two large positive residuals associated with zero year-classes. With these outliers removed, the residuals were normally distributed. The variances of the residuals from the different size classes of crabs were tested for homogeneity with an *F*-ratio test. There were no significant differences between size classes for any of the stocks.

The standard deviation of residuals is of the order 0.3 to 0.5, except with the Pribilof Islands zero abundance indices, in which case the offset added to prevent undefined logarithms substantially affects the magnitude of the residuals and resulted in a residual standard deviation of 0.89. When the residuals for the zero year classes were

We created a FORTRAN program to perform Monte Carlo simulations by extending the original two-stage FORTRAN model, delpop6.for, to incorporate the third stage. This program a) uses a data set that fits the model perfectly (output from the baseline run), b) prompts the user for the number of Monte Carlo replicates, the standard deviation and correlation of measurement errors, and the standard deviation of equation errors, c) simulates the uncorrelated equation errors and assumes these relative abundance indices are representative of the true population, d) simulates correlated or uncorrelated measurement errors on the true abundance indices from step (c), and e) fits the simulated observed data with the three-stage model as many times as desired. We used delpop6.for to perform identical Monte Carlo simulations with the two-stage model for comparison.

Equation errors exist when the true population abundance is not precisely predicted by the transition equations. We simulated the equation errors by altering the input (fitted) survey indices with the following calculations and assuming the new abundance indices represent the true population.

$$rec_1 = \hat{rec}_1$$

$$post_1 = \hat{post}_1$$

$$rec_{t+1} = \left[\frac{\hat{pre}_t \; molt_t \phi}{\theta} e^{-M_t} \right] \cdot e^{z*std - var/2}$$

$$post_{t+1} = \left[(rec_t/\phi + post_t) e^{-M_t} - qC_t e^{-M_t(1-T_t)} \right] \cdot e^{z*std - var/2},$$

where rec_t and $post_t$ represent the true relative abundances of recruits and post recruits and thus are not superscripted, $\hat{pre}_t$, $\hat{rec}_t$ and $\hat{post}_t$ are the fitted indices from the baseline run, z is a random standard normal deviate, *std* is the standard deviation and *var* is the variance of the equation errors. In the simulations examining equation error only, these simulated "true" relative abundance indices are equivalent to the observed indices as there would be no measurement error.

uncorrelated errors. We performed 1000 replicates and calculated the mean and standard deviation of the bootstrapped fits.

RESULTS AND DISCUSSION

St. Matthew Island Blue King Crab

For the St. Matthew blue king crab stock, commercial catch and survey indices were available from 1980 to 1997. The pre-recruit and recruit size classes ranged from 105 to 119 mm and 120 to 133 mm carapace length, respectively. The input data file is in Table 1a and the bootstrap output is provided in Table 2a. The standard deviation of the residuals from the baseline fit and subsequently used in the bootstrap replicates was 0.36. The bootstrap runs resulted in a very small (-0.038) bias in the catchability coefficient and a considerably smaller (0.004) bias in the mean estimate of the catchability of pre-recruits relative to post-recruits (θ). The bootstrapped average percent bias of mean legal abundance was 0.427 and the average coefficient of variation of legal abundance was 15.29. The three-stage model legal and mature crab abundance estimates and the bootstrapped 95% confidence interval about legal and mature crab abundance are portrayed in Figures 10 a & b. The bootstrapped abundance means coincide nicely with the model output and indicate the population abundance continues to increase.

We performed some additional analyses using the St. Matthew stock as a representative example. We performed Monte Carlo simulations assuming correlated and uncorrelated measurement errors, equation errors and mixed equation and measurement errors. From the residual analysis, we observed that the standard deviation of the pre-recruit, recruit and post-recruit measurement errors for the St. Matthew Island stock is 0.36. Furthermore, the pre-recruit, recruit and post-recruit measurement errors are correlated to some degree from 0 to 1 (between 0.59 and 0.70 for the St. Matthew Island stock). This is most likely because the relative abundance indices come from the same survey. We would expect equation errors to exist when some of the input parameters, such as the estimates of natural mortality, change during the time series. These errors

Figure 3 shows the average bias of the legal abundance estimates for each year in the runs with uncorrelated measurement errors. The average bias of the legal abundance for each year from the two-stage model increases and becomes more negative as the standard deviation of measurement errors increases (Figure 3). The largest bias occurs during 1982-1985 when the population abundance was decreasing to very low levels. The average yearly bias of the three-stage model (Figure 3) also increases and becomes more negative as the standard deviation of measurement errors increases. However, in comparison to the two-stage model, the magnitude of the bias with the three-stage model is much greater during the period from 1982-1985 and less during the remainder of the time series.

In general, one may expect a slightly positive bias in the abundance estimates because the simulated lognormal equation errors cause some large positive deviations from the fitted input data; however, we simulated the lognormal measurement errors to have mean 1.0. This causes the median of the measurement errors to be less than 1.0. As the standard deviation of the measurement errors increases, the median shifts to a lower and lower value (0.94 with a standard deviation of 0.3 and 0.81 with a standard deviation of 0.7). Furthermore, with a standard deviation of 0.3 and 0.5, there was a significant correlation ($p < 0.07$ that the correlation is zero) between the median of the measurement error for one run and the average percent bias of the population estimates of the run. As a result, as the standard deviation increases, the bias becomes more negative.

The percent bias of legal abundance is quite large during the period from 1982-1985. During the intermediate years (1982-1987), the legal abundance decreases and becomes quite low in comparison to the earlier and later years. The percent bias is most likely amplified during the years of low abundance because of the logarithmic transform in the objective function. The simulated relative abundance estimates can become very small for these intermediate years, especially as the standard deviation of the measurement error increases. The logarithm in the objective function places greater emphasis on the residuals during the years of low abundance and the model tries hard to fit these small values. This bias may be more extreme with the three-stage model than with the two-stage model because there are three residuals associated with the small cohorts rather than two.

natural survival and thus inversely related to M. Thus, estimates of θ should be positively related to molt probability. A small fraction of pre-recruits may molt directly into the post-recruit size range without being recruits. However this is offset by a small fraction of recruits whose molt increment is insufficient to put them in the post-recruit stage.

Errors in molt probability or pre-recruit natural mortality directly influence pre-recruit abundance estimates. For example, if we assume that pre-recruit and recruit mortality equal post-recruit mortality (when in fact it is higher for smaller crabs), θ would be overestimated and pre-recruit abundance would be underestimated. Thus, accurate estimates of the absolute abundance of pre-recruits depend on good estimates of molt probability and pre-recruit natural mortality. Estimates of both pre-recruit catchability and recruit catchability are inversely related to estimates of post-recruit catchability (Figures 6d and 6e). However, as the three-stage model compensates for errors in recruit catchability by changing pre-recruit catchability, errors in pre-recruit catchability increase the sum of squared residuals much more than errors in recruit catchability (Figure 6c).

As we set the instantaneous natural mortality rate to 0.3 for all years, we compare our St. Matthew Island results with the results from Zheng et al.'s (1997a) two-stage CSA with M_t set to 0.3 and q estimated. The abundance estimates appear to follow those from the two-stage CSA nicely, although the three-stage model predicts slightly lower legal abundances for all but 5 years (Figure 7a). This model smoothed and moderated abundance levels through time in comparison with the two-stage model, with the peak in 1982 reduced from about 4.5 to 3.9 million crabs. The model estimated the catchability of pre-recruits relative to post-recruits to be 0.516. The catchability coefficients and mean square errors from the two- and three-stage CSAs are comparable (Table 5). Note that because the objective function in Zheng et al. (1997a) is different from the objective function we employ, we approximate the sum of squared residuals using the delpop7.for FORTRAN program.

Pribilof Islands Blue King Crab

The pre-recruit class includes crabs with carapace length between 120 and 134, and the carapace length for the recruit class ranges from 135 to 148. Data are available million crabs). The two-stage model predicts higher abundances in 1990, 1991 and 1992. The catchability of pre-recruits relative to post-recruits at 0.625 is slightly larger than the value estimated for St. Matthew, perhaps due to the larger size of this class. The catchability coefficient is estimated to be 1.405 in the three-stage model and is very similar to the q from the two-stage model. The sum of squared residuals at 25.5 is quite high in the three-stage model, with the 1989 pre-recruit cohort contributing over 70% of the sum of squared residuals. Although the survey index for the pre-recruits is zero in 1989, the model predicts a small, positive value because it uses the pre-recruit abundance to estimate the recruit abundance in the following year and the survey found a substantial number of recruits in 1990. This cohort carries over into the 1991 post-recruit estimation. The residuals are accentuated in these smaller classes due to the logarithm in the objective function. A comparison of the catchability coefficient, sum of squared residuals, number of degrees of freedom and the mean squared error between the two- and three-stage CSAs is provided in Table 5.

Bristol Bay Red King Crab

The pre-recruit stage is defined to be those crabs with carapace length between 120 and 134 mm, and the recruit stage is defined to contain new shell crabs with carapace length between 135 and 149 mm. Catch and survey estimates are available for the years 1973 to 1997. The input file used in the three-stage model and the bootstrap output are in Tables 1c and 2c. The standard deviation of the residuals calculated in the baseline run of the three-stage model and used in the bootstrap was 0.29. The bootstrapped average percent bias of mean legal abundance is -0.059 and the average coefficient of variation of legal abundance is 12.86. Figures 12 a & b contain the model and bootstrap mean legal and mature crab abundance estimates and 95% confidence intervals about the mean bootstrapped estimate. The output indicates that the Bristol Bay red king crab population abundance has not increased in recent years and remains at a level similar to that of the early eighties, following a large decrease in abundance and high catches.

We can compare the output from the three-stage CSA model with the output from three other methods: the two-stage catch survey analysis (Collie and Kruse 1998), the indices with the three-stage model. The two-stage CSA is not able to estimate recruit abundance in this last year; thus the unsmoothed survey index must be used. The three-stage model can also be used to estimate the abundance of mature male king crabs, because the size of pre-recruits corresponds approximately to the size at maturity of male king crabs (Somerton and MacIntosh 1983). This is important for stock managers as the commercial quota is based upon estimates of both legal and mature crab abundance.

The harvest strategy for these three king crab stocks includes setting an annual guideline harvest level (GHL) each season. The GHL for the Bristol Bay red king crab stock is set to 10% of the mature male abundance if the biomass of spawning females (ESB) is below 55 million pounds and to 15% of the mature male abundance if the ESB is greater than 55 million pounds. However, the GHL is capped so that no more than 50% of the legal male crabs may be harvested each year. In recent years, it has been possible to set the GHL of 15% of the mature male abundance (Zheng et al. 1997b). The St. Matthew Island blue king crab stock GHL is set at 20% of mature male abundance, because the stock is above the threshold of 0.6 million males (Zheng et al. 1997b). To avoid by-catch problems, an aggregate GHL is set for the Pribilof Islands blue and red king crab stocks based upon the abundance of mature male crabs (Zheng et al. 1997b).

The three-stage model uses more data than the two-stage model and therefore has a higher ratio of observations to parameters. For the three-stage model only two more parameters need to be estimated, one relative abundance estimate and θ. The bootstrap simulations indicate that θ is well defined in this model. The standard error of θ from the simulations for St. Matthew Island, the Pribilof Islands and the Bristol Bay king crab stocks were 0.060, 0.101, and 0.083, respectively. This resulted in quite narrow confidence intervals for θ. In only one case (Pribilof Islands) was the Mean Square Error of the three-stage model larger than that of the corresponding two-stage model (Table 5). The high sum of squared residuals in this case resulted from the zero abundance indices in 1988 and 1989.

The sensitivity analyses reveal that the three-stage model is able to smooth uncorrelated measurement errors better than the two-stage formulation. As a result, the bootstrapped confidence intervals about the legal abundance estimates should be narrower

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Table 1. Input files for 3-stage catch-survey analysis.

a) St. Matthew Island blue king crab input file.

Year	pre-recruit abundance index	recruit abundance index	post-recruit abundance index	commercial catch (millions)	pre-recruit weight (Lbs.)	rec & post-rec weight (Lbs.)	pre-recruit natural mortality	post-rec & rec natural mortality	timing of commercial catch	pre-recruit molt probability
1980	2.588	1.699	1.197	0.033	4.5	4.5	0.3	0.3	0.068	0.63
1981	1.480	1.195	1.648	1.046	4.4	4.4	0.3	0.3	0.052	0.63
1982	2.615	3.617	3.263	1.936	4.6	4.6	0.3	0.3	0.068	0.63
1983	1.639	1.399	1.956	1.932	4.8	4.8	0.3	0.3	0.121	0.63
1984	0.500	0.788	0.762	0.841	4.5	4.5	0.3	0.3	0.096	0.63
1985	0.431	0.541	0.708	0.485	5.0	5.0	0.3	0.3	0.137	0.63
1986	0.425	0.164	0.185	0.220	4.6	4.6	0.3	0.3	0.137	0.63
1987	0.757	0.492	0.292	0.235	4.6	4.6	0.3	0.3	0.137	0.63
1988	0.703	0.417	0.411	0.302	4.4	4.4	0.3	0.3	0.137	0.63
1989	1.235	0.940	0.954	0.248	4.7	4.7	0.3	0.3	0.134	0.63
1990	0.957	0.954	1.164	0.391	4.4	4.4	0.3	0.3	0.140	0.63
1991	1.636	1.353	0.889	0.727	4.6	4.6	0.3	0.3	0.178	0.63
1992	1.582	1.338	1.247	0.545	4.6	4.6	0.3	0.3	0.142	0.63
1993	1.994	1.605	2.000	0.630	4.8	4.8	0.3	0.3	0.178	0.63
1994	1.350	1.246	1.120	0.827	4.6	4.6	0.3	0.3	0.178	0.63
1995	1.321	0.993	0.902	0.667	4.8	4.8	0.3	0.3	0.178	0.63
1996	1.970	1.950	1.331	0.661	4.6	4.6	0.3	0.3	0.178	0.63
1997	2.319	2.213	1.853	NA	NA	NA	NA	NA	NA	NA

b) Pribilof Islands blue king crab input file.

Year	pre-recruit abundance index	recruit abundance index	post-recruit abundance index	commercial catch (millions)	pre-recruit weight (Lbs.)	rec & post-rec weight (Lbs.)	pre-recruit natural mortality	post-rec & rec natural mortality	timing of commercial catch	pre-recruit molt probability
1980	1.283	1.434	4.165	1.497	7.3	7.3	0.3	0.3	0.252	0.75
1981	0.717	0.686	3.179	1.202	7.6	7.6	0.3	0.3	0.249	0.75
1982	0.313	0.629	1.750	0.588	7.5	7.5	0.3	0.3	0.175	0.75
1983	0.618	0.369	1.075	0.276	7.9	7.9	0.3	0.3	0.173	0.75
1984	0.233	0.236	0.375	0.040	7.6	7.6	0.3	0.3	0.142	0.75
1985	0.163	0.147	0.239	0.078	6.9	6.9	0.3	0.3	0.192	0.75
1986	0.018	0.098	0.394	0.037	7.0	7.0	0.3	0.3	0.233	0.75
1987	0.071	0.068	0.731	0.095	7.4	7.4	0.3	0.3	0.274	0.75
1988	0.000	0.034	0.164	0.000	7.4	7.4	0.3	0.3	0.000	0.75
1989	0.000	0.000	0.211	0.000	7.4	7.4	0.3	0.3	0.000	0.75
1990	0.658	0.234	0.094	0.000	7.4	7.4	0.3	0.3	0.000	0.75
1991	0.793	0.614	0.623	0.000	7.4	7.4	0.3	0.3	0.000	0.75
1992	0.730	0.374	0.741	0.000	7.4	7.4	0.3	0.3	0.000	0.75
1993	0.640	0.318	0.658	0.000	7.4	7.4	0.3	0.3	0.000	0.75
1994	0.314	0.183	0.651	0.000	7.4	7.4	0.3	0.3	0.000	0.75
1995	0.842	0.332	1.669	0.174	7.3	7.3	0.3	0.3	0.175	0.75
1996	0.938	0.145	1.071	0.124	7.3	7.3	0.3	0.3	0.175	0.75
1997	0.261	0.282	0.540	NA	NA	NA	NA	NA	NA	NA

c) Bristol Bay red king crab input file.

Year	pre-recruit abundance index	recruit abundance index	post-recruit abundance index	commercial catch (millions)	pre-recruit weight (Lbs.)	rec & post-rec weight (Lbs.)	pre-recruit natural mortality	post-rec & rec natural mortality	timing of commercial catch	pre-recruit molt probability
1973	14.180	7.043	3.826	4.826	5.6	5.6	0.189	0.189	0.23	0.908
1974	20.033	13.647	7.172	7.710	5.5	5.5	0.189	0.189	0.23	0.908
1975	20.181	14.070	9.739	8.745	5.7	5.7	0.189	0.189	0.23	0.908
1976	28.472	16.892	13.539	10.603	6.0	6.0	0.189	0.189	0.28	0.908
1977	35.693	23.506	15.298	11.733	5.9	5.9	0.189	0.189	0.32	0.908
1978	32.160	29.719	20.341	14.746	5.8	5.8	0.189	0.189	0.25	0.908
1979	21.926	16.487	16.498	16.809	6.4	6.4	0.189	0.189	0.25	0.908
1980	16.603	20.262	17.797	20.845	6.2	6.2	0.991	0.991	0.25	0.539
1981	8.452	2.635	7.362	5.308	6.3	6.3	0.991	0.991	0.26	0.539
1982	8.308	2.379	1.820	0.541	5.6	5.6	0.991	0.991	0.24	0.539
1983	4.690	0.793	0.590	0.000	5.4	5.4	0.991	0.991	0.00	0.539
1984	5.146	2.017	1.287	0.794	5.2	5.2	0.991	0.991	0.27	0.539
1985	5.666	1.929	0.527	0.796	5.5	5.5	0.189	0.189	0.25	0.765
1986	6.487	3.645	1.316	2.100	5.4	5.4	0.189	0.189	0.25	0.765
1987	7.895	4.203	3.909	2.122	5.8	5.8	0.189	0.189	0.25	0.765
1988	4.030	3.526	3.337	1.236	6.0	6.0	0.189	0.189	0.25	0.765
1989	6.010	3.868	7.995	1.685	6.1	6.1	0.189	0.189	0.25	0.765
1990	4.537	2.609	6.220	3.120	6.5	6.5	0.189	0.189	0.35	0.765
1991	2.834	2.899	6.086	2.630	6.5	6.5	0.189	0.189	0.35	0.765
1992	3.047	1.212	3.824	1.197	6.7	6.7	0.189	0.189	0.35	0.539
1993	6.137	1.028	6.293	2.261	6.6	6.6	0.189	0.189	0.35	0.539
1994	4.006	1.501	3.680	0.000	0.0	0.0	0.189	0.189	0.00	0.539
1995	1.806	0.961	3.238	0.000	0.0	0.0	0.189	0.189	0.00	0.539
1996	1.989	0.950	4.672	1.249	6.7	6.7	0.189	0.189	0.35	0.765
1997	3.233	2.983	6.495	NA	NA	NA	NA	NA	NA	NA

2a. St. Matthew Island output continued

CATCHABILITY COEFFICIENT

```
 INITIAL GUESS:    1.000        95% CONFDENCE INTERVAL
             ESTIMATE    STD ERR    LOWER      UPPER
 1ST PASS      1.105      0.363     0.366      1.843
BOOTSTRAP      1.067      0.122     0.818      1.315
DIFFERENCE    -0.038=BIAS
```

PRE-RECRUIT CATCHABILITY

```
 INITIAL GUESS:    1.000        95% CONFDENCE INTERVAL
             ESTIMATE    STD ERR    LOWER      UPPER
 1ST PASS      0.516      0.357    -0.211      1.244
BOOTSTRAP      0.520      0.060     0.398      0.643
DIFFERENCE     0.004=BIAS
```

PARAMETER SUMMARY

NUMBER OF YEARS = 18

NUMBER OF STAGE CLASSES = 3

NUMBER OF RESIDUAL ERRORS = 53, AS FOLLOWS:

17 FOR PRE-RECRUIT MEASUREMENT ERRORS(ALL YEARS BUT LAST),
18 FOR RECRUIT MEASUREMENT ERRORS (ONE EACH YEAR),
18 FOR POST-RECRUIT MEASUREMENT ERRORS (ONE EACH YEAR),

NUMBER OF PARAMETERS TO BE ESTIMATED = 21, AS FOLLOWS:

ONE FOR TRUE POST-RECRUIT RELATIVE ABUNDANCE IN FIRST YEAR,
ONE FOR TRUE RECRUIT RELATIVE ABUNDANCE IN FIRST YEAR,
ONE FOR TRUE PRE-RECRUIT RELATIVE ABUNDANCE FOR EACH YEAR
(EXCEPT THE LAST YEAR), AND ONE FOR Q.

DEGREES OF FREEDOM = 32 (NO. OF RESIDUALS MINUS NO. OF PARAMETERS)

PARAMETERS ESTIMATED INDEPENDENT OF MODEL

RECRUIT CATCHABILITY = 1.00 TIMES ADULT CATCHABILITY

PRE-RECRUIT CATCHABILITY = 1.00 TIMES ADULT CATCHABILITY

RELATIVE ERROR WEIGHTS

```
PRE-RECRUIT OBSERVATION ERROR    1.00
RECRUIT OBSERVATION ERROR        1.00
POST-RECRUIT OBSERVATION ERROR   1.00
```

2b. Pribilof Island output continued

NON-LINEAR LEAST-SQUARES FIT

FITTING CRITERIA

```
 1. FUNCTION TOLERANCE  0.142E-13      THIS IS SATISFIED IF THE NORM
                                       OF THE FUNCTION IS LESS THAN
                                       THE ABSOLUTE FUNCTION TOLERANCE

 2. GRADIENT TOLERANCE  0.345E-03      THIS IS SATISISFIED IF THE NORM
                                       OF THE SCALED GRADIENT IS LESS THAN
                                       THE GIVEN GRADIENT TOLERANCE

 3. STEP TOLERANCE      0.242E-08      THIS IS SATISFIED IF THE SCALED DISTANCE
                                       BETWEEN THE LAST TWO STEPS
                                       IS LESS THAN THE STEP TOLERANCE
```

SUM OF LOGARITHMIC RESIDUALS FROM BASELINE FIT =25.548

STANDARD DEVIATION OF RESIDUAL ERRORS USED IN BOOTSTRAP = 0.49

STANDARD DEVIATION OF RESIDUAL ERRORS FROM BASELINE FIT = 0.89

NUMBER OF MONTE CARLO REPLICATES = 1000

AVERAGE PERCENT BIAS OF MEAN LEGAL ABUNDANCE = 0.757

AVERAGE COEFFICIENT OF VARIATION OF LEGAL ABUNDANCE = 26.68

NUMBER OF NON-CONVERGENT TRIALS = 8

2c. Bristol Bay output continued

POPULATION ESTIMATES IN MILLIONS

	-----------BEST ESTIMATES--------------					--------------------BOOTSTRAP--------------------								
YEAR	PREREC	RECRUIT	POSTREC	LEGAL	MATURE	LEGAL MEAN	LEGAL BIAS	LEGAL STD ERR	MATURE MEAN	MATURE BIAS	MATURE STD ERR	COMMERC CATCH	LEGAL HARVEST RATE	LEGAL HARVEST RATE
73	18.616	9.260	4.762	14.022	32.638	14.105	0.082	2.064	32.697	0.059	3.603	4.826	0.344	0.148
74	21.799	13.997	7.435	21.432	43.231	21.482	0.051	2.796	43.117	-0.113	4.393	7.710	0.360	0.178
75	23.047	16.390	11.075	27.465	50.513	27.384	-0.081	3.424	50.316	-0.197	5.396	8.745	0.318	0.173
76	30.361	17.329	15.175	32.504	62.864	32.349	-0.154	4.222	62.975	0.111	6.364	10.603	0.326	0.169
77	35.374	22.828	17.652	40.480	75.853	40.551	0.071	4.982	75.760	-0.093	6.576	11.733	0.290	0.155
78	29.032	26.597	23.191	49.787	78.820	49.723	-0.065	5.155	78.605	-0.215	6.075	14.746	0.296	0.187
79	29.018	21.829	28.416	50.245	79.263	50.079	-0.166	4.811	79.212	-0.051	4.512	16.809	0.335	0.212
80	17.320	21.818	27.005	48.822	66.143	48.771	-0.051	3.586	66.299	0.156	4.356	20.845	0.427	0.315
81	10.534	3.468	8.215	11.684	22.218	11.706	0.023	1.329	22.219	0.001	2.451	5.308	0.454	0.239
82	7.666	2.109	1.789	3.898	11.565	3.904	0.005	0.641	11.586	0.021	1.790	0.541	0.139	0.047
83	8.427	1.535	1.193	2.728	11.155	2.733	0.005	0.423	11.222	0.067	1.633	0.000	0.000	0.000
84	9.326	1.688	1.013	2.701	12.027	2.715	0.014	0.358	12.004	-0.023	1.634	0.794	0.294	0.066
85	7.839	1.868	0.618	2.485	10.324	2.483	-0.002	0.351	10.305	-0.019	1.337	0.796	0.320	0.077
86	7.508	4.961	1.366	6.327	13.835	6.315	-0.012	0.870	13.798	-0.037	1.567	2.100	0.332	0.152
87	8.495	4.751	3.415	8.166	16.661	8.141	-0.026	1.085	16.606	-0.055	1.860	2.122	0.260	0.127
88	5.917	5.376	4.918	10.294	16.211	10.254	-0.040	1.309	16.117	-0.094	1.754	1.236	0.120	0.076
89	6.049	3.745	7.449	11.193	17.242	11.126	-0.067	1.314	17.194	-0.048	1.681	1.685	0.151	0.098
90	5.500	3.828	7.803	11.632	17.132	11.588	-0.044	1.262	17.077	-0.055	1.567	3.120	0.268	0.182
91	2.926	3.481	6.869	10.350	13.276	10.307	-0.043	1.182	13.265	-0.011	1.343	2.630	0.254	0.198
92	3.202	1.852	6.242	8.093	11.296	8.078	-0.015	1.060	11.313	0.017	1.308	1.197	0.148	0.106
93	5.440	1.429	5.641	7.070	12.510	7.072	0.002	0.951	12.518	0.008	1.612	2.261	0.320	0.181
94	3.683	2.428	3.853	6.281	9.965	6.285	0.004	1.009	9.965	0.001	1.382	0.000	0.000	0.000
95	2.436	1.644	5.199	6.844	9.280	6.845	0.002	0.960	9.288	0.008	1.177	0.000	0.000	0.000
96	3.606	1.087	5.665	6.752	10.359	6.757	0.004	0.870	10.379	0.020	1.331	1.249	0.185	0.121
97	3.817	2.282	4.485	6.767	10.584	6.781	0.014	0.986	10.706	0.122	NA	NA	NA	NA

CATCHABILITY COEFFICIENT

INITIAL GUESS:	1.000		95% CONFDENCE INTERVAL	
	ESTIMATE	STD ERR	LOWER	UPPER
1ST PASS	0.851	0.457	-0.069	1.772
BOOTSTRAP	0.833	0.076	0.679	0.986
DIFFERENCE	-0.019=BIAS			

PRE-RECRUIT CATCHABILITY

INITIAL GUESS:	1.000		95% CONFDENCE INTERVAL	
	ESTIMATE	STD ERR	LOWER	UPPER
1ST PASS	0.995	0.473	0.043	1.947
BOOTSTRAP	1.000	0.083	0.832	1.168
DIFFERENCE	0.005=BIAS			

2c. Bristol Bay output continued

SUM OF LOGARITHMIC RESIDUALS FROM BASELINE FIT = 3.962

STANDARD DEVIATION OF RESIDUAL ERRORS USED IN BOOTSTRAP = 0.29

STANDARD DEVIATION OF RESIDUAL ERRORS FROM BASELINE FIT = 0.29

NUMBER OF MONTE CARLO REPLICATES = 1000

AVERAGE PERCENT BIAS OF MEAN LEGAL ABUNDANCE = -0.059

AVERAGE COEFFICIENT OF VARIATION OF LEGAL ABUNDANCE = 12.86

NUMBER OF NON-CONVERGENT TRIALS = 0

Table 4. Results of the Monte Carlo simulations of the two- and three- stage CSA. Results are for the St. Matthew Island stock.

Standard deviation of measurement error	Correlation of measurement error	Standard deviation of equation error	Bias of q estimates		Standard error of q estimates		Average % bias of legal abundance estimates		Average magnitude of the % bias of legal abundance estimates		Average CV of legal abundance estimates		Number of replicates that converged	
			2-stage	3-stage	2-stage	3-stage	2-stage	3-stage	2-stage	3-stage	2-stage	3-stage	2-stage	3-stage
0.3	0	0	-0.01	-0.03	0.11	0.11	-0.6	0.3	0.7	0.2	15.29	13.22	999	999
0.5	0	0	-0.01	-0.06	0.18	0.18	-2.2	-0.2	2.5	0.8	26.72	24.06	998	1000
0.7	0	0	-0.02	-0.10	0.25	0.24	-4.9	-2.5	5.3	2.8	38.36	37.35	995	998
0.9	0	0	-0.02	-0.14	0.31	0.30	-9.0	-6.4	9.7	6.3	51.02	54.94	995	983
0.3	0.5	0	-0.02	-0.04	0.11	0.11	0.7	1.4	0.6	1.2	14.71	13.42	1000	1000
0.5	0.5	0	-0.06	-0.09	0.17	0.18	0.8	2.4	1.4	2.4	25.66	24.66	999	1000
0.7	0.5	0	-0.08	-0.15	0.23	0.23	-0.9	1.1	2.8	4.5	37.96	39.37	997	995
0.9	0.5	0	-0.10	-0.21	0.29	0.29	-4.3	-2.2	6.1	7.0	50.93	59.55	979	985
0	0	0.1	0.01	0.00	0.04	0.04	-0.3	-0.3	0.4	0.4	11.00	12.83	988	983
0	0	0.3	0.07	0.05	0.14	0.14	-3.2	-5.2	3.2	5.2	46.69	58.94	989	931
0.3	0	0.1	-0.01	-0.03	0.12	0.12	-0.1	0.5	0.4	0.6	19.56	19.23	998	993
0.3	0.5	0.1	-0.02	0.00	0.11	0.04	0.6	1.3	0.5	1.3	19.28	19.41	1000	995

Table 5. Comparison of the two- and three-stage catch survey analyses.

	St. Matthew Island		Pribilof Islands		Bristol Bay		
	Two-stage	Three-stage	Two-stage	Three-stage	Two-stage 1975-1994	Two-stage 1973-1997	Three-stage 1973-1997
Catchability Coefficient	1.04	1.105	1.40	1.41	0.95	0.828	0.851
Degrees of Freedom	16	32	16	32	18	23	46
Sum of squared residuals	2.087	4.063	3.014	25.548	1.293	2.146	3.962
Mean Square Error	0.130	0.127	0.189	0.798	0.072	0.093	0.086

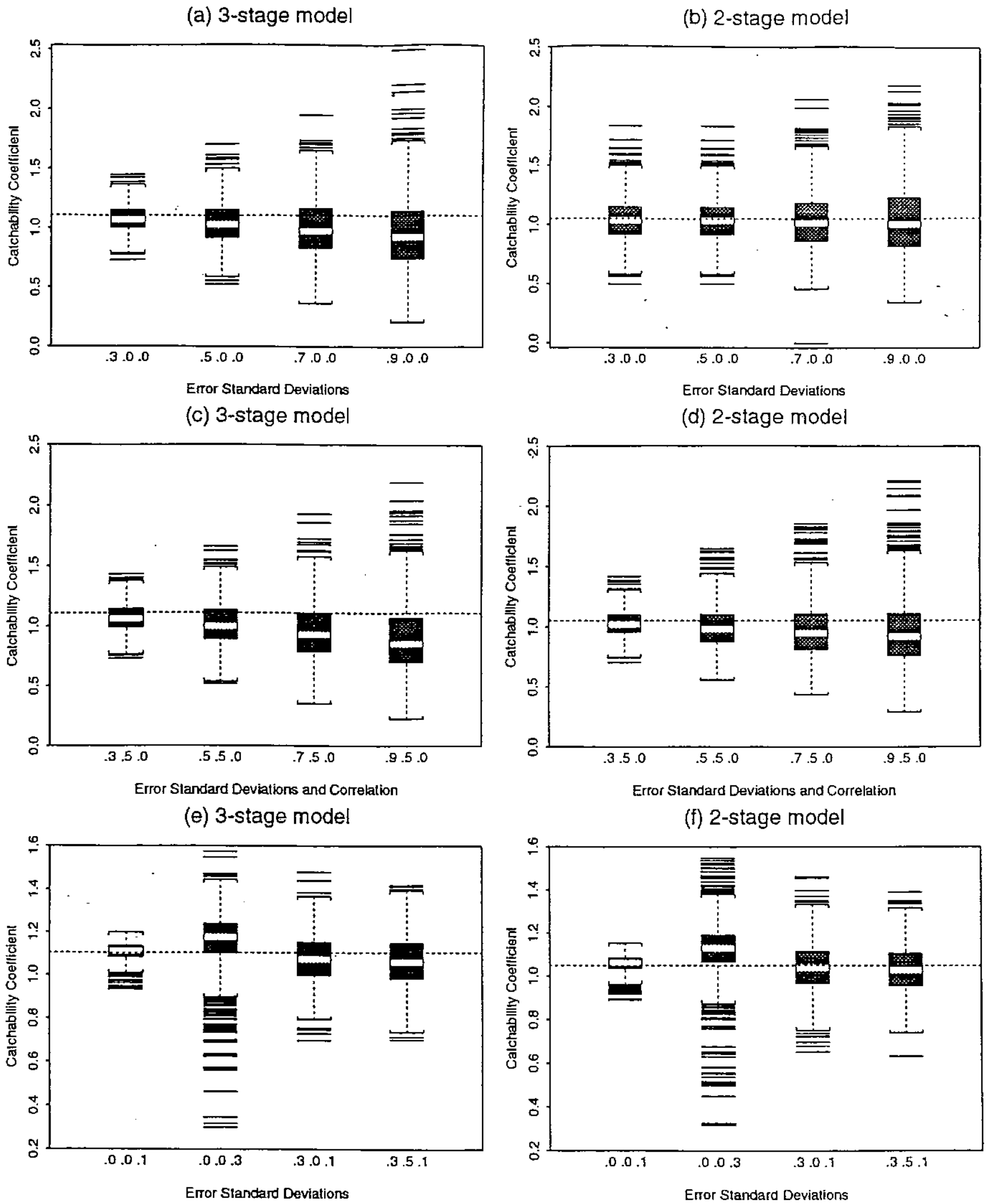

Figure 2. Distributions of the catchability coefficients estimated in the Monte Carlo simulations of the 2- and 3- stage CSA. Each box plot summarizes the distribution of 1000 q values. The white bar in the interior of the box is the median. The height of the box is equal to the interquartile distance (IQD). The whiskers extend 15X the IQD, or to the extreme range of the data, whichever is less. Individual lines beyond the whiskers are outliers. The three numbers under each box indicate the standard deviation of measurement errors, the correlation of measurement errors, and equation error standard deviation (from left to right).

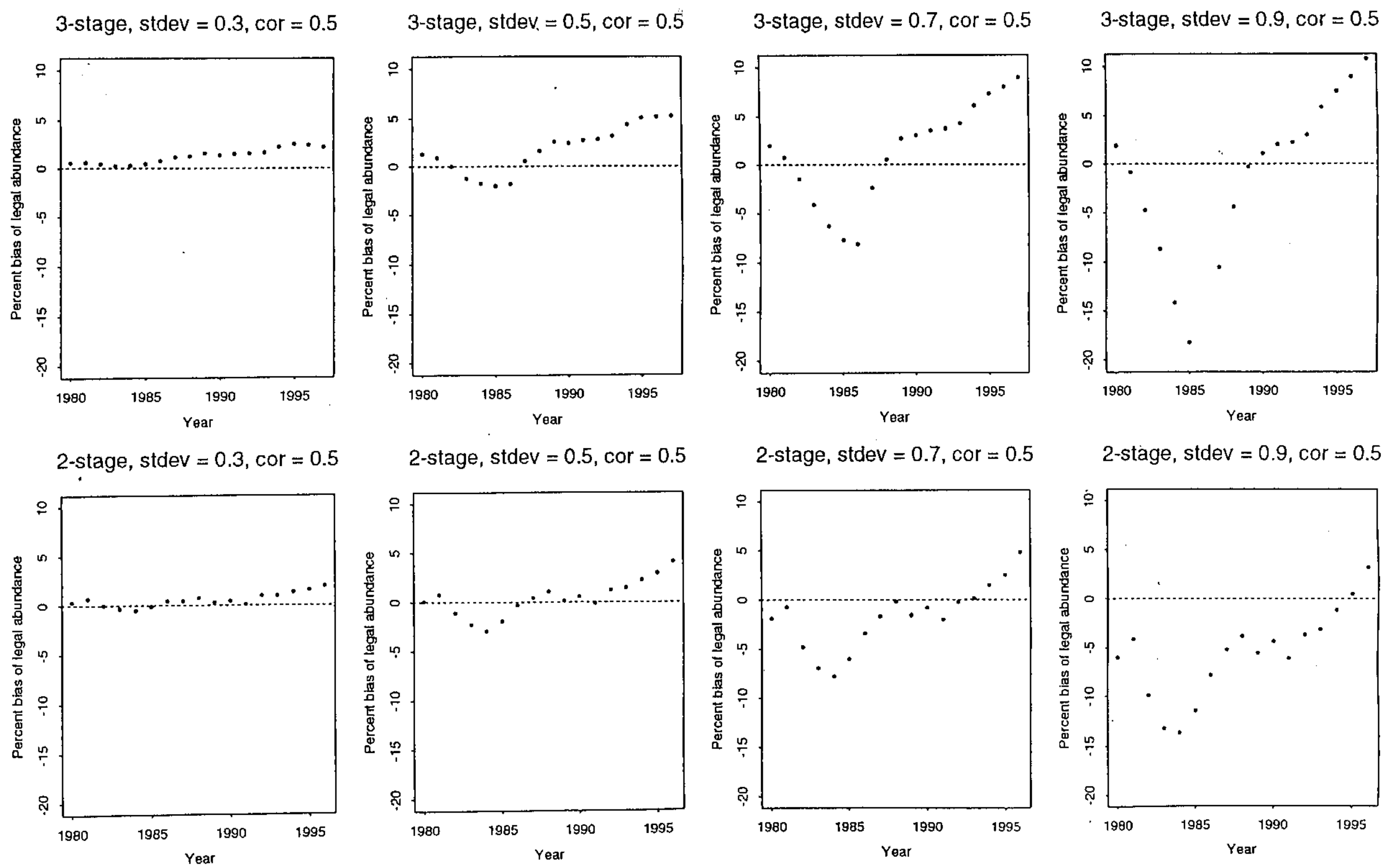

Figure 4. Percent bias by year of legal abundance from the Monte Carlo simulations with the two-stage and three-stage models with correlated measurement errors.

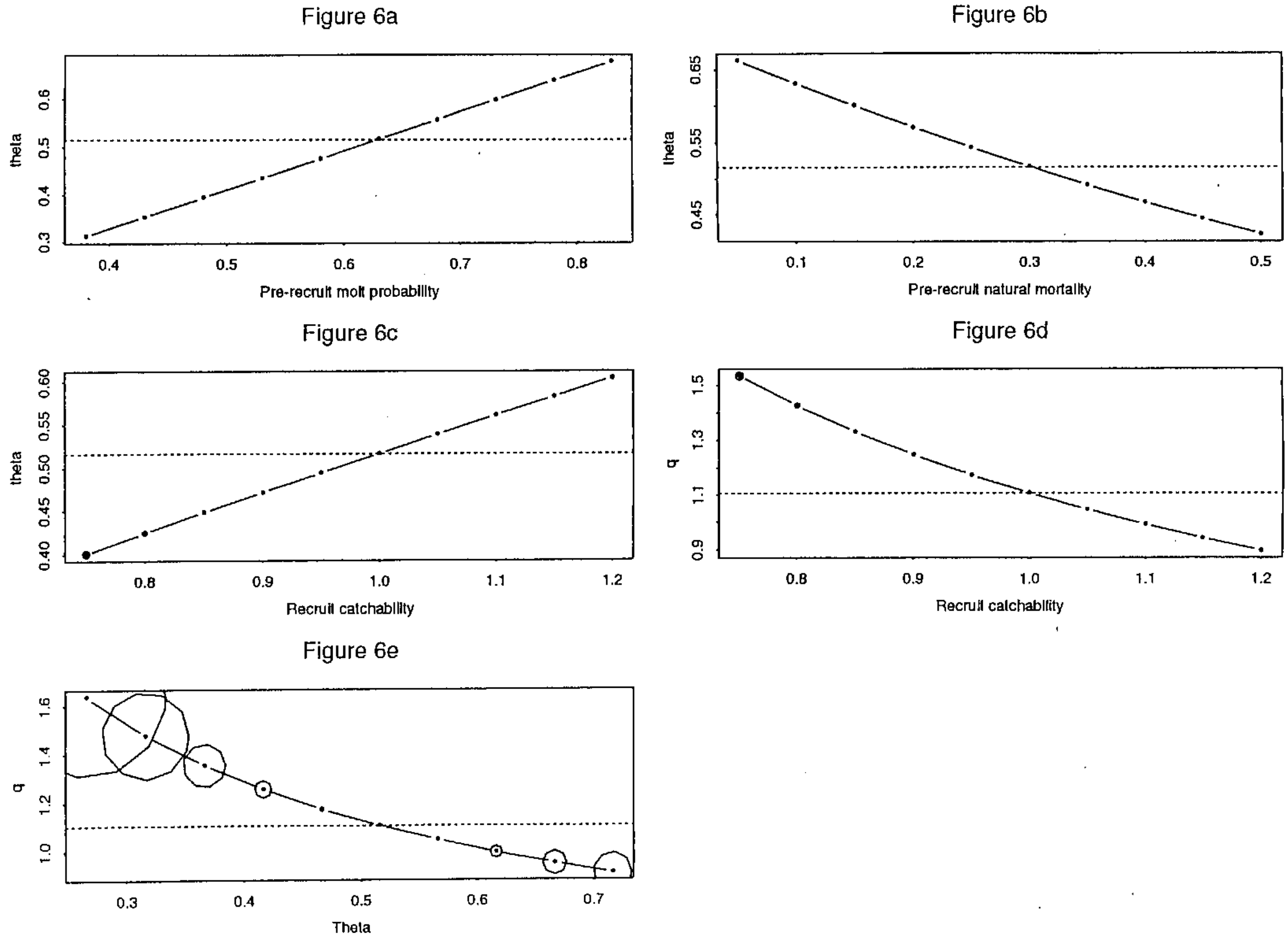

Figure 6. Sensitivity of the estimated post-recruit catchability coefficient (q) and pre-recruit catchability (θ) to errors in specifying the input values of pre-recruit molt probability, pre-recruit natural mortality, recruit catchability and θ. The correct values were $q = 1.105$, $\theta = 0.516$, molt probability = 0.63, natural mortality = 0.3, recruit catchability = 1.

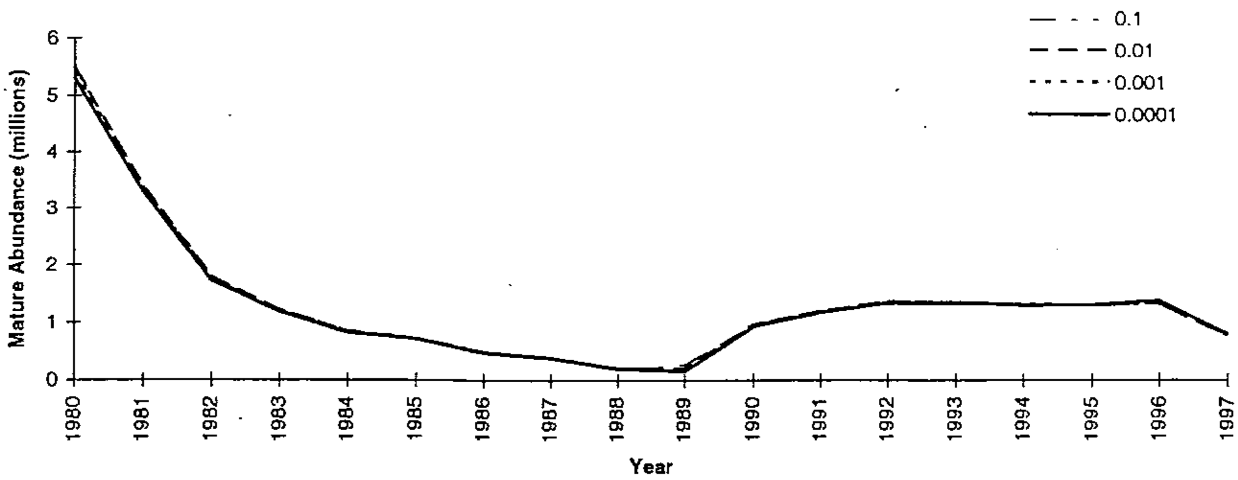

Figure 8a. Mature Crabs.

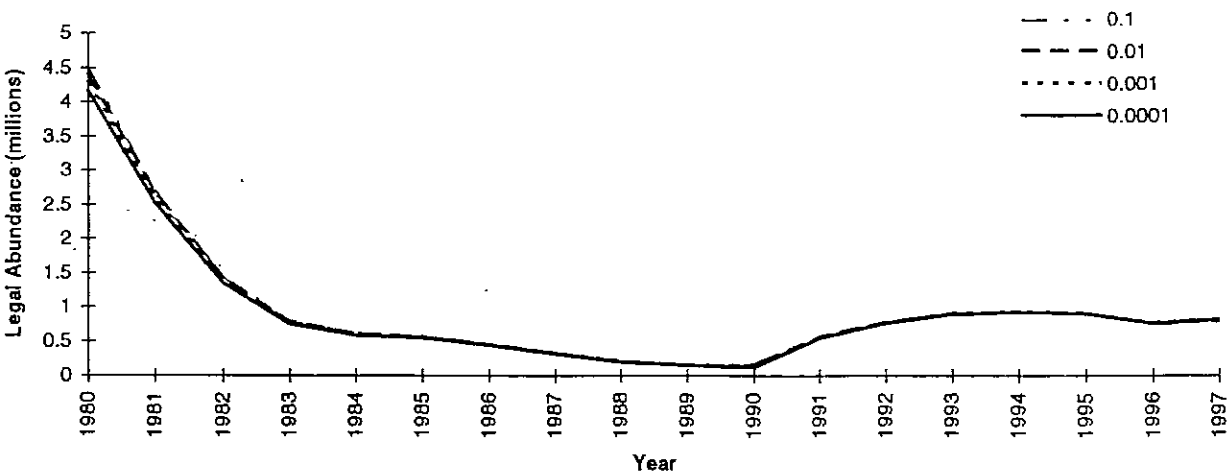

Figure 8b. Legal Crabs.

Figure 8. Comparison of the estimates of the Pribilof Islands blue king crab mature and legal crab abundance using a range of offset terms in the objective function.

Figure 12a. Bristol Bay Red King Crab Legal Abundance

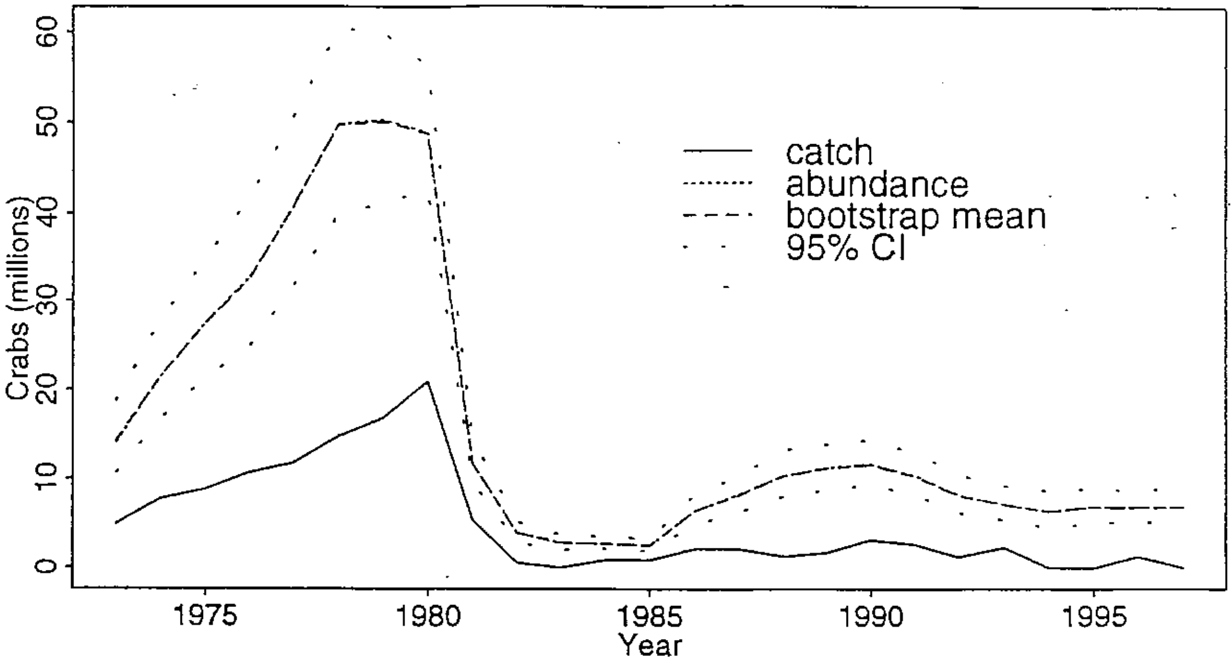

Figure 12b. Bristol Bay Red King Crab Mature Abundance

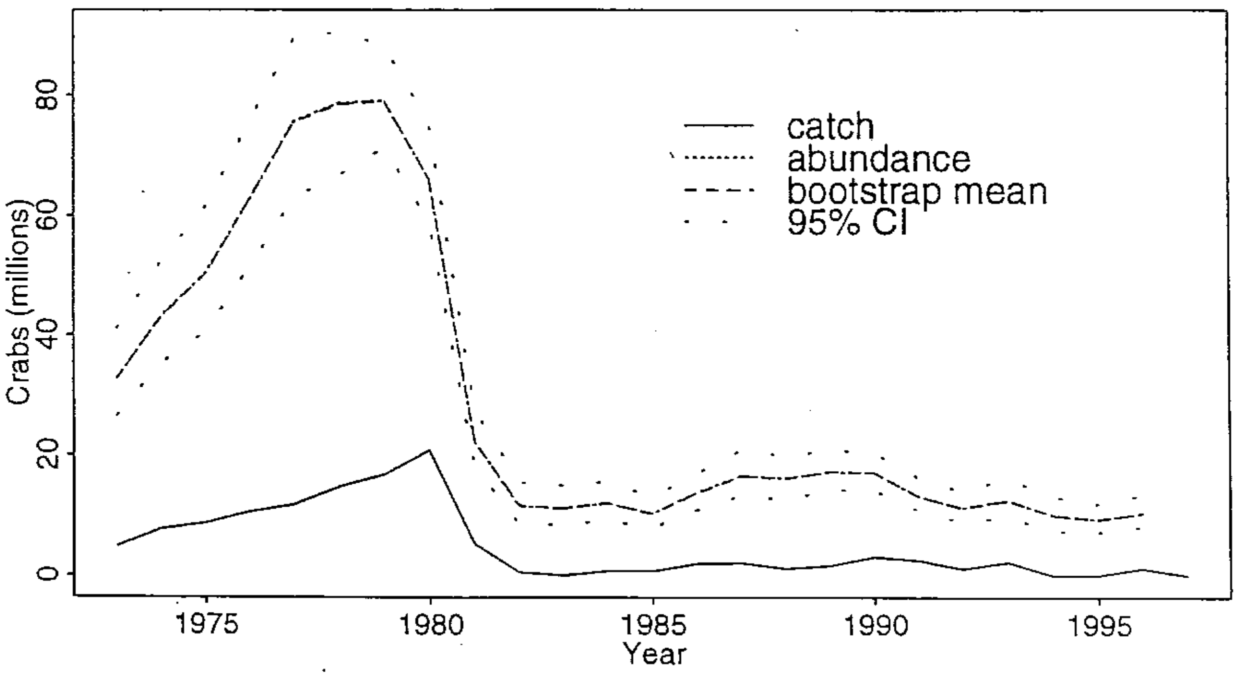

Figure 12. Legal and mature crab abundances and bootstrapped 95% confidence intervals for the Bristol Bay red king crab stock.