Snail kite breakpoint analysis

The Southern snail kite population underwent a rapid change in age structure between 2007 and 2010 that resulted in a population now dominated by senescent individuals (Reichert et al., 2016). Therefore, we first tested whether this change in age structure would manifest itself as a change in population dynamics by fitting the standard Gompertz density dependence model with a breakpoint. We let the model parameters, a (reproductive rate) and b (density dependence), before and after this breakpoint differ. We did not include any environmental covariates at this stage in our analysis. Our breakpoint model is:

$$X(y+1) = \begin{cases} a_{\text{pre}} + b_{\text{pre}}X(y) + \varepsilon(y) & \text{for } y \leq \tau, \\ a_{\text{post}} + b_{\text{post}}X(y) + \varepsilon(y) & \text{for } y > \tau. \end{cases} \tag{S1}$$

Here y goes from 1997 to 2013 and τ is the breakpoint. We fit τ by profiling over the likelihood between the years of 2002-2009. We then calculated BIC values for the standard Gompertz model and the change point model to determine which was more parsimonious.

Once the presence of a breakpoint was determined, we analyzed the influence of environmental covariates on the abundance of snail kites in their southern range from 1997-τ, where τ was the estimated breakpoint in the Gompertz model from the breakpoint analysis. We did not include observations after the breakpoint in this analysis because we expected this to add only 3-6 years of data, which we deemed insufficient to fit a density dependent model with an environmental covariate. We used a suite of environmental covariates that were previously hypothesized to be important for snail kite reproduction and survival (Reichert et al., 2011). We also tested a weighted geometric covariate constructed from daily water level measurements.

Results

We first determined whether the southern snail kite population has qualitatively changed through time. We found that the breakpoint model was more parsimonious than a model with no breakpoints ($\Delta \text{BIC} = 8.9$). Our maximum likelihood estimate for the breakpoint was $\hat{\tau} = 2007$, consistent with the change in population structure documented by Reichert et al. (2016). Model parameters pre- and post-breakpoint were estimated as (reported as mean (se)) $\hat{a}_{\text{pre}} = 2.58$ (2.31), $\hat{a}_{\text{post}} = 8.99$ (3.18), $\hat{b}_{\text{pre}} = 0.62$ (0.04), and $\hat{b}_{\text{post}} = -0.47$ (0.08). These values correspond to average per-capita rates of increase over these time periods of 0.9297 and 0.7810 for pre- and post-breakpoint, respectively. Our estimated parameters in the breakpoint model (equation 7) predict a pre-2007 equilibrium of 888 (43) individuals that subsequently dropped to 452 (14) individuals post-2007. In both cases, the fitted models display a positive equilibrium indicating the possibility that the population will not decline to extinction. We note that this calculation does not account for the possibility of stochastic population extinction. Post-2007 results must be treated as preliminary because only 6 data points are available for this period and the system may be undergoing complex changes that are not captured by our model.

The ultimate outcomes of this demographic shift in snail kite populations are still unclear. Invasive apple snails are linked to food-handling difficulties in juvenile kites (Darby et al., 2007; Cattau et al., 2010; Pias et al., 2012), suggesting a causal mechanism for the demographic shift documented by Reichert et al. (2016). However, the potential of invasive snails to reach higher densities than native snails has also been linked to increased breeding rates and juvenile survival in the northern subpopulation of snail kites (Cattau et al., 2016). In the absence of clear mechanisms driving the demographic shift, it is not clear how to weight these two potential outcomes at this time.

References

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