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COMMENTARY

Hawaiian forest bird trends: Using log-linear models to assess long-term trends is supported by model diagnostics and assumptions (reply to Freed and Cann 2013)

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ABSTRACT

Freed and Cann (2013) criticized our use of linear models to assess trends in the status of Hawaiian forest birds through time (Camp et al. 2009a, 2009b, 2010) by questioning our sampling scheme, whether we met model assumptions, and whether we ignored short-term changes in the population time series. In the present paper, we address these concerns and reiterate that our results do not support the position of Freed and Cann (2013) that the forest birds in the Hakalau Forest National Wildlife Refuge (NWR) are declining, or that the federally listed endangered birds are showing signs of imminent collapse. On the contrary, our data indicate that the 21-year long-term trends for native birds in Hakalau Forest NWR are stable to increasing, especially in areas that have received active management.

Keywords: Hawaiian forest birds, log-linear models, model diagnostics, trends

Tendencias en aves de bosque Hawaianas: El uso de modelos logarítmicos lineales para evaluar tendencias a largo plazo es respaldado por supuestos y diagnósticos del modelo (respuesta a Freed y Cann 2013)

RESUMEN

Freed y Cann (2013) criticaron nuestro uso de modelos lineales para evaluar las tendencias en el estado de las aves de bosque en Hawai a través del tiempo (Camp et al. 2009a, 2009b, 2010) al cuestionar nuestro uso del esquema de muestreo, si hemos cumplido con los supuestos del modelo, y si hemos ignorado cambios a corto plazo en las series temporales en las poblaciones. En este artículo, respondemos a estas inquietudes y reiteramos que nuestros resultados no apoyan la posición de Freed y Cann (2013) que las aves de bosque en el Refugio Nacional Forestal Hakalau (NWR) están disminuyendo, o que las aves en peligro de extinción según la lista federal están mostrando signos de un inminente colapso. Por el contrario, nuestros datos indican que las tendencias a largo plazo por 21 años para las aves nativas en el NWR Forestal Hakalau son estables o van en aumento, especialmente en las áreas manejadas activamente.

Palabras clave: aves de bosque Hawaianas, modelos logarítmicos lineales, diagnósticos del modelo, tendencias

Hawaiian forest bird monitoring consists of determining the status of populations and tracking that status through time—a time series of bird abundances—with the goals of informing management decisions and discriminating among competing hypotheses about how populations respond to environmental change and management actions. In Camp et al. (2009a, 2009b, 2010), we defined population trend as the long-term, overall directional change in abundance over time. Determining population trends is the primary objective of many monitoring programs and the use of linear models to summarize the

general population trend is well-established (Geissler and Noon 1981, Droege 1990, Barker and Sauer 1992, Thomas 1996, Urquhart and Kincaid 1999, Thomas et al. 2004). However, Freed and Cann (2010, 2013) criticized our analyses of long-term trends in Hawaiian forest birds (Camp et al. 2009a, 2009b, 2010) in 3 ways, namely: 1) our sampling scheme; 2) a perceived lack of model diagnostics and evaluation of model assumptions; and 3) a lack of testing for change-points in the time series. Below we address these 3 concerns and close with summary thoughts on forest bird conservation in Hawai'i.

Sampling Scheme

Most wildlife abundance surveys are a combination of design-based and model-based strategies (e.g., Skalski 1994). Design-based strategies rely on probability-based sampling schemes such as systematic random sampling, as was used in the original Hawai'i Forest Bird Survey (Scott et al. 1986). In the original sampling scheme, stations were established 100–250 m apart along transects that were spaced 3–5 km apart (Scott et al. 1986). Subsequent surveys also applied systematic random sampling to establish count stations ~150 m apart with varying distances between transects (Camp et al. 2009a, 2009b). Since both sampling schemes are probability-based, both schemes allow unbiased summary estimates that can be compared (Thompson 2002). Assessing trends in populations requires a fixed sampling frame; however, it does not necessarily require that the sampling stations remain fixed. To account for differences in survey sampling frames, we (Camp et al. 2009a, 2009b, 2010) delineated the area consistently surveyed and drew conclusions only about the population that fell within the area that was exposed to sampling in all surveys.

Model Diagnostics and Assumptions

Freed and Cann's (2010, 2013) suggestion that we did not conduct model diagnostics is false. We conducted both standard and Bayesian model diagnostics to discern the appropriateness of using continuous, log-linear regression to describe population patterns, and we stated "[d]iagnostics demonstrated that the log-linear regressions of bird trends met all model assumptions" (Camp et al. 2010:201) because we found no evidence of violation of model assumptions for the 2 time series we examined (1987–2007 and 1999–2007). We included diagnostics and further analyses (as described below) in Camp et al. (2009a), but due to limited print space these were left out of Camp et al. (2010). Here, we include residual plots of linear regression models (Supplemental Material [Appendix A](#)) and Bayesian-based diagnostic plots (Supplemental Material [Appendix B](#)), and we continue to assert that these diagnostics support the appropriateness of linear regression models and indicate little to no evidence of unequal variances or nonnormality in the residuals from our log-linear model of annual density.

We used the standard statistical procedure of log-transforming population densities to control error variance (Neter et al. 1996). Although residual plots are useful for assessing whether the variance of the error terms is constant, their interpretation is somewhat subjective, and concluding definitively between residuals expressing a pattern or providing an adequate fit can be difficult. This is especially true of our time series with fewer than 30 points. Therefore, we used the modified Levene test to provide a



FIGURE 1. Male Hawai'i 'Ākepa (*Loxops coccineus coccineus*). These endangered Hawaiian honeycreepers are 1 of only 18 extant species from more than 50 Drepanidinae that evolved in the Hawaiian Islands. This specialist insectivore is found only in montane old-growth forest on the island of Hawai'i and uses its crossed bill to open leaf buds and expose the insects, primarily microleps and spiders, on which it feeds. Photo credit: Jack Jeffrey, www.JackJeffreyphoto.com

formal quantitative test of the appropriateness of a log-linear model (Neter et al. 1996). This modified Levene test allows assessment of the absolute deviations of the residuals about the group medians and thus is more robust. There was no evidence that the error variances differed among groups for any species by strata or trend period (Supplemental Material [Appendix C](#)).

Observations that occur close together in time are often more similar than those that are farther apart (i.e. serial or temporal correlation), and this dependence among observations can complicate the estimation of variance. Residual plots are useful for assessing nonindependence of error terms by plotting the residuals against time. We found little evidence in our time series of any correlation between proximate error terms. We further tested for temporal autocorrelation using the 'acf' function in program R (R version 2.7.0, 2008-04-22; R Development Core Team 2008) to determine which lag autocorrelation removed serial correlation. The temporal independence model had the lowest Δ AIC value for 11 species (Supplemental Material [Appendix D](#)). Only the 'Ākiapōlā'au (*Hemignathus munroi*) showed limited evidence of serial autocorrelation, but the temporal independence model was within 3 AIC units, thus the more universally parsimonious temporal independence model

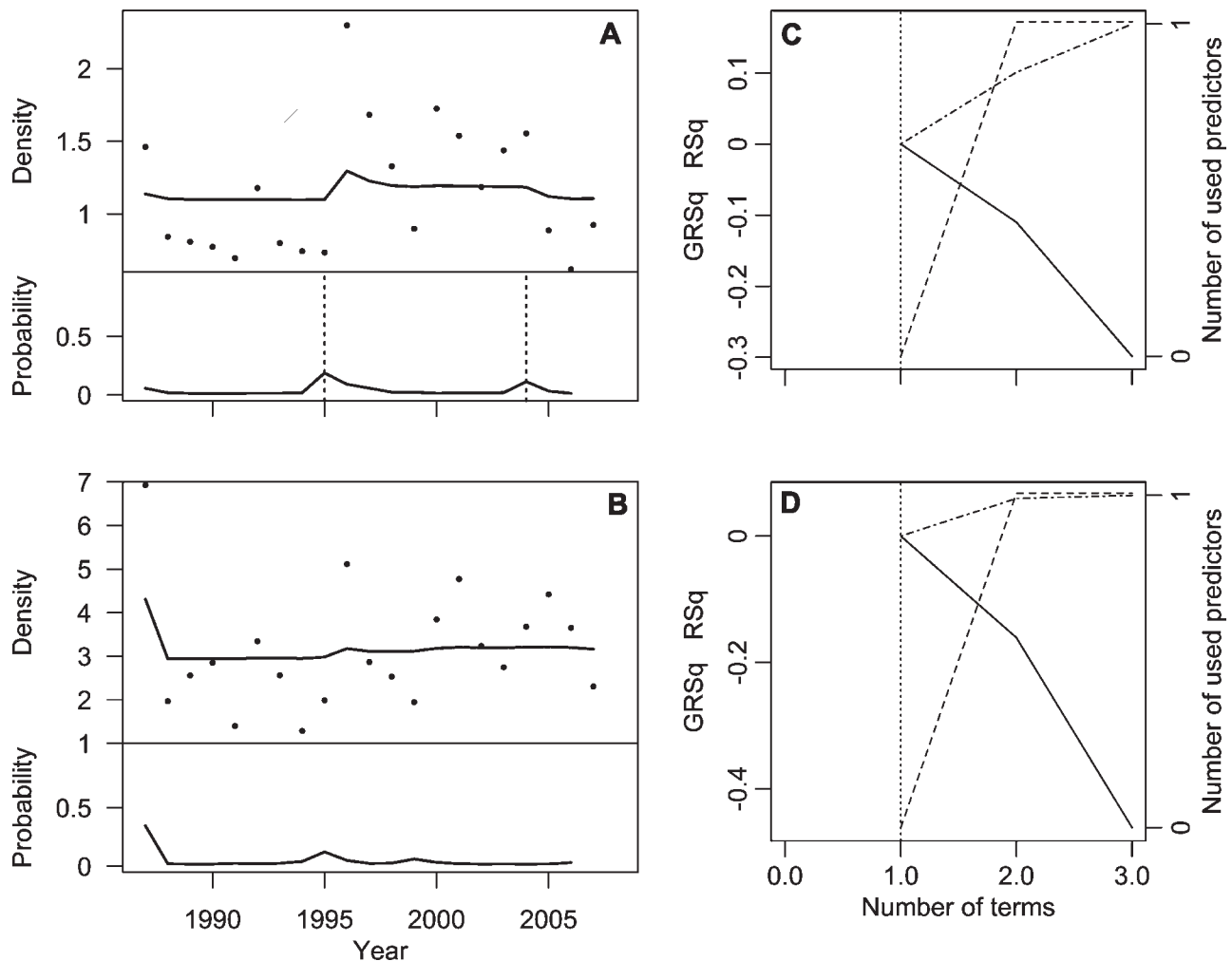


FIGURE 2. Change-point assessment of bird densities in open forest from 1987 to 2007 using Bayesian change point (bcp) and adaptive regression spline (ars) analyses for Hawai'i 'Ākepa (**A**, **C**, respectively) and Japanese White-eye (**B**, **D**, respectively). The Bayesian change-point procedure produces a probability distribution showing the posterior probability of a change-point at each location in the sequence. The upper portion of the bcp graphics shows the annual density estimates (birds ha^{-1} ; points) along with the posterior mean at each annual survey ("Density"; line). The lower portion of the plot shows the weight of evidence for a change-point along the time series (as indicated by the Bayesian posterior probabilities; "Probability"). We interpreted the likelihood of a change-point with 4 categories of evidence derived from the posterior odds: weak, moderate, strong, or very strong. We defined the categories based on the posterior probabilities (P) as follows: weak if $P < 0.5$; moderate if $0.5 \leq P < 0.7$; strong if $0.7 \leq P < 0.9$; and very strong if $P \geq 0.9$. The vertical dashed lines indicate likely breakpoints; however, we found only weak evidence for the presence of change-points in the 'Ākepa time series and no evidence in the Japanese White-eye time series. Adaptive regression spline analysis fits piecewise linear regression to the time series iteratively with a knot at each time t , and the model selected minimizes the residual sum-of-squares (RSq; dash-dot line) as the number of terms is reduced. The optimal number of parameters in the final model is identified using a generalized cross-validation (GRSq; solid line) procedure standardized by the number of terms (intercept and knots) and number of predictors used (the independent variable time in these analyses; long dashed line); thus, a parsimonious model is obtained that best represents trajectories in the time series while penalizing for additional knots and avoiding overfitting the data. For both species, the intercept-only model was selected and no knots were identified (indicated by the short dashed line). Results from both change-point assessment methods indicate that for both species a single slope may be used to characterize trends in abundance.

was chosen. Neter et al. (1996:103) stated that "residual outliers can be identified from residual plots against X " and used the rule of thumb that the dataset should contain fewer than 4 outliers. We found few (range 0–2) outliers in any of the datasets. Finally, normal probability

plots of residuals by species indicated that the distribution of the error terms was nearly linear and suggested agreement with normality for all strata and trend periods. Based upon all these diagnostics, we believe log-linear models are appropriate to describe Hawaiian forest

passerine trends, contrary to the assertion by Freed and Cann (2010, 2013).

Change-points in the Time Series

In Camp et al. (2009a, 2009b, 2010), our objective for monitoring bird populations was to assess the overall trend of the time series, not to describe short-term fluctuations. However, as we stated in Camp et al. (2009b, 2010), a long-term trend may be composed of short-term fluctuations or trajectories that vary over time and that may persist for only a few years. Relying on short-term trajectories to describe population patterns can be misleading if extrapolated. However, short-term trajectories can also be illuminating, especially as they may indicate the start of a shift in the long-term trend. Therefore, we assessed trends in Hawaiian forest passerines over 2 time periods: long-term trends in bird densities for a 21-year period (1987–2007) in open forest and pasture; and shorter near-term trajectories in open forest, closed forest, and pasture calculated for a 9-year period (1999–2007) when these tracts were surveyed concurrently.

Camp et al. (2010) applied a breaking point in 1999 based on changes in the sampling frame and to allow for comparisons when the 3 habitat strata (open forest, closed forest, and pasture) were concurrently surveyed. Freed and Cann (2010, 2013) provided biological justifications for their assignment of a breaking point in 2000. As examples, we present here general change-point assessments of Hawai'i 'Ākepa (*Loxops coccineus coccineus*, hereafter 'Ākepa; Figure 1) and Japanese White-eye (*Zosterops japonicas*, hereafter White-eye) densities in an open forest stratum from 1987 to 2007 using package 'bcp' in R (Erdman and Emerson 2007). This procedure identifies "steps" in the time series where means differ among segments (Erdman and Emerson 2007). We found only weak evidence for the presence of change-points in the time series, none of which occurred in 2000 (Figure 2A and 2B). In addition, we used adaptive regression spline analysis to identify the relationships in a series of linear regressions at different intervals of the 'Ākepa and White-eye time series using package 'earth' in R (R Development Core Team 2008). This procedure identifies points, termed 'knots,' where the slopes in the linear relationships change (Friedman 1991). No knots were identified for either species (Figure 2C and 2D). Therefore, the results from both analyses suggest that a single slope may be used to characterize trends in abundance for each species, and the time series do not support an inflection in 2000 as applied by Freed and Cann (2010, 2013).

Conclusion

L. Freed and R. Cann believe that forest birds at Hakalau, particularly the Hawai'i 'Ākepa, are in decline (Freed et al.

2008, Freed and Cann 2009). L. Freed, R. Cann, and their students have studied the 'Ākepa for more than 20 years (see citations in Freed and Cann 2013), and their data and expertise are valuable. Thus, the U.S. Fish and Wildlife Service solicited scientific review of the available data to assess whether the 'Ākepa population at Hakalau had declined, through 3 separate evaluations: 1) 8 members of the Hawai'i Forest Bird Recovery Team (Scott 2006); 2) a 2-day workshop held October 8–9, 2008, with 37 participating scientists and managers (Scott 2008a); and 3) solicitation of expert opinion from 8 independent scientists (Scott 2008b). In all, 48 scientists reviewed or conducted original analyses of the survey data, and the general consensus was similar to our conclusions for all 12 study species in the Hakalau Forest NWR—that although the 'Ākepa population had fluctuated over time, there was no evidence of a long-term decline. The debate has also been extensively described in Dalton (2008), Lempinen (2008), and Tummons (2009). However, we reiterate the caution from Camp et al. (2009a:196) that "more recent mixed results may indicate emergent problems" for all birds in Hakalau, and we advocate continued surveys and vigilance in this critical bird area.

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