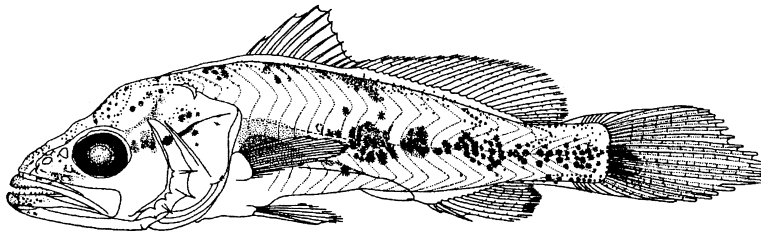




POWER ANALYSIS FOR DETECTING TRENDS IN JUVENILE SPOTTED SEATROUT  
ABUNDANCE IN FLORIDA BAY

BY

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The spotted seatrout (*Cynoscion nebulosus*) is considered a key species relative to the implementation of the Comprehensive Everglades Restoration Plan (CERP). One of the goals of the CERP is to increase freshwater flows to Florida Bay. Increased freshwater flows can have potential positive and negative impacts on spotted seatrout populations. At low salinities, the planktonic eggs of spotted seatrout sink to the bottom and are not viable (Alshuth and Gilmore, 1994; Holt and Holt, 2002). On the other hand, increased freshwater flows can alleviate hypersaline conditions that could result in an expansion of the distribution of the early life stages of spotted seatrout (Thayer et al., 1999; Florida Department of Environmental Protection<sup>1</sup>). Thus it would be useful to develop a monitoring program that can detect changes in seatrout abundance on time scales short enough to be useful to resource managers.

The NOAA Center for Coastal Fisheries and Habitat Research (NOAA) has made sporadic collections of juvenile seatrout using otter trawls since 1984 (see Powell et al, 2004). The results suggest that it might be useful to sample for seatrout in as many as eight different areas or basins (Figure 1): Bradley Key, Sandy Key, Johnson Key, Palm Key, Snake Bight, Central, Whipray and Crocodile Dragover. Unfortunately, logistical constraints are likely to limit the number of tows to about 40 per month over a period of six months each year. Inasmuch as few seatrout are caught in any given tow and the proportion of tows with zero seatrout is often high, it is important to determine how best to allocate this limited sampling effort among the various basins so that any trends in abundance may be detected with sufficient statistical confidence.

In developing an optimal sampling design one must be concerned with two types of errors: type 1, the conclusion that a trend exists when in fact it does not, and type 2, the conclusion that a no trend exists when in fact one does. Consider, for example, the case where the abundance of a population  $A$  is postulated to increase linearly with elapsed time  $t$  at a rate of  $r$  percent per year:

$$(1) \quad A_t = A_0 + rA_0(t - 1)$$

If the  $i$ 'th tow covers  $f_i$  units of bottom area and each unit of bottom area contains a proportion  $q$  of the total population, a possible model for the observed catch would be

$$(2) \quad c_i = (b_0 + b_1(t_i - 1))f_i + \varepsilon_i$$

where  $b_0$  is the intercept parameter ( $=qA_0$ ),  $b_1$  is the slope ( $=qrA_0$ ) and the  $\varepsilon_i$  are normally distributed observation errors with mean zero and standard deviation  $\sigma$ . In that case the maximum likelihood estimator for the slope  $b_1$  is

$$(3) \quad \hat{b}_1 = \frac{\sum_{i=1}^n (t_i - \bar{t})(c_i - \bar{c})}{\sum_{i=1}^n (t_i - \bar{t})^2}$$

where  $n$  is the total number of points in the regression and the overbar indicates the sample mean.

A trend in abundance is deemed to be statistically significant if the probability  $p$  is low that an estimate as large or larger than  $\hat{b}_1$  would be obtained if in fact the null hypothesis  $H_0$  were true (i.e., if the  $c_i$  were truly normal-distributed with mean  $b_0 f_i$  and standard deviation  $\sigma$ ). The  $p$ -level that defines ‘low’, often denoted by the symbol  $\alpha$ , is typically set at 0.05 or less. In cases where  $p > \alpha$ , it can be fairly stated that procedure failed to reject the null hypothesis of no trend. Many times, however, the failure to reject  $H_0$  is interpreted as acceptance of it. As Peterman (1990) pointed out, this jump in logic is not justified unless the probability of committing a type 2 error,  $\beta$ , is sufficiently low.

The quantity  $1-\beta$  is commonly referred to as the power of the statistical procedure. In this context it is the probability of correctly identifying the existence of a trend. In the case of equation 2, and its log-linear counterpart, Gerrodette (1987) has derived formulae expressing power as a function of  $n$ ,  $r$ ,  $\alpha$  and  $\sigma$ . However, the distribution of seatrout catches from the otter trawl is highly skewed and includes a large number of zeroes; hence, neither the normal or lognormal models are appropriate. Instead, the catches from most of the basins appear to follow the negative binomial distribution (Figure 2). Analytical formulae analogous to those of Gerrodette (1987) are difficult to derive for a negative binomial error structure. In this paper, we use simulations to determine the power of negative binomial-based regressions of equation 2 to detect various rates of increase.

## Methods

The simulated data were generated to resemble the actual historical distribution of catches (see Table 1) and assuming the density population was increasing at a linear rate according to equation 1. The expected catch per 1000m<sup>2</sup> in the first year,  $qA_0$ , was set equal the mean values observed during tows in the least productive basin (Crocodile Dragover, 0.1 trout per 1000m<sup>2</sup>) and most productive basin (Johnson Key and Sandy Key, 6 trout per 1000m<sup>2</sup>). The area  $f$  covered by any given tow was drawn with replacement from the distribution of historical values. Thus, the expected catch of the  $i$ 'th simulated tow in each basin was

$$(4) \quad E[c_i] = \begin{cases} 0.1 f_i (1 + r(t_i - 1)) & \text{Crocodile Dragover} \\ 6.0 f_i (1 + r(t_i - 1)) & \text{Johnson Key} \end{cases}$$

The observed catch corresponding to (4) was drawn with replacement from a Poisson distribution in the case of Crocodile Dragover and a negative binomial distribution with the dispersion coefficient  $K$  equal to 0.4 in the case of Johnson Key,

$$(5) \quad P[c_i] = \begin{cases} \frac{e^{-E[c_i]} E[c_i]^{c_i}}{\Gamma(c_i + 1)} & \text{Crocodile Dragover} \\ \frac{\Gamma(K + c_i)}{\Gamma(K)\Gamma(c_i + 1)} \left( \frac{E[c_i]}{E[c_i] + K} \right)^{c_i} \left( \frac{K}{E[c_i] + K} \right)^K & \text{Johnson Key} \end{cases}$$

The procedure indicated by equations 4 and 5 was repeated  $n$  times each year to simulate a data set

obtained from a regular sampling program in each area. A total of 500 data sets were so generated for each assumed level of  $r$  and  $n$ . The value of  $\alpha$  was fixed in all experiments to 0.05. The value of  $\sigma^2$  is implicit to the assumed distributions, being equal to  $E[c]$  in the case of the Poisson distribution and equal to  $E[c]+E[c]^2/K$  in the case of the negative binomial. The same number of samples were assumed to be taken each year.

Each simulated data set was analyzed using a negative-binomial based regression of the linear predictor in equation 2. Maximum likelihood estimates for the parameters ( $K$ ,  $b_0$  and  $b_1$ ) were obtained by minimizing the negative log-likelihood expression

$$(6) \quad L(C|b_0, b_1, K) = \sum_{i=1}^{nY} \ln \Gamma(c_i + 1) + \ln \Gamma(K) - \ln \Gamma(K + c_i) - c_i \ln \left( \frac{E[c_i]}{E[c_i] + K} \right) - K \ln \left( \frac{K}{E[c_i] + K} \right)$$

$$E[c_i] = f_i[b_0 + b_1(t_i - 1)]$$

where  $Y$  is the number of years, the offset  $f_i$  is treated as though it were known with negligible error and  $\Gamma$  represents the gamma function. The minimization was accomplished numerically using the routines provided in the software package AD Model Builder<sup>1</sup>.

The likelihood ratio test statistic  $\lambda$  was computed for each sample to determine if the value of the slope parameter was significantly different from zero:

$$(7) \quad \lambda = 2[L(C|\hat{b}_0, 0, K) - L(C|\hat{b}_0, \hat{b}_1, K)]$$

where  $\hat{b}_0$  and  $\hat{b}_1$  represent the maximum likelihood estimates. The value of  $\lambda$  is approximately Chi-Square distributed with 1 degree of freedom; hence, for  $\alpha = 0.05$ ,  $H_0$  is rejected when  $\lambda > 3.84$ . The power of the regression procedure to correctly identify an increasing trend was quantified by dividing the number of data sets where  $H_0$  was rejected (and the estimated slope was positive) by the total number of data sets analyzed (500).

## Results and Discussion

The statistical power of any test is a function of sample size  $n$ , sample distribution  $P(c)$  and the degree to which reality differs from  $H_0$  (here quantified by the magnitude of  $r$ ). Here we examined the effect of a range of values for  $n$  and  $r$  under two alternative distributions: a Poisson distribution with mean 0.1, representing the sparse, scattered population of seatrout in Crocodile Dragover basin, and a negative binomial distribution with high dispersion (low  $K$ ), representing the more dense, clumped populations in Johnson and Sandy Key basins.

The power of the regressions to detect changes in seatrout densities (power) after three years is summarized in Figure 3. It is apparent that, in sparsely populated areas like Crocodile Dragover, even 80 trawls per year are insufficient to allow detection of rapid changes in abundance with reasonable power (0.8 or above). The situation is somewhat better for more densely populated areas

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<sup>1</sup>Otter Research Ltd. 2001. An introduction to AD Model Builder Version 4.5. Box 2040, Sidney B.C. V8L 3S3, Canada. 141 p.

like the Johnson Key area, but even with 80 trawls per year the population would need to change by more than 50% per year in order to be detectable with a power of 0.8. The power curves for regressions based on nine years of data are more optimistic (Fig. 4). As few as 40 samples per year enabled the regressions to detect changes of 30% yr<sup>-1</sup> with high power, even in the sparsely populated Crocodile Dragover basin. Changes of only 10% yr<sup>-1</sup> could be detected in Johnson Key basin with 80 samples per year. Note that the power associated with nine years of sampling 20 times per year (180 total samples) is substantially greater than the power associated with three years of sampling 80 times per year (240 total samples), thus confirming the obvious point that regressions perform better with increasing contrast in the data.

Statistical power also depends on the probability of Type 1 error ( $\alpha$ ). Heretofore we have assumed  $\alpha$  will be set equal to the oft-used value of 0.05. However, the choice of  $\alpha$  ought to depend on the consequences of falsely rejecting the null hypothesis. As Peterman (1990) points out, the cost of type 2 errors often exceeds the cost of type 1 errors in the context of natural resource management. This argues in favor of developing sampling schemes that lead to a statistical power of at least  $1-\alpha$ . Alternatively, with a fixed sampling scheme one can effectively increase the power of the regression by increasing the value of  $\alpha$ . In effect, a large value of  $\alpha$  means one is more likely to reject  $H_0$ , and therefore more likely to ‘accept’ the alternative when it is true. To examine this, we repeated the above power analysis using a value for  $\alpha$  of 0.2 (Fig. 5). The power to discern low rates of increase was substantially improved for both basins, however 40 samples per year remained too few to enable powerful regressions with only three years of data.

In summary, if the goal is to detect long term changes in the abundance of juvenile seatrout in each basin, reasonable power will probably be achieved with 40 samples yr<sup>-1</sup> per basin. This is true even for relatively unproductive basins like Crocodile Dragover. However, in order to detect shorter-term changes (within 3 yrs) with reasonable power, then the number of samples will have to be increased. About 80 samples yr<sup>-1</sup> would seem to be sufficient for productive basins like Johnson Key, but more would be needed for unproductive basins like Crocodile Dragover.

The analyses presented may be overly pessimistic for the more densely populated areas like Johnson Key in that the observed distributions include the effect of inter-annual fluctuations in sea trout abundance and choice of sampling locations. In that case the sample variances will be inflated, resulting in underestimates of  $K$  and power. Unfortunately, there were insufficient samples from any given year to develop year-specific distributions for this study. However, it will be possible to develop more representative probability distributions after the first year of the proposed sampling, at which time the current power analysis can easily be updated.

Logistical constraints limit the number of samples to about 240 per year. Thus, the analyses above would suggest that only six areas can be sampled with sufficient intensity for powerful long-term regressions and only two or three areas with sufficient intensity for powerful short-term regressions. It may be advantageous to employ a stratified random sampling design where each basin (or even smaller unit) is sampled independently. While the estimates for the abundance trends in each basin may not be very powerful, the estimates for a combination of ecologically similar basins will be much more so. We suggest combining Johnson Key, Bradley Key, Sandy Key, and Palm Key basins as one area (Western zone), and Snake Bight, Central, Whipray, and Crocodile Dragover basins as another (Central zone). The Western zone is ecologically similar in seagrass composition and standing crop, sediment depth, tidal amplitude, circulation, and salinity and comprises the most productive juvenile spotted seatrout habitat in Florida Bay (Chester and Thayer,



1990). The Central zone is characterized as an area of restricted circulation, persistent hypersaline conditions and low spotted seatrout densities (Thayer and Chester, 1989; Orlando et al., 1997). It is also an area that could receive increased freshwater inflow from restoration activities, which may enhance juvenile spotted seatrout abundances if the frequency, duration, or spatial extent of hypersaline events is reduced (Thayer et al., 1999) or decrease egg viability if salinities become mesohaline (Alshuth and Gilmore, 1994; Holt and Holt, 2002). The Western zone will be used to establish an efficient annual abundance index that will monitor the health of the most productive spotted seatrout habitat in Florida Bay. The Central zone will be used to establish an annual abundance index that will monitor the potential changes in abundance of spotted seatrout in this area with regards to increased freshwater flow and correlate these changes with environmental correlates.

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**Table 1.** Sample statistics from historical trawls in the eight basins ( $n$  = number of trawls,  $\bar{f}$  = average area trawled in 1000 m<sup>2</sup>,  $\bar{c}_{obs}$  = mean of observed catch,  $\bar{c}_{std}$  = mean of standardized catch,  $V_{std}$  = variance in standardized catch,  $CV_{std}$  is the coefficient of variation,  $K$  is the negative binomial dispersion coefficient and  $\bar{c}_{1000}$  is the mean catch per 1000 m<sup>2</sup>. Negative binomial distributions with large (infinite)  $K$  values are equivalent to the Poisson distribution. Note that the variances and means of the observed catches are affected by the area swept by the trawl, which varied non randomly among samples for different basins (and within basins among years). To account for this the catches were standardized relative to the area covered during an average tow as described in the caption of Fig. 2.

Basin	$n$	$\bar{f}$	$\bar{c}_{obs}$	$\bar{c}_{std}$	$V_{std}$	$CV_{std}$	$K$	$\bar{c}_{1000}$
Bradley	14	0.86	1.57	2.29	34.53	2.57	0.16	3.06
Central	40	0.71	0.30	0.48	1.23	2.33	0.30	0.60
Crocodile	49	0.81	0.08	0.08	0.08	3.39	infinity	0.10
Johnson	19	0.69	4.58	4.42	31.15	1.26	0.73	5.93
Palm	1	0.20	2.00	7.00				10.03
Sandy	17	0.71	2.06	4.76	115.57	2.26	0.20	6.28
Snake	24	0.64	1.62	2.54	22.52	1.87	0.32	3.43
Whipray	49	0.76	0.10	0.12	0.15	3.18	0.52	0.13
Averages	213	0.74	1.54	2.71	29.32	2.42	0.37	3.70

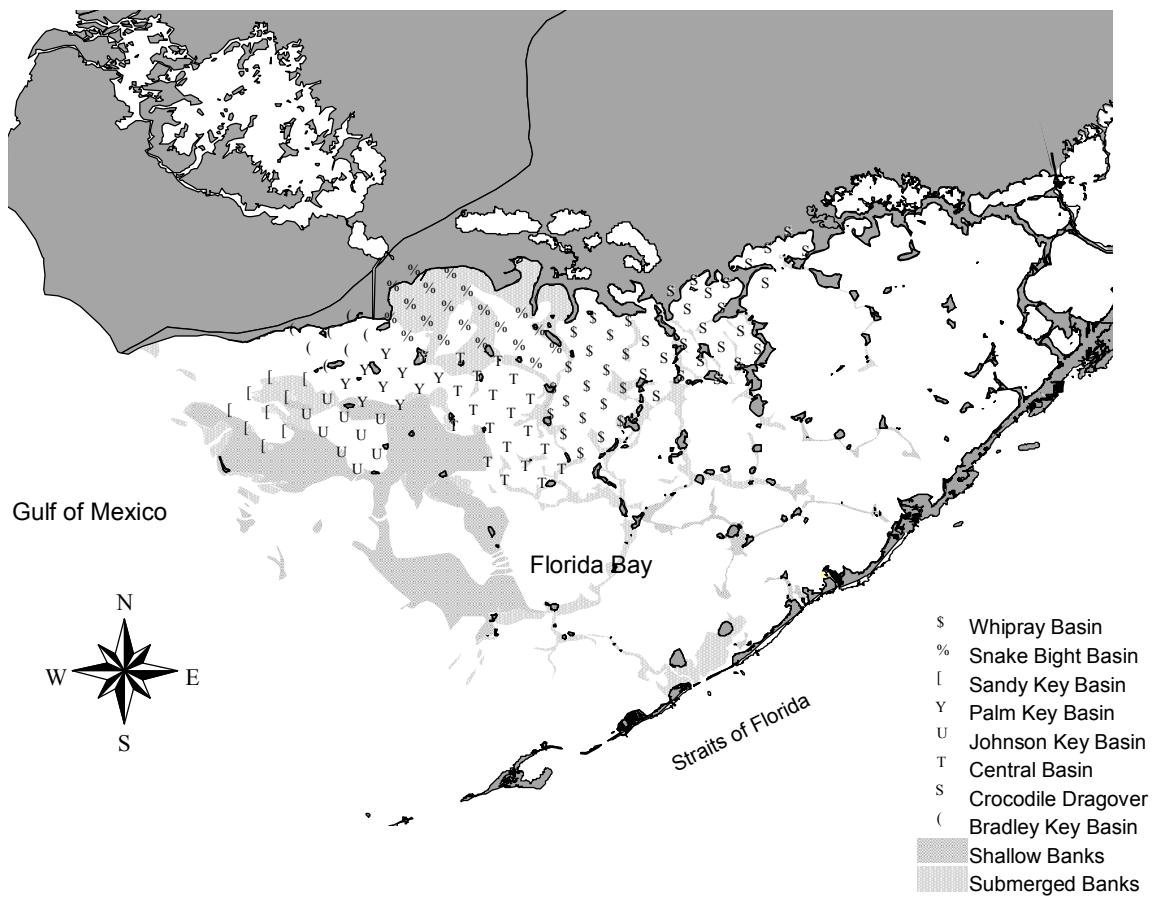
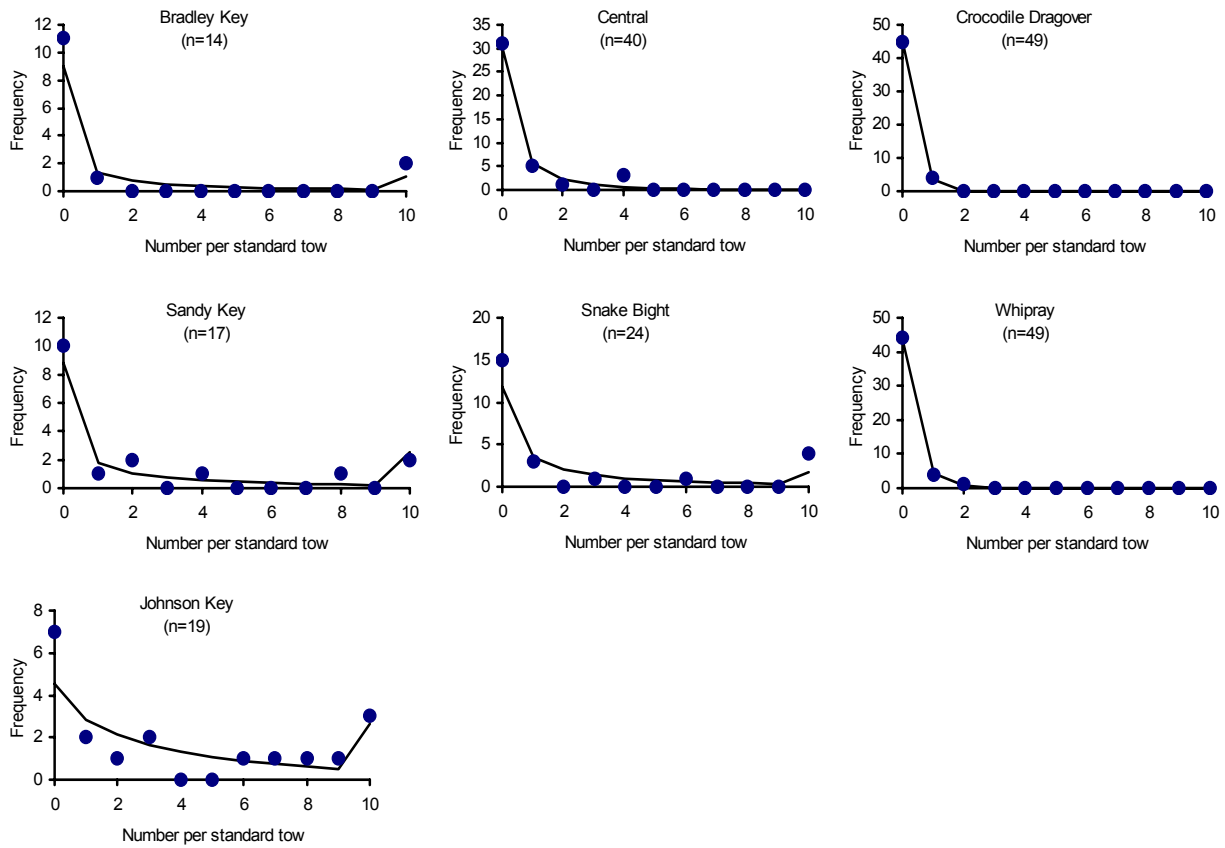


Figure 1. Location of sampling stations in Florida Bay. Each symbol is centered in a cell 1800m on a side. Samples were taken with a small otter trawl at the center of each cell (where possible). The area sampled was calculated from the distance towed and the mouth opening of the net.



**Figure 2.** Negative binomial distributions (lines) fit to historical catches of juvenile seatrout from each basin (dots). Inasmuch as the area swept varied considerably from sample to sample, the historical catches were standardized by dividing through by the area swept relative to the overall average. The dispersion coefficients were then estimated by fitting the negative binomial distributions to the adjusted historical catches. The fit is remarkably good considering that the samples were taken over several years at locations that varied non-randomly through time.

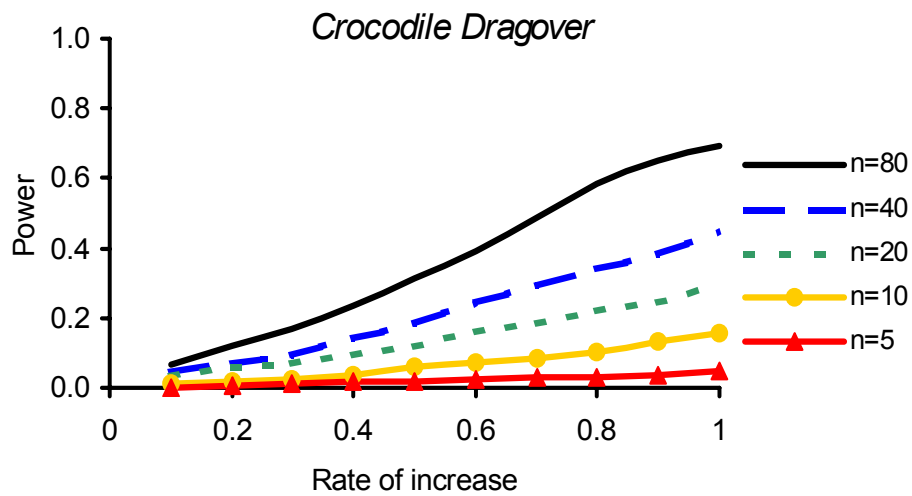
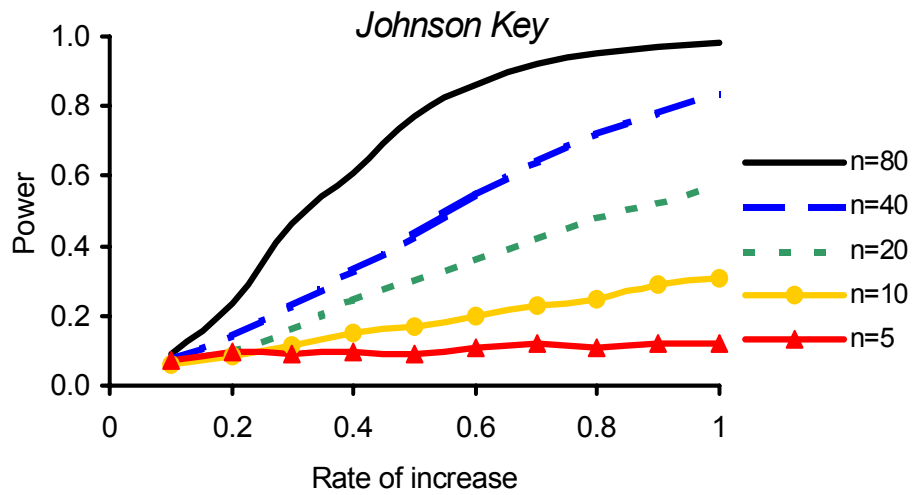


Figure 3. Power of negative binomial regressions to correctly discern the existence of an increasing trend in juvenile seatrout abundance after 3 years of sampling in areas with distributional characteristics resembling Crocodile Dragover and Johnson Key basins. The curves shown assume  $\alpha = 0.05$ .

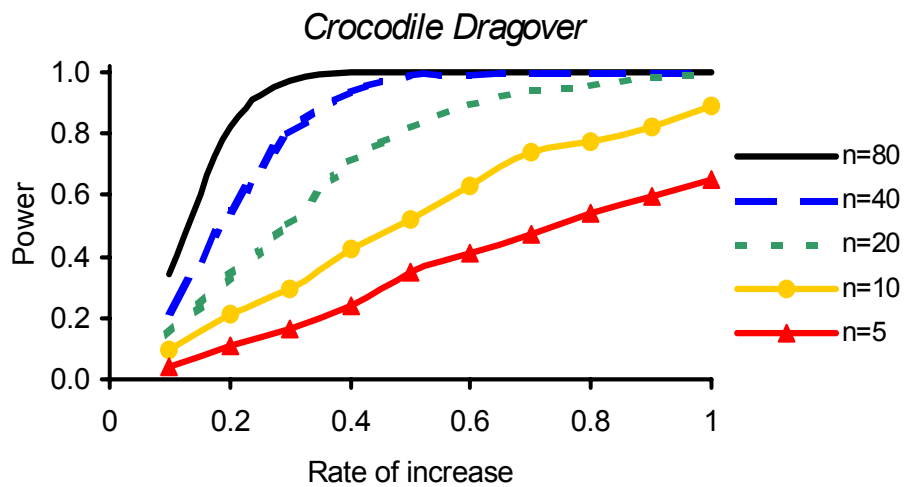
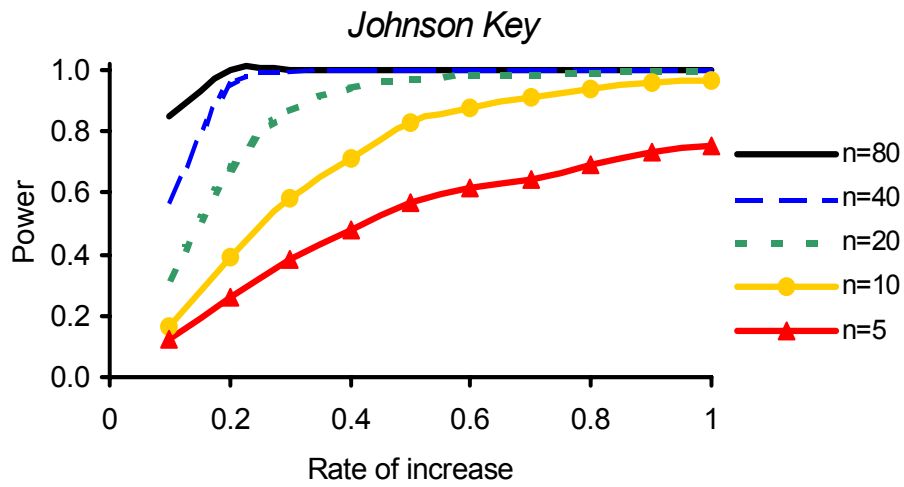


Figure 4. Power of negative binomial regressions to correctly discern the existence of an increasing trend in juvenile seatrout abundance after 9 years of sampling in areas with distributional characteristics resembling Crocodile Dragover and Johnson Key basins. The curves shown assume  $\alpha = 0.05$ .

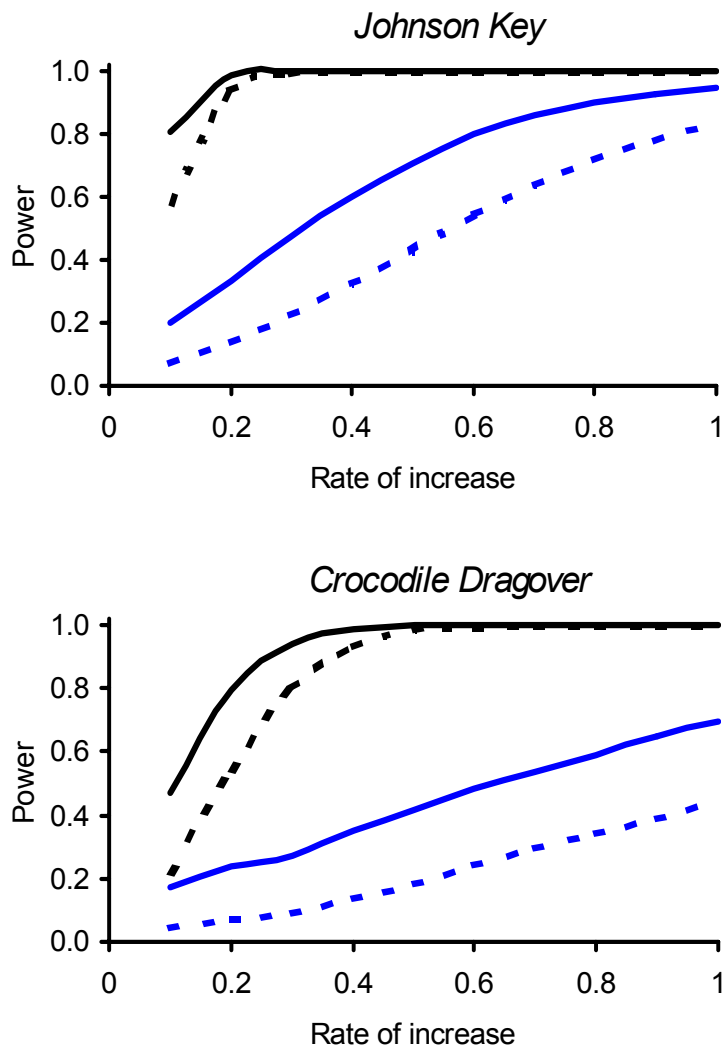


Figure 5. Power of negative binomial regressions to correctly discern the existence of an increasing trend in juvenile seatrout abundance when  $\alpha = 0.20$  (solid curves) and  $\alpha = 0.05$  (dotted curves). The top two curves represent a 9 yr sampling program and the bottom curves represent a 3 yr program (40 samples yr<sup>-1</sup>).