Integrating multiple data types from a novel gear combination into a standardized fisheries index for vermilion snapper (*Rhomboplites aurorubens*)

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Abstract

Standardized chevron trap sampling has been used since 1990 to monitor reef fish along the southeast Atlantic coast. Since 2011, video cameras have been paired with chevron traps creating two semi-independent fisheries indices. Here we develop a State-Space Model for vermilion snapper to combine both chevron trap catches and video counts into a single integrated index for stock assessment. The index spans the time frame of 1990-2016 and accounts for variation in sampling efficiency of both sampling gears as well as covariates describing the spatial distribution of fish. The index is meant to describe population trends of vermilion snapper in the region. Index values for 2015-2016 include a calibration factor to account for a change in camera type.

Background

Many economically important reef fish species along the southeast US Atlantic coast have been monitored using fishery-independent chevron fish traps since 1990. Since 2011, cameras have been attached to chevron traps to provide an additional index of reef fish abundance. Early research comparing trap catches to video counts showed substantial variation between the two (Bacheler et al. 2013), likely due to differences in how environmental conditions influenced the ability of traps and videos to detect various species of fish (Bacheler et al. 2014, Coggins et al. 2014). For instance, vermilion snapper and gray triggerfish were more likely caught in traps when water temperature was warm, and observed on video when water was clear (Bacheler et al. 2014). At a 2015 stock assessment workshop for red snapper and gray triggerfish (SEDAR 41), chevron trap and video data were used to compute separate indices of abundance that were subsequently combined following the method of Conn (2010). Workshop attendees noted that the gears lacked independence since cameras were attached to traps, but attendees were also unwilling to discard one of the indices because no other fishery-independent indices were available and because both gear types were considered informative. The method we propose here combines trap and video data into a single time series while accounting for the lack of independence between the two gears.

One methodological approach to combine trap and video data is through the use of hierarchical model structures that can separate aspects of the ecological process of interest from aspects of the observation process (Gelman et al. 2007, Royle and Dorazio 2008). There are few effective ways to achieve this separation with count-based data, but two examples include *N*-mixture models (Royle 2004) and State-Space Models (SSM, Schnute 1994). The application of *N*-mixture models to fish is fairly new in the fisheries literature and quite rare (but see Webster et al. 2008, Flowers and Hightower 2013, Chambert et al. 2016, Scheerer et al. 2017). The paucity of examples of *N*-mixture models applied to fish is likely a result of the stringent assumptions required by these models. Because *N*-mixture models rely on the variance of replicate count data to separate the abundance from the detection process, strict population closure and a binomial sampling process are required for useful model performance (Barker et al. 2017). Indeed, preliminary analysis of vermilion snapper data indicated random extra-binomial variation in the replicate camera counts and dependence of the camera counts on the chevron trap due to its depleting effects on the local abundance during the first ~100 min of sampling.

Alternatively, State-Space Models have a long history in fisheries (e.g. Schnute 1994, Maunder et al. 2013, Shertzer et al. 2016) and have been applied to integrate multiple data types into a single index (e.g. Conn 2010, Staton et al. 2017). Because SSMs do not rely on the assumption of binomial sampling to estimate "true" abundance and detection probability, they require fewer assumptions. SSMs are typically applied to time series data and assume that catch (trap catch or camera counts) is a random variable drawn from a specified distribution with a mean that is equal to the true relative abundance each year. For the parameters of this model to be estimable, the assumption is also made that the true relative abundance is non-independent among years, which is a biologically valid assumption for most biota with multi-year lifespans.

Here we develop a novel fishery-independent index of abundance for vermilion snapper in the US South Atlantic through the development and application of a State-Space Model using trap and video data collected by the Marine Resources Monitoring, Assessment, and Prediction (MARMAP) program (1990-2016) and the Southeast Fishery-Independent Survey (2010-2016). Collectively, these two fishery-independent sampling programs are referred to as the Southeast Reef Fish Survey (SERFS). The SSM has three key features that make it particularly useful for this application: (i) The model incorporates the chevron trap catches and camera counts into a single index and has the potential to incorporate additional information as available. (ii) The model corrects for shifts in the sampling frame by modeling temporal variation at the meta-population level separate from spatial variation at the sub-population level. (iii) The model corrects for changes in sampling efficiency due to temporal and spatial variation in the environment through the use of covariates of detection and random effects.

Data and Treatment

There were 15,629 chevron trap samples available covering a period of 27 years (1990-2016). For the time period of 2011-2016, the chevron traps were fitted with a video camera resulting in 7,644 41-frame video samples available. For analysis, we used un-transformed catch of the chevron trap and the sum of the counts across the 41 camera frames (*SumCount*). We chose to use the *SumCount* of the camera data because (i) preliminary analysis indicated that modeling each of 41 camera frames for each video sample substantially increase computation time, (ii) *SumCount* changes linearly with the mean count (Bacheler and Carmichael 2014), which is often the preferred camera metric (Conn 2011, Schobernd et al. 2014), and (iii) using the *SumCount* preserves the discrete nature of the camera counts allowing for the use of derivations of the Poisson distribution to describe both the chevron trap and camera observation processes.

We applied several data filters to either simplify predictor variables, remove records with missing predictor variables, or to remove unusual values. We removed any data points in which the survey video was considered unreadable by an analyst (e.g., too dark, corrupt video file), or if the trapping event was flagged for any irregularity that could have affected catch rates (e.g., trap dragged or bounced). Additionally, any survey video for which fewer than 41 video frames were read (*n* =150) was removed from the full data set. Standardizing the number or readable frames for any data point was essential due to our use of *SumCount* as a response variable. We also identified any chevron trap or video sample in which corresponding predictor variables were missing and removed them from the final data set. After the filtering process, the final data set contained 13,903 chevron trap samples, of which 6,767 had corresponding video camera samples (Table 1).

The Model

We fit the chevron trap catch and video *SumCount* data to a State-Space Model (SSM) that described patterns in vermilion snapper relative abundance through space and time. Our SSM was formulated in a hierarchical framework with a sub-model that described patterns in "true" relative abundance and two secondary sub-models that described the observation of the "true" relative abundance with chevron traps and video cameras. By modeling the abundance process and observation process with separate sub-models we were able to separate observation error from process error and account for some aspects of systematic variation in sampling efficiency (i.e. detection probability).

Our model describes changes in the standardized relative abundance (hereafter referred to simply as abundance, N_t) from year to year with an exponential growth model as:

$$\log(N_t) = \log(N_{t-1}) + r_t \tag{1}$$

where r_t represents the log-scale change in abundance between time *t*-1 and time *t*. Abundance was treated as an unobserved (latent) variable, and represents the time series of primary interest (i.e., the standardized index). The parameter r_t was modeled as a random variable on the log scale drawn from a normal distribution as:

$$r_t \sim \text{Normal}(\bar{r}, \sigma) \tag{2}$$

where $\bar{r}$ is the expected population change between time *t*-1 and *t*, and σ is the standard deviation, representing the magnitude of process error.

Spatial variation in abundance across sample sites each year was modeled as:

$$n_{s,t} = \log(N_t) + cov_{s,t}^{n} + \varepsilon^{abun} \tag{3}$$

where the term $\log(N_t)$ is the year specific intercept of the linear model, $cov_{s,t}^{n}$ is a linear combination of spatial covariates, and ε^{abun} describes random spatial variation in abundance that is unexplained by the covariate structure.

We approximated the chevron trap catches ($c_{s,t}^{trap}$) and the camera *SumCounts* ($c_{s,t}^{cam}$) as deviates drawn from Poisson log-Normal distributions, which are similar in character to negative binomial distributions (Nitzoufras 2009, p. 315-317), but can demonstrate better mixing properties than negative binomial distributions when applied in Bayesian programs such as JAGS. We specified these models as:

$$c_{s,t}^{trap} \sim \text{Poisson}\left(e^{n_{s,t}+cov_{t,j}^{trap}+\varepsilon^{trap}}\right) \tag{4}$$

$$c_{s,t}^{cam} \sim \text{Poisson}\left(e^{n_{s,t}+cov_{t,j}^{cam}+\varepsilon^{cam}+\nu_t}\right) \tag{5}$$

where the mean on the log scale is the site-specific abundance $n_{s,t}$ plus a linear combination of environmental and sampling covariates (i.e. $cov_{t,j}^{trap}$ and $cov_{t,j}^{cam}$) to account for systematic variation in sampling efficiency. The parameters ε^{trap} and ε^{cam} are gear-specific log Normal distributed random observation errors modeled as, $\varepsilon_{s,t} \sim Normal(0,\sigma)$, with a mean of zero and an estimated standard deviation specific to each sampling method (i.e. σ^{trap} and σ^{cam}). The parameter ν_t is a fixed value (i.e. log(1.72)) that accounts for the increased field of view of the video cameras used in 2015 and 2016.

Model Covariates

We incorporated a suite of covariates into our abundance and observation models. We selected covariates based on two key considerations. Our first consideration was to separate covariates that influenced the spatial distribution of fish from those that influenced temporal patterns in fish abundance. This was important because spatial and temporal patterns of abundance are modeled in two separate hierarchical layers (i.e. equation 1 and 3) to create a distinction between the fishery index, i.e. temporal patters in abundance at the meta-population level (N_t), from spatial variation in the data due to patterns in the spatial distribution of fish and shifts in the sampling frame through time ($n_{s,t}$). Thus, we include a main and quadradic effect of latitude (*lat* and *lat*^{2}), longitude (*lon* and *lon*^{2}) and depth (*depth* and *depth*^{2}), as well as the potential interaction between latitude and longitude as:

$$\begin{aligned} cov_{s,t}^{n} = {} & \beta_1 lat_{s.t} + \beta_2 lat_{st}^2 + \beta_3 depth_{s,t} + \beta_4 depth_{s,t}^2 + \beta_5 lon_{s,t} + \\ & \beta_6 lon_{s,t}^2 + \beta_7 lat_{s,t} lon_{s,t}. \end{aligned} \tag{6}$$

Our second key consideration was to separate covariates of the abundance and detection processes. This was important because our model likely has limited ability to disentangle systematic patterns in abundance from systematic patterns in detection when they are similar. Thus, we do not expect to be able to resolve the effects of covariates that have similar influences on patterns in abundance as they do on patterns in detection (Barker et al. 2017). Under this consideration, the most useful covariates for predictive purposes are those that either, (i) only influence the abundance or the detection process, or (ii) have very different influences on the abundance and detection processes. Thus, we included main and quadratic effects of trap soak time (*E* and *E*^{2}), main and quadradic effects of temperature (*temp* and *temp*^{2}), water turbidity (*turb*), percent hardbottom substrate (*sub*), bottom relief (*relf*), current direction (*dir1* and *dir2*), and attached biota (*bio*) into our chevron trap observation model as:

$$\begin{aligned} cov_{s,t}^{trap} = {} & \eta_1 E_{s,t} + \eta_2 E_{s,t}^2 + \eta_3 temp_{s,t} + \eta_4 temp_{s,t}^2 + \eta_5 turb_{s,t} + \eta_6 sub_{s,t} + \\ & \eta_7 relf_{s,t} + \eta_8 dir1_{s,t} + \eta_9 dir2_{s,t} + \eta_{10} bio_{s,t}. \end{aligned} \tag{7}$$

In the camera detection sub-model, we included turbidity, current direction, main and quadratic effects of bottom temperature, percent hardbottom substrate and attached biota as:

$$\begin{aligned} cov_{s,t}^{cam} = {} & \varphi_1 + \varphi_2 turb_{s,t} + \varphi_3 dir1_{s,t} + \varphi_4 dir2_{s,t} + \varphi_5 temp_{s,t} \\ & + \varphi_6 temp_{s,t}^2 + \varphi_7 sub_{s,t} + \varphi_8 relf_{s,t} + \varphi_9 bio_{s,t} \end{aligned} \tag{8}$$

where φ_1 allows for a systematic difference in the detection probability of the camera relative to the chevron trap. All covariates definitions are provided in Table 2 and JAGS model code is provided in Appendix A.

Model Fit Test

We evaluated the fit of eight general model error structures using a posterior-predictive check (Hooten and Hobbs 2015, Broms et al. 2016). The eight model error structures included models that either included or excluded the random variables ε^{abun}, ε^{trap}, and/or ε^{cam}. Because these parameters are random effects, they offer little predictive advantage when included in our models, however, evaluating how their inclusion or exclusion impacts general model fit is necessary to accurately describe the magnitude and shape of the residual error, to partition the residual error between biological and observation processes and to appropriately estimate the uncertainty in our model predictions (Kery and Schaub 2012).

To perform the model fit evaluation, we first randomly selected 100 data points from each of six data categories to validate the fit of our models. Our categories were, (i) trap catches = zero prior to 2011, (ii) trap catches = zero post 2010, (iii) trap catches > zero prior to 2011, (iv) trap catches > zero post 2010, (v) camera *SumCounts* = zero, and (vi) camera *SumCounts* > zero. We expected that understanding how our model fit each of these data types would provide comprehensive insight into the model's ability to back predict our fishery index. For each selected data point, we simulated the corresponding trap or video count from the posterior distributions of our model parameters and calculated a Pearson Chi-squared statistic for each simulated and observed data point. We then summed the Chi-squared values across data category to create six fit metrics. To assess whether the observed values of the fit metrics were likely given the assumptions of the models, we used the posterior samples of the simulated data to approximate the sampling distribution of these statistics for each data point. We reported the total number of validation data points where the observed Chi-squared statistic (χ^2) was within the 95% credible intervals of its predicted distribution for each data type.

Variable Selection

We assessed the importance of different covariates for describing variation in counts for the model with the simplest error structure judged to adequately fit the data. We expected that information theoretic approaches to variable selection, such as AIC and DIC, would likely be unreliable when applied to our SSM because of the complex nature of the hierarchical structured random effects (Celeux et al. 2006, Millar 2009, Hooten and Hobbs 2015, Broms et al. 2016). Thus, we applied two alternative procedures for comparison. The first procedure was a Bayesian mixture model approach where each covariate effect parameter is multiplied by an “inclusion parameter” in the model (Royle and Dorazio 2008). The inclusion parameter is a Bernoulli trial with a prior probability of 0.5. When the parameter takes the value of one, the covariate influences the likelihood and when the parameter takes the value of zero it does not. The mean of the posterior sample of the inclusion parameters represents the probability that the “best” model includes the covariate. Values ≥ 0.5 indicate that models including the covariate have optimal predictive properties (Barbieri 2004). Thus, we used inclusion probabilities of ≥ 0.5 as an approximate indicator of statistical significance of the parameter. An added benefit of this variable selection procedure is that all model predictions are automatically model averaged. However, the procedure can substantially increase the time needed to perform the necessary MCMC iterations and the results can be sensitive to priors (Hooten and Hobbs 2015). The second method of variable selection was a simplified procedure based on credible interval overlap with zero that is common in the ecological literature (e.g., White et al. 2013, Beesley et al. 2014, King et al. 2016). Thus, for the simplest error structure with adequate fit, we evaluated support for each covariate by assessing if the 95% Bayesian credible intervals overlap with zero. Parameters whose 95% credible intervals excluded zero were considered ‘statistically significant.’

Model Fitting Methods

The posterior distributions of all parameters were estimated using a Gibbs sampler implemented in JAGS (Plummer 2003). We called JAGS from program R (R Core Team 2015) using the library R2jags (Su and Yajima 2015). All prior distributions of log-scale covariate effect parameters were specified as diffuse normal distributions. Standard deviation parameters were specified as Gamma distributions with shape parameters equal to 0.01 and were verified to not influence the range of posterior distributions. Inference was drawn from 10,000 posterior samples taken from two chains of 500,000 samples. We discarded the first 250,000 values of each chain to remove the effects of initial values and thinned the chain to every 50th value. Convergence of all models was diagnosed by visual inspection of trace plots and Gelman-Rubin statistic ($\hat{R} \leq 1.1$ indicate model convergence, Gelman et al. 2004).

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Appendix A. State-Space Model JAGS code

```
model{
#PREDICTIONS FOR MODEL FIT
 for(i in 1:400){
 tc.exp[i] <- trp_exp[ttnum[i]]
 tc.pred[i] ~ dpois(trp_exp[ttnum[i]])
 }
 for(i in 1:200){
 cc.exp[i]  <- cam_exp[ccnum[i]]
 cc.pred[i] ~ dpois(cam_exp[ccnum[i]])
 }
#MODEL FOR TIME PERIOD 2011-2016
 #CAMERA OBSERVATION MODEL
 for(i in 1:cn){
 cc[i] ~ dpois(cam_exp[i])
 cam_exp[i] <- exp(N[i]+log_pc[i]+epic[i]+camcorr[i])
 epic[i] ~ dnorm(0,tau[2]) T(-10,10)
 #TRAP OBSERVATION MODEL
 tc[i] ~ dpois(trp_exp[i])
 trp_exp[i]  <- exp(N[i]+log_pt[i]+log_ptc[i]+epit[i])
 epit[i] ~ dnorm(0,tau[1]) T(-10,10)
 #ABUNDANCE MODEL
 N[i] <- lam_cov[i] + Npred[year[i]] + epin[i]
 epin[i] ~ dnorm(0,tau[4]) T(-10,10)
 }
#MODEL FOR TIME PERIOD 1990-2010
 for(i in (cn+1):n){
 #TRAP OBSERVATION MODEL
 tc[i] ~ dpois(trp_exp[i])
 trp_exp[i]<- exp(N[i]+log_pt[i]+epit[i])
 epit[i] ~ dnorm(0,tau[1]) T(-10,10)
 #ABUNDANCE MODEL
 N[i] <- lam_cov[i] + Npred[year[i]] + epin[i]
 epin[i] ~ dnorm(0,tau[4]) T(-10,10)
 }
#COVARIATE VECTORS
 #Abundance covariates
  lam_cov[1:n] <- w[1]*bet[1]*lat[] + w[2]*bet[2]*lat2[] + w[3]*bet[3]*depth[] +
              w[4]*bet[4]*depth2[] + w[5]*bet[5]*lon[] + w[6]*bet[6]*lon2[] +
              w[7]*bet[7]*lat[]*lon[]
 #Trap detection covariates
  log_pt[1:n] <- w[8]*eta[1]*effort[] + w[9]*eta[2]*effort2[] + w[10]*eta[3]*temp[] +
             w[11]*eta[4]*temp2[]
  log_ptc[1:cn] <- w[12]*eta[5]*turb[] + w[13]*eta[6]*substrate[] + w[14]*eta[7]*relief[] +
              w[15]*eta[8]*dir1[] + w[16]*eta[9]*dir2[] + w[17]*eta[10]*biota[]
 #Camera detection covariates
```

```
  log_pc[1:cn] <- phi[1] + w[18]*phi[2]*turb[] + w[19]*phi[3]*dir1[] + w[20]*phi[4]*dir2[] +
            w[21]*phi[5]*ctemp[] + w[22]*phi[6]*ctemp2[] + w[23]*phi[7]*substrate[] +
            w[24]*phi[8]*relief[] + w[25]*phi[9]*biota[]

#TEMPORAL ABUNDANCE PROCESS MODEL (exponential population growth)
 for(i in 2:nyr){
 Npred[i] <- Npred[i-1] + r[i]
 r[i] ~ dnorm(rmu,tau[3])
 }
 Npred[1] ~ dnorm(0,.1)
 r[1] ~ dnorm(rmu,tau[3])
 rmu ~ dnorm(0,.1)
#PRIOR DISTRIBUTIONS
 for(i in 1:7){bet[i] ~ dnorm(0,.1)}
 for(i in 1:10){eta[i] ~ dnorm(0,.1)}
 for(i in 1:9){phi[i] ~ dnorm(0,.1)}
 for(i in 1:5){
 tau[i] <- pow(sig[i],-2)
 sig[i] ~ dt(0,1/(0.3^2),2) T(0,10)
 }
#VARIABLE SELECTION
 for(i in 1:25){w[i] <-1}#~ dbern(.5)}
}
```