# Abundance Indices of Red Hind Collected in Caribbean SEAMAP Surveys from Southwest Puerto Rico 

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# Abundance Indices of Red Hind Collected in Caribbean 

 SEAMAP Surveys from Southwest Puerto RicoG. Walter Ingram, Jr.

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Since 1991 a fishery-independent survey under the support of the Southeast Area Monitoring and Assessment Program - Caribbean (SEAMAP-C) has been carried out in the southwest coast of Puerto Rico (P.R.). Pagán (2002) summarized these data, which are intended to be used for longterm monitoring of local fisheries, including abundances and ecology. Here this information was used to ascertain abundance trends of red hind to be used as input to stock assessment models.
For the SEDAR 35, the time series of data between 1991 and 2011 were used to develop abundance indices for red hind for the U.S. Caribbean off the southwest coast of Puerto Rico. Initially, SEAMAP-C data were evaluated to determine the efficacy of their use for development of abundance indices of areas around both Puerto Rico and the U.S. Virgin Islands, using multiple gear-types (handline and traps) and catch data-types (catch in numbers or weight). Preliminary analyses indicated a sparseness of complete catch and effort for red hind in the USVI area, sparseness in the continuity of the time series of the trap data, and a higher variability in the weight data. Therefore, handline catch-per-unit-effort (CPUE) data in numbers of rind hind collected off the southwest coast of Puerto Rico were used to develop abundance indices. Figure 1 shows the distribution of CPUE.

The delta-lognormal index of relative abundance ( $I_{y}$ ) as described by Lo et al. (1992) was estimated as

## (1) $I_{y}=c_{y} p_{y}$,

where $c_{y}$ is the estimate of mean CPUE for positive catches only for year $y ; p_{y}$ is the estimate of mean probability of occurrence during year $y$. Both $c_{y}$ and $p_{y}$ were estimated using generalized linear models. Data used to estimate abundance for positive catches (c) and probability of occurrence ( $p$ ) were assumed to have a lognormal distribution and a binomial distribution, respectively, and modeled using the following equations:
(2) $\ln (\mathbf{c})=\mathbf{X} \boldsymbol{\beta}+\boldsymbol{\varepsilon}$
and

$$
\begin{equation*}
\mathbf{p}=\frac{e^{\mathbf{X} \boldsymbol{\beta}+\varepsilon}}{1+e^{\mathbf{X} \boldsymbol{\beta}+\varepsilon}}, \text { respectively } \tag{3}
\end{equation*}
$$

where $\mathbf{c}$ is a vector of the positive catch data, $\mathbf{p}$ is a vector of the presence/absence data, $\mathbf{X}$ is the design matrix for main effects, $\boldsymbol{\beta}$ is the parameter vector for main effects, and $\boldsymbol{\varepsilon}$ is a vector of independent normally distributed errors with expectation zero and variance $\sigma^{2}$.

The GLIMMIX and MIXED procedures in SAS (v. 9.1, 2004) were used to develop the binomial and lognormal submodels, respectively. Similar covariates were tested for inclusion for both submodels: water depth (m), geographic spawning aggregation marine protected area (MPA) variable (" 0 " for outside MPA and " 1 " for inside MPA), spawning season variable [if month in $(12,1,2)$ then spawning season is " 1 ", otherwise spawning season is " 0 "'], and year. A backward selection procedure was used to determine which variables were to be included into each submodel based on type 3 analyses with a level of significance for inclusion of $\alpha=0.05$. If year was not significant then it was forced into each submodel in order to estimate least-squares means for each year, which are predicted annual population margins (i.e., they estimate the marginal annual means as if over a balanced population).

Therefore, $c_{y}$ and $p_{y}$ were estimated as least-squares means for each year along with their corresponding standard errors, $\operatorname{SE}\left(c_{y}\right)$ and $\operatorname{SE}\left(p_{y}\right)$, respectively. From these estimates, $I_{y}$ was calculated, as in equation (5), and its variance calculated as

$$
\begin{equation*}
V\left(I_{y}\right) \approx V\left(c_{y}\right) p_{y}^{2}+c_{y}^{2} V\left(p_{y}\right)+2 c_{y} p_{y} \operatorname{Cov}(c, p), \tag{4}
\end{equation*}
$$

where,

$$
\begin{equation*}
\operatorname{Cov}(c, p) \approx \rho_{\mathrm{c}, \mathrm{p}}\left[\operatorname{SE}\left(c_{y}\right) \operatorname{SE}\left(p_{y}\right)\right], \tag{5}
\end{equation*}
$$

and $\rho_{\mathrm{c}, \mathrm{p}}$ denotes correlation of $c$ and $p$ among years.
The backward selection procedure used to develop the delta-lognormal model is summarized in Table 1. All variables were retained in each submodel as highly significant (i.e. $p<0.0001$ ). Figure 2 summarizes indices of red hind, developed using a delta-lognormal model. Figures 3 and 4 provide diagnostics for each of the submodels in the index development. In Figures 3 and 4, the approximately normal distribution of the residuals of the submodels is indicated. Finally, a length-frequency histogram for red hind (Figure 5) collected during this survey was developed.

## Literature Cited

LO, N. C. H., L.D. Jacobson, and J.L. Squire. 1992. Indices of relative abundance from fish spotter data based on delta-lognormal models. Can. J. Fish. Aquat. Sci. 49: 2515-1526.

PAGÁN, F. E. 2002. Caribbean-SEAMAP Program Reef Fish Data Analysis Survey, Final Report. Prepared for UPR Sea Grant College Program/NMFS Cooperative Southeast Area Monitoring and Assessment Program - Caribbean (SEAMAP-C), University of Puerto Rico Sea Grant College Program, Mayagüez, Puerto Rico. 66 pages.

Figure 1. Distribution of CPUE (\# per 5 hook hours) for handlines in the SEAMAP-C Survey from 1991-2011. Nonzero CPUEs ranged from 0.77 to 70.72 red hind per 5 hook hours (white to red $=$ lowest to greatest CPUE). Note: numerous stations have the same latitude and longitude over the course of the time series, resulting in some stations being masked by others.


Table 1. Backward selection procedure for building delta-lognormal submodels for red snapper collected during Bottom Longline Surveys in the Gulf of Mexico.

| Model Run \#1 | Binomial Submodel Type 3 Tests ( AIC $=9542.2$ ) |  |  |  |  |  | Lognormal Submodel Type 3 Tests$(A I C=3040.7)$ |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Effect | Num $D F$ | Den $D F$ | Chi- <br> Square | F <br> Value | Pr $>$ ChiSq | $P r>F$ | Num <br> DF | $\begin{gathered} \text { Den } \\ D F \end{gathered}$ | F Value | $P r>F$ |
| year | 12 | 2065 | 172.39 | 14.37 | <. 0001 | <. 0001 | 13 | 1196 | 15.59 | $<.0001$ |
| spawning season | 1 | 2065 | 31.48 | 31.48 | <. 0001 | <. 0001 | 1 | 1196 | 51.70 | <. 0001 |
| spawning aggregation area | 1 | 2065 | 146.61 | 146.61 | $<.0001$ | <. 0001 | 1 | 1196 | 111.88 | <. 0001 |
| depth | 1 | 2065 | 66.79 | 66.79 | <. 0001 | <. 0001 | 1 | 1196 | 220.96 | <. 0001 |

Figure 2. Abundance indices for red hind collected during SEAMAP-C Surveys using handlines off southwest Puerto Rico. STDcpue is the index scaled to a mean of one over the time series. Obscpue is the average nominal CPUE, and LCI and UCI are $95 \%$ confidence limits. In the table below, the frequency listed is nominal frequency, $N$ is the number of bottom longline stations, Index is the abundance index in CPUE units, Scaled Index is the index scaled to a mean of one over the time series, $C V$ is the coefficient of variation on the index value, and $L C L$ and $U C L$ are $95 \%$ confidence limits.

STDcpue


|  | PLOT | $\leftrightarrow$ STDcpue$---U C I$ |  | LCI <br> obscpue |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Survey Year | Frequency | $N$ | Index | Scaled <br> Index | CV | LCL | UCL |
| 1991 | 1.00000 | 94 | 11.4812 | 3.12356 | 0.10921 | 2.51231 | 3.88352 |
| 1992 | 0.55807 | 353 | 5.6761 | 1.54423 | 0.06933 | 1.34451 | 1.77361 |
| 1993 | 0.63683 | 391 | 3.8949 | 1.05965 | 0.06174 | 0.93668 | 1.19878 |
| 1994 | 0.58960 | 346 | 3.9435 | 1.07286 | 0.06935 | 0.93408 | 1.23226 |
| 1995 | 0.34091 | 21 | 0.8398 | 0.22847 | 0.32135 | 0.12205 | 0.42768 |
| 1997 | 0.50926 | 216 | 5.0971 | 1.38672 | 0.09161 | 1.15500 | 1.66493 |
| 1998 | 0.71739 | 92 | 8.3987 | 2.28494 | 0.11251 | 1.82580 | 2.85954 |
| 1999 | 0.68508 | 181 | 4.6077 | 1.25357 | 0.08556 | 1.05674 | 1.48706 |
| 2000 | 0.42000 | 100 | 2.5857 | 0.70347 | 0.15401 | 0.51791 | 0.95551 |
| 2001 | 0.29268 | 82 | 0.4921 | 0.13387 | 0.20469 | 0.08927 | 0.20074 |
| 2005 | 0.39412 | 170 | 2.1517 | 0.58540 | 0.12060 | 0.46034 | 0.74443 |
| 2006 | 0.10526 | 57 | 0.2496 | 0.06790 | 0.10875 | 0.05466 | 0.08435 |
| 2010 | 0.19444 | 36 | 0.9580 | 0.26065 | 0.38386 | 0.12417 | 0.54711 |
| 2011 | 0.61538 | 13 | 1.0833 | 0.29471 | 0.32526 | 0.15630 | 0.55570 |

Figure 3. Diagnostic residual QQplot of the binomial submodel.


Figure 4. Diagnostic residual QQplot of the lognormal submodel.


Figure 5. Length frequency of red hind collected during SEAMAP-C Surveys using handlines off southwest Puerto Rico. $\mathrm{N}=8598$.


