**The Regime Shift Detector: a model to identify changes in dynamic rules governing populations**

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**Abstract**

1: Environmental factors may interact with internal rules of population regulation, sometimes perturbing systems to alternate dynamic states. Yet, pinpointing when sustained state changes occur in naturally fluctuating populations is difficult. An analytical approach that can identify the timing and magnitude of such changes, or “regime shifts”, would facilitate understanding of abrupt ecological transitions with potential to inform management of species of economic or conservation concern.

2: We developed a generalizable model, the “Regime Shift Detector”, for identifying changes in the parameters of a simple density dependent model governing the temporal fluctuations of a population. The model is a generalizable tool comprised of a suite of functions for examining population time series data for the presence, location, and magnitude of shifts. The model uses an iterative approach to fitting subsets of time series data, and then ranks the fit of a particular break point combination using model selection to assign a relative weight of each break. We examined the performance of this model with simulated data and two real-world case studies each with >20-years of data: one species with an invasion dynamic, the multicolored Asian ladybeetle (*Harmonia axyridis*), and one that has been declining, the eastern monarch butterfly (*Danaus plexippus*).

3: We found that under low environmental/sampling variation, the break point sets selected by the Regime Shift Detector contained the simulation parameters with 70%-100 accuracy, with the most complex parameterization conditions (i.e. time series with many break points) least likely to be detected by the model. In these complex cases, the Regime Shift Detector generally identified the true break point in the simulated data but were also likely to identify additional potential breaks in the time series data. The weighting tool generally separated breaks intentionally placed in simulated data to those due to sampling error, although the magnitude of the difference varied with other simulation parameters.

4: In our case study examining the invasion process of Asian ladybeetles, the Regime Shift Detector identified shifts in population cycling associated with known variation in prey availability. The results for the eastern monarch population were more ambiguous, with greater uncertainty about the number and location of breaks in the time series data: several equivalently performing break point combinations had widely divergent weights associated with their break points, suggesting multiple, super-imposed biological processes are driving the dynamics of this species.

5: The Regime Shift Detector functions as a method for identifying possible break points within time series data, and the weighting tool provides a means of quantifying the strength of evidence for each break point. When interpreted in the context of known species biology, the Regime Shift Detector has the potential to aid management decisions and identify critical drivers of change in species’ dynamics. In an era of rapid global change, such tools can improve understanding of the conditions under which population dynamics shift to other states.

**Introduction**

Population dynamics are governed by internal, biotic rules and also abiotic factors, leading to both stochastic and deterministic forces governing abundance patterns (Bjørnstad and Grenfell 2001). External perturbations to population processes can lead to regime shifts, where the internal rules that govern fluctuations in population abundance transition to another state (Hare and Mantua 2000, Carpenter et al. 2008). Understanding how and when external environmental factors interact with internal density dependent regulation remains a fundamental challenge in population ecology (Sutherland et al. 2013, Eason et al. 2016).

Density dependent tools for modelling population time series were developed and championed during the 1950s and 60s. Examples include the Ricker and Beverton-Holt models, which were initially developed for fisheries management (Ricker 1954, Beverton and Holt 1957) and describe the expected population size in year *t* as a function of the population size in year *t-1*. The accuracy of these simple density dependent models is generally highest for populations fluctuating around their carrying capacity (Sabo et al. 2004), with compensatory density dependence and no lag effects (Bjørnstad and Grenfell 2001). Although this deterministic approach to population modelling has largely fallen out of favor for more complex strategies involving nonlinear stochastic elements (May 1976, Bjørnstad and Grenfell 2001, Barraquand et al. 2017, Boettiger 2018), simple dynamic models remain useful, in large part due to easily interpretably and ecologically meaningful parameters (Gadrich and Katriel 2016). Differences in parameter values between populations, or a change within a single population, can suggest differences in environmental constraints governing a population, providing a quantitative measure of environmental change impacts (Forchhammer and Asferg 2000, Berryman and Lima 2006, Zipkin et al. 2009, Bahlai, vander Werf, et al. 2015).

Although theoretically straightforward, identifying abrupt transitions in ecological systems is challenging using real-world data due to a lack of systematic approaches and noise in naturally produced time series data (Bestelmeyer et al. 2011). In many cases, transition points are applied to time series data *ad hoc*, based on data visualization or specific hypotheses surrounding factors affecting population fluctuations (Hare and Mantua 2000, Toms and Lesperance 2003, Weimerskirch et al. 2003, Berryman and Lima 2006, Knapp et al. 2012), creating the potential for biases in selecting break points. Break point analysis tools eliminate this bias by locating change points with a variety of optimization strategies, including linear and moving average methods (Braun and Muller 1998, Zeileis et al. 2001, Killick and Eckley 2014, Priyadarshana and Sofronov 2015). However, these methods do not work on data with internal, density dependent structure inherent to population time series data. Density-dependent population growth has the potential to mask transition points. For example, transient dynamics occurring immediately after a temporary disturbance can result in a change in population size, but not necessarily in the rules governing population fluctuations. Wavelet analysis has been applied to population time series to address changes in cycling patterns (Jenouvrier et al. 2005) but this method also does not account for density-dependent processes as an explicit mechanism governing changes in abundance (Cazelles et al. 2008). A robust, unbiased tool for detecting regime shifts would simultaneously allow us to identify when shifts in population cycling processes occur and further quantify the specific changes to the underlying dynamic driving population size changes.

In this paper, we develop a generalizable tool, the Regime Shift Detector (RSD), for identifying shifts in dynamic regimes within density-dependent populations using time series data. We illustrate our approach using the Ricker model because of its simplicity and high performance under a variety of realistic environmental scenarios. Yet, the techniques described in our paper can be readily adapted for other model structures, including more complicated processes such as seasonal periodicity or lag effects. We describe the basic structure of our model and how it can be used to evaluate the presence, location, and magnitude of shifts in population parameters governing dynamics. We demonstrate the utility of our model through a series of simulations and apply the model to real-world case studies of two populations of conservation and economic concern. First, we examine the invasion process of the multicolored Asian ladybeetle (*Harmonia axyridis*), a cosmopolitan invasive, in the two decades following its arrival in Midwestern US agricultural ecosystems. Then, we examine the declining eastern monarch butterfly (*Danaus plexippus*) population using census data collected on its overwintering grounds in Mexico over a similar two decade period. In our ladybeetle case study, the RSD model identified shifts in population cycling associated with known variation in prey availability, with a moderately high weight break associated with prey arrival and a moderately low weight break associated with management actions against the prey. The results for the monarch population were more ambiguous, with greater uncertainty about the number and location of breaks in the time series data. Several equivalently performing break point combinations had divergent weights associated with their specific break points, suggesting multiple, super-imposed biological processes driving the dynamics of this species.

The RSD model functions as a method for identifying hypothetical break points within time series data, and the weighting tool provides a means of quantifying the strength of evidence for each break point. When interpreted in the context of known species biology, the RSD model has the potential to aid management decisions, identify critical drivers of change in species’ dynamics, help determine where best to focus additional research efforts. In an era of rapid global change, such tools can improve understanding of the conditions under which population dynamics shift.

**The Regime Shift Detector model**

Fort the purposes of our analyses, we assume that the population of interest follows a Ricker model structure such that the population size in time t+1, , is dependent on the population size in time t, , the carrying capacity of the system, , and the per-capita annual growth rate, (Turchin 2003):

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We further assume that observed annual population abundance is partially stochastic and may be influenced by either environmental variation and/or sampling error. We include an error term to represent this noise, which follows a normal distribution centered around zero with a variance of . The parameters K, r, and are estimated from the population time series data (N1, N2, … N*t*). The Ricker model is a useful starting point for breakpoint analyses because 1) it does not rely on any external information (abundance in time *t* is a function of only abundance in time *t*-1); 2) only three parameters need to be estimated, and those parameters have ecologically meaningful interpretations; and 3) it is an extremely flexible distribution, taking a variety of forms, from linear to compensatory to over-compensatory, and thus has a wide range of applications across a variety of taxa (Ricker 1954, Brook and Bradshaw 2006).

To build the RSD model, we use an iterative, model-selection process to determine if, and when, shifts in parameter values occur within a given time series. To achieve this, we first fit the Ricker model to the entire time series of available data. Then the population time series is subdivided into all possible combinations of 2, 3, …, n subsets of sequential data points (hereafter, ‘break point combination’) and the Ricker model is fit to each of the subsets produced for each break point combination. We constrain break point combinations to include only subsets with at least four sequential data points.

After fitting each subset for a given break point combination, we evaluate the candidate set of models by calculating the Akaike Information Criteria for small sample sizes (AICc) value for each segment and summing them accordingly (Hall et al. 2013). Fits for break point combinations with comparatively lower AICc values are considered to have better performance. Models with AICc value differences of two units or less are considered equivalent (Burnham and Anderson 2002). To evaluate the strength of evidence for an identified break in the time series, we extend the relative variable importance method (Burnham and Anderson 2002). To do this, we compute the Akaike weight *w*i for every potential break point across all combinations and sum the Akaike weights for a potential break point across all break point combinations. We selected AICc as our information criterion to use for model selection within the RSD model because it provided a balance of simplicity and sensitivity, however, we also completed a parallel analysis with an identical procedure, using AIC as the information criterion for decision-making, which is documented in appendix S2. AIC blah blah sensitivity vs specificity

The RSD model is implemented as a series of R functions to enable a user to quickly generate a list of potential break points for a population time series dataset. The model (and all subsequent simulations and case studies) were scripted and run in R Version 3.3.3 (R Development Core Team 2017). All data manipulations, analyses and figure scripts, including the complete development history, are publicly available in a Github repository at <https://github.com/cbahlai/monarch_regime>. We summarize the role of each function in the script within the supplemental files (see S1).

*Simulation study*

We conducted a series of simulations to test the accuracy of the RSD model under a variety of scenarios. For a given time series, the RSD model produces a set of equally performing break point combinations for cases in which model fits produce equivalent AICc values (i.e. within 2 units of the best-performing fit). We tested the performance of the RSD model under a variety of plausible parameter spaces. To do this, we let *N1* = 3000, *r = 2* and *K = 2000* and then achieve a stable population by running the Ricker model for 20 years. We then modified *r* and *K* individually by a set of intervals from their starting values ±(0%, 10%, 25%, 50%, 75%) while holding all other parameters constant. We examined the effect of the size of *r* on model performance by creating scenarios with different starting values of *r* (0.5, 1, 1.5, 2). We also evaluated how the magnitude of stochasticity in the system (as measured by the error term ) influenced model performance. For generalizability of our simulation results, we simulated error as a percentage of the mean population size, rather than as absolute value (described in the model above). For each (true) annual population size in the simulated dataset, a random value was selected from a normal curve of mean 0 and standard deviation of (where = 1%, 2%, 5%, 10%, 15%)*.* To scale the standard deviation to the population size used in the simulations, and the expected value of N(t+1) was multiplied by this value to simulate . Each of these scenarios was run on 250 simulated datasets for breakpoint combinations with 0, 1, 2 and 3, respectively. We also tested the impact of time series length by modifying length of the simulated time series at five year intervals (over a range from 15 – 30 years) while holding the parameters constant.

We examined the RSD model’s performance for all test scenarios from two perspectives. First, we evaluated the ability of the model to detect scenario initialization conditions within the set of the best fitting break point combinations (i.e. the top ranked break point combination, and those break point combinations whose AICc values fell within two units of the top ranked). Then, we examined the performance of the singular top-ranked break point combination (regardless of the presence of break point combinations with equivalent performance) in greater depth. We also examined the performance of the break-point weighting tool from the perspective of its average and ‘worst-case’ weightings of correct and erroneous break points.

The number of breaks and their locations were detected within the top performing break point combination sets with >70% accuracy under nearly all parameterization scenarios, and this accuracy was consistent to values of error nearing 15% (Fig. 1). The RSD model correctly identified the simulated break point combinations (when considering all top performing models) in virtually 100% of scenarios initiated with two break points, >90% of scenarios initiated with one break point and >80% of zero break simulations. These results remained roughly consistent regardless of the value of the variance (sigma squared) determining the annual amount of environmental/sampling noise (Fig. 1 A). A very similar trend of model performance was observed over varying starting values of *r*, with roughly consistent performance of the RSD model amongst the equivalent performing break point combinations, regardless of *r*, with accuracy reduced at extreme values of *r* ( Fig. 1 B). The RSD model had the highest accuracy with larger shifts in K (>10%; Fig 1. C) and relatively smaller changes to *r* (<25%; Fig. 1 D). This result is somewhat counter-intuitive, as we would generally expect large shifts in all parameters to be more easily detected. However, because the Ricker model produces chaotic dynamics with high values of r (r > 2.3) a large shift in parameters could potentially result in a situation where multiple break point fits would perform equally well. Finally, the accuracy of the RSD model decreased as scenario length increased, likely because of the factorial increase in potential break point combinations with additional data in the time series (Fig. 1 E).

The breakpoint weighting analysis revealed that in the vast majority of cases, the average weight of a true break exceeded a value of 0.8 (Fig. 2), whereas the weight of erroneous breaks averaged less than 0.2 in weight. The notable exception occurs when true breaks resulted from very small shifts in K (Fig. 2 C).

**Applications**

We tested the performance of the RSD model with two cases using population time series data from field observation studies. Both case studies involve approximately two decades of observations of economically or culturally important insect species: one case examines an invasion process and the other examines a population decline, both occurring over the same time period in recent history.

Multicolored Asian ladybeetles in southwestern Michigan

The 1994 invasion of multicolored Asian ladybeetles to southwestern Michigan, United States was documented in monitoring data collected on agriculturally-important Coccinellidae (ladybeetles) in landscapes dominated by field crops. Population density of ladybeetles is monitored in 10 plant communities weekly over the growing season using yellow sticky card glue traps starting in 1989 at the Kellogg Biological Station at Michigan State University. We used data on the captures of adults at the site from 1994-2017, culled at day of year 222 (August 10) to minimize the effect of year-to-year variation in the sampling period. We then calculated the average number of adults captured per trap, across all traps deployed within a sampling year, and used this value as the dependent variable in our analysis. Detailed sampling methodology is available in previous work (Bahlai et al. 2013, Bahlai, Colunga-Garcia, et al. 2015, Bahlai, vander Werf, et al. 2015).

Two break points, one occurring after 2000 and one occurring after 2005, were observed in the top break point combination model (Fig. 3 A, AICc=-18.02). However, the RSD model indicated that two additional break point combinations, a single break after 2000 (AICc=-17.46), and a no break series (AICc=-17.64), had equivalent performance. Break weight analysis suggested a weight of 0.56 for the 2000 break, and a weight of 0.29 for the break after 2005. Although the weights of both of these break points fall into an intermediate range of support, we expect that natural systems would behave in a less idealized manner, thus we conclude that there is reasonably strong evidence of a shift in dynamic rule after 2000, and a moderate-weak evidence for a shift after 2005. The shift from ‘phase A’ to ‘phase B’ in 2000 is characterized by substantial increases in the values of K and r, with approximate increases of 75% and 40% over their initial estimates, respectively (Table 1). The shift from 'phase B' to 'phase C' in 2005 is characterized by a return to parameter estimates that were nearly identical to those observed for ‘phase A’ (Table 1, Fig. 3 B).

These observations can be explained in the context of the known ecology of this ladybeetle. Dynamics of the ladybeetle invasion appear to be closely coupled with prey availability (Bahlai and Sears 2009, Heimpel et al. 2010, Rhainds et al. 2010, Bahlai, Colunga-Garcia, et al. 2015), which, in turn, is driven by documented pest management practices (neonicotinoid insecticide use; Bahlai, vander Werf, et al. 2015) leading to relatively simple pulsed change. The first shift in the dynamics of the Asian ladybeetle*,* after 2000, corresponds to the well documented arrival and establishment of a preferred prey item from its native range, soybean aphid, to North America (Ragsdale et al. 2004, Wu et al. 2004). The invasion of this aphid dramatically increased resources available to *H.axyridis* in habitats where the beetles were already well-established (Bahlai et al. 2013), supporting both a higher carrying capacity and a greater intrinsic growth rate. The second shift, after 2005, was weaker is more difficult to directly explain, as the prey item still persists in the landscapes where *H. axyridis* occurs. However, landscape-scale use of neonicotinoid insecticides decreased prey numbers, particularly during the spring when aphids are colonizing new hosts, which could be limiting early season reproduction of ladybeetles(Bahlai, vander Werf, et al. 2015)*.* Indeed, in this case, we would expect a weaker shift in dynamics as the prey item is incompletely controlled, and control tactics were not uniformly adopted across the prey’s range all at one time.

Monarch butterflies in Mexican overwintering grounds

The eastern population of the North American monarch butterfly (*Danaus plexippus*) is migratory, with the majority of individuals overwintering in large aggregations in Oyamel fir forests within the transvolcanic mountains in the central region of Mexico (Urquhart and Urquhart 1978). Monarchs are highly dispersed over their breeding season, occupying landscapes throughout the agricultural belt in central and eastern United States and southern Canada (Flockhart et al. 2017). As such, estimates of the overwintering population size can provide a convenient and inclusive annual metric of the size of the eastern migratory population (Prysby and Oberhauser 2004). This population of monarchs has been in dramatic decline in recent decades, although the degree and cause of this decline is hotly debated (Sarkar 2017). We used data on the total area occupied by monarchs from 1995 to 2017 (based on early winter surveys conducted in December), compiled by the World Wildlife Fund Mexico (available at MonarchWatch; Lovett 2017).

The RSD model estimated that the best break point combination fit for the monarch overwintering density data was a single break after 2003 (Fig. 4; AICc=120.18). However, the model indicated that two additional break point combinations, a single break after 2006 (AICc=121.87), and a two break combination of 2003 and 2008 (AICc=-121.86), had equivalent performance. The weight analysis suggested weights of 0.49, 0.14 and 0.26, for 2003, 2006 and 2008 respectively. As above, with our ladybeetle case study, the strength of evidence was strongest for the first break in 2003, and weaker for the secondary break. The shift corresponds with a >50% reduction in K at 2003, and, if the secondary break is taken at 2008, a further reduction of K nearing 50% again at that point (Table 2; Fig. 4 B).

Abiotic drivers of monarch population dynamics are complex and can interact at local, regional, and continental scales (Saunders et al. 2017). Loss of milkweed hostplants due to changing agricultural practices on Midwestern breeding grounds (Hartzler 2010, Pleasants and Oberhauser 2013) is hypothesized to be a major cause of the decline. However, other studies have implicated climate (Zipkin et al. 2012), extreme weather events (Brower et al. 2004), changing habitat availability on wintering grounds (Vidal and Rendón-Salinas 2014), and mortality during the fall migration (Davis and Altizer 2015) as possible factors influencing monarch population dynamics. With many super-imposed drivers, monarch dynamics are likely to be driven by both press and pulsed processes, making the detection of discrete break points associated with regime shifts more difficult.

Thus, there is biological support for essentially all the break points selected by our model- or, indeed, changes occurring in a combination of pulsed and smooth processes. For example, changing herbicide use practices in central North America have largely eliminated milkweed hostplants from agricultural field crops, with fairly consistent, low levels of milkweed on the landscape starting from about 2003-2005 (Zaya et al. 2017). Although glyphosate tolerant soybeans and maize were introduced to the US market in 1996 and 1998 respectively (Duke and Powles 2009), actual glyphosate use lagged behind, with dramatic increases in use of the pesticide in 1998- 2003 in soybean, and 2007-2008 in maize (Baker 2017).

**Discussion**

The RSD model provides a novel and objective tool for evaluating changes in parameters, such as carrying capacity and growth rates, that govern natural populations. As illustrated with our case studies, model results not only identify and quantify parameters changes, but can provide insight into the potential drivers in the systems under study and help focus the time frames that should be examined more closely. We illustrated the RSD with the Ricker model as the functional form governing population dynamics. However, the central dynamic model could be changed or modified to incorporated more complicated population processes.

The model in the RSD is a compromise between sensitivity and simplicity. We found that, in general, results were more easily interpreted when using a conservative information criterion to select results in simulations, and thus, we recommend users of the RSD model use AICc when examining new data. However, there may be cases where it is desirable to gain a more liberal estimate of changes in patterns: in this case, the more sensitive AIC can be used to rank break point combinations. We found final results of the RSD model were similar, regardless of the information criterion used, except that using AIC was more likely to indicate more candidate breaks, and weight both true and erroneous breaks with higher values (Appendix S2). Thus, this more sensitive approach may be most useful in the context of hypothesis generation, rather than as an explicit hypothesis test.

We recommend users carefully consider the limitations of the tool in the context of the raw data presented: if phases of change are close together (e.g., less than 3-4 years or time periods), the resultant variation may reduce the model’s sensitivity for detecting shifts in the data. For instance, we use the discrete form of the Ricker model, with a yearly time step, but end users can modify model structure and temporal resolution appropriate to their systems and available data. As is, the results of the model should be interpreted with caution in populations undergoing rapid change in their environments or internal dynamics. We also observed that the likelihood of identifying erroneous break points increased as time series length increased. The reason for this is twofold- first, as the series lengthens, the set of possible breakpoint combinations increases geometrically, thus creating many more combinations for the RSD model to potentially chose from. Secondly, as the number of data points increases, the AICc penalty for small sample sizes approaches zero, so there is minimal penalty for over-parameterizing a model fit on a longer time series. Thus, in cases where a long time series exists, but a particular time period is of interest, the RSD model could be used on the time period of interest alone to minimize the likelihood of distracting or erroneous results.

In both of these evaluations, we found that the RSD model was able to detect scenario conditions in practically all cases, but presented a problem with respect to over-sensitivity: essentially, more ‘suspected’ break points were identified by the model than were intentionally placed in the simulated data, creating ambiguities in interpretation. Thus, both the ‘model set’ and the ‘top model’ approach could be used to identify a list of potential break points and break point combinations, and an additional tool could be used to evaluate the strength of evidence for each. In our simulations, we found that, on average, ‘true’ breaks based on scenario conditions and erroneous breaks could be easily discerned by their computed weights, while erroneous breaks typically averaged less than 0.2 in weight, whereas in most scenarios, true breaks had weights of >0.8 under nearly all simulated conditions (Fig. 2).

Applying these insights to our case studies upon evaluating our case studies, we found interpretation of the ladybeetle example was relatively straightforward (Fig. 3). Our top break point combination and the equivalently-performing set did not contain contradictory information: each candidate set was simply a subset of breakpoints from the most complex set, and only two break points were found. Both of these break points were associated with moderate or greater weights, although the values of these break weights were both intermediate to the weights of ‘true’ and ‘erroneous’ breaks found in the simulations, suggesting breaks in natural systems do not behave as cleanly as those in simulated data. The monarch butterfly case study was more ambiguous (Fig. 4). Although the top two break point weights were nearly identical to those observed in the ladybeetle study, the top-ranked break point combination only had one break, and the set of equivalently performing break point combinations had varied structures. Weights of the two ‘strongest’ breaks were numerically similar to those of the ladybeetle case study, but model selection results suggest additional, superimposed processes may be affecting monarch population dynamics and creating a noisier signal.

We used simulations to understand how changing various inputs affected the likelihood of the RSD model in identifying the conditions under which the data were produced. Performance of the RSD model declined with increasing levels of stochasticity, or error, in the data, a behavior that is expected of any statistical tool. Yet, performance was relatively stable amongst model sets across the range of noise tested in our experiment (Fig. 1 A). Other input conditions also impacted the performance of the RSD model. The effect of dynamic shift size was dependent on which parameter was changed and by how much (Figs. 1 C, D). Larger shifts in *K* were more detectable both by the top break point combination and within the equivalent break point combinations set (Fig. 1 C). However, increasing change in *r* made it less likely for the parameterization conditions to be detected, but this effect varied in strength between parameterization complexity and whether the break point set or just the top break point combination was considered (Figs. 1, 2 D). Although larger shifts in regression parameters would, intuitively, lead to a higher likelihood of detection, these larger shifts in *r* would also be more likely to induce large variations in transient dynamics in the years immediately following the shift, potentially making the timing of shifts more difficult to pinpoint. Similarly, longer time series yielded results that were more error prone (Fig. 1-2 E). This likely because, firstly, there were simply more possible break-point combinations for the model to select from, and secondly, because the penalty for increasing parameterization (i.e. AICc) would decrease as sample sizes grew, leading to increasing likelihood of identifying extra breaks.

When interpreted in the context of known species biology, the RSD model has the potential to aide management decisions and identify, and rank critical drivers of change in internal dynamics of a population. Our modeling framework should be useful in this era of rapid global change affecting species dynamics, as it can help evaluate population changes relative to internal regulators.

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**Table 1:** Ricker model fits for each phase between break points resulting from fitting population data of *Harmonia axyridis* from Kellogg Biological Station, 1994-2015. Regression parameters r represent the per capita yearly intrinsic rate of increase and K the carrying capacity, based on population numbers expressed as average number of adult *H. axyridis* captured per trap, per year. The ‘Phase’ column gives a shorthand for referring to the data subsetting structure indicated by the Regime Shift Detector model.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Data**  **structure** | **Phase** | **Years in subset** | **r ( ± SE)** | **K ( ± SE)** |
| Two breaks | A | 1994-2000 | 1.3 ± 0.3 | 0.31 ± 0.02 |
|  | B | 2001-2005 | 2.3 ± 0.3 | 0.43 ± 0.03 |
|  | C | 2006-2013 | 1.6 ± 0.3 | 0.27 ± 0.03 |
|  |  |  |  |  |

**Table 2.** Ricker model fits for each phase between break points resulting from fitting population data documenting the area occupied by overwintering Monarch butterflies in their winter habitat in the Mexico, 1995-2016. Regression parameters r represent the per capita yearly intrinsic rate of increase and K the carrying capacity, in units of hectares occupied. The ‘Phase’ column gives a shorthand for referring to the data subsetting structure indicated by the Regime Shift Detector model.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Data structure** | **Phase** | **Years in subset** | **r ( ± SE)** | **K ( ± SE)** |
| Two breaks | A | 1995-2003 | 1.0 ± 0.5 | 10.1 ± 1.9 |
|  | B | 2004-2008 | 1.6 ± 0.2 | 5.6 ± 0.3 |
|  | C | 2009-2016 | 1.2 ± 0.4 | 2.8 ± 0.5 |
|  |  |  |  |  |

**Figure captions**

Figure 1: **Performance the Regime Shift Detector model under varying conditions.** Proportion of results where initial conditions were detected by the top break point combination (circles) or within the equivalent model set (triangles) under A) varied noise (in the form of normally distributed error) B) varied starting values of the r constant, C) varied % changes in the K constant in the Ricker model D) varied % changes in r, the intrinsic rate of increase in the Ricker model and E) simulated time series length. Sets of 0, 1, 2 and 3 break points were randomly generated from within the set of possible values each scenario was iterated 250 times.

Figure 2: **Average break weight of break points found under varying parameterization conditions.** Break weight is computed based on a modification of “Relative Variable Importance” formula, where each break point is multiplied by the Akaike weight of each model in which it appears. Average weights of break points identified by the regime shift detector model reflecting true parameterization conditions (circles) or erroneous breaks suggested by the model (triangles) under A) varied noise (in the form of normally distributed error) B) varied starting values of the r constant, C) varied % changes in the K constant in the Ricker model D) varied % changes in r, the intrinsic rate of increase in the Ricker model and E) simulated time series length. Sets of 0, 1, 2 and 3 break points were randomly generated from within the set of possible values each scenario was iterated 250 times.

Figure 3: **Regime shift detector breaks and Ricker model fits for an invasive ladybeetle**. Population data documenting the invasion of *Harmonia axyridis*, a ladybeetle native to eastern Asia, to plots at the Kellogg Biological Station in southwestern Michigan, USA, 1994-2015 A) Time series documenting average number of adults captured, per trap, per year. Vertical blue lines indicate timings of shifts in dynamics, as indicated by the regime shift detector model. B) Ricker fits of phases of population dynamics as indicated by the regime shift detector model.

Figure 4: **Regime Shift Detector breaks and Ricker model fits for a species of conservation concern.** Population data documents the area occupied by overwintering Monarch butterflies in their winter habitat in the Mexico, 1995-2017. A) Time series documenting raw data of estimated area occupied by overwintering monarchs by year. Vertical blue line indicates timing of a shift in dynamics, as indicated by the regime shift detector model. B) Ricker fits of phases of population dynamics as indicated by the regime shift detector model.