

**Supplementary Material: Minimum time required to detect population trends:
the need for long-term monitoring programs**

Easton R. White*

Address:

Center for Population Biology, University of California-Davis, Davis, California 95616 USA

*Corresponding author: eawhite@ucdavis.edu

June 22, 2017

Contents

S1 Detailed example of subsampling and power calculations	S2
S2 Additional results from the main manuscript	S3
S2.1 Predictors of minimum time required	S3
S2.2 Minimum time required and biological correlates	S5
S2.3 Minimum time series and biological class	S7
S2.4 Sensitivity analysis of significance level and power	S8
S3 Minimum time calculations testing exponential growth	S8
S4 Simulations with more complicated population model	S10
S5 Minimum time required to estimate geometric growth rate	S11
S6 Using Generalized additive model to identify significant trends	S13
References	S15

Data and code for all the figures and tables can be found at (<https://github.com/erwhite1/time-series-project>). All analyses were run using R (R Core Team 2016).

S1 Detailed example of subsampling and power calculations

Here, we illustrate how we performed the subsampling and power calculations for a specific population. We provide more detail here than in the main manuscript. As an example, we examine a 35-year time series of Bigeye tuna (*Thunnus obesus*), one species in the Global Population Dynamics Database (NERC Centre for Population Biology 2010). Simple linear regression indicates a significant decrease for this population with an estimated slope coefficient of -0.0189581. We assume that this significant increase over 35 years is in fact the “true trend“. In statistical jargon, the 35-year trend is an effect that is actually present; we can reject the null hypothesis of no trend. We can then use this as a benchmark to see if subsamples of the time series also indicate a significant increase.

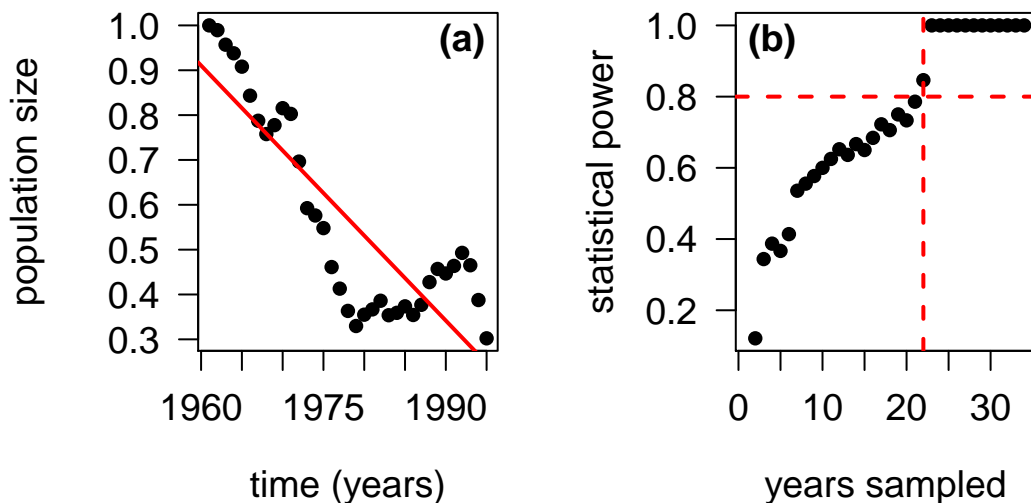


Figure A1: (a) Population size of Bigeye tuna (*Thunnus obesus*) over time. The line is the best fit line from linear regression. (b) Statistical power for different subsets of the time series in panel a.

We then perform a subsampling routine to estimate the minimum time required T_{min} (similar to Gerber, DeMaster, and Kareiva (1999)). This is the same routine we used for the results in the main manuscript.

1. We first extract all contiguous subsamples of the time series. This leads to 34 two-year subsamples, 33 two-year subsamples, and so forth until a single 35-year subsample.
2. For each subsample, we conduct linear regression and extract model coefficients and p-values.
3. We can call each set of subsamples, of the same length, a set. The fraction of subsamples within a set that show significant trends (significant slope coefficient α less than 0.05) is the statistical power. It is important to note that we only consider subsamples to be significant if they are significant in the same direction as the complete 35-year time series. In other words, we are conducting a one-tailed test.

4. We can then plot statistical power as a function of time series length (Fig. A1b). As expected, we can see that power increases with the more years that are sampled.
5. Then, we determine an appropriate level of statistical power that we find acceptable. Traditionally, this has been at 0.8, however, this is purely historical. Statistical power of 0.8 implies if a true trend is present, or there is a real change in abundance, then we will detect this trend 0.8 fraction of the time.
6. We then determine the minimum time series length (T_{min}) required to achieve that level of statistical power. Here, T_{min} is the first point in Fig. A1b where following points are also above 0.8. In this example, T_{min} is 22.

Therefore, a minimum of 22 years of continuous monitoring are required (for 0.8 statistical power at 0.05 significance level) to determine long-term changes in abundance.

S2 Additional results from the main manuscript

S2.1 Predictors of minimum time required

In the main text, we explained how the minimum time required strongly correlated with the trend strength, temporal autocorrelation, and variance in population size. Here, we use a generalized linear model framework with a Poisson error structure to determine explanatory variables of the minimum time required. We use the same 878 populations as in the main text. In figure A2, we show a set of residual plots for the regression. We then show the coefficient estimates and levels of significance in table A1.

Table A1: Output of generalized linear model to examine predictors of the minimum time required for determining long-term population trends.

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.7405513	0.0242742	154.09595	0
abs_overall_trend	-104.0533454	3.0941097	-33.62949	0
autocorrelation	-0.4899533	0.0431769	-11.34757	0
variance	18.7366110	0.6404458	29.25557	0

Our model with trend strength, autocorrelation, variance, and generation length accounted for 72.45% of the variation in the minimum time required (Table A1). However, we also found trend strength and variance to be strongly correlated with one another. Therefore, we ran two additional models with either trend strength or variance, but not both together. This resulted in lower explained deviance (analogue to R^2) of 53.03% and 45.03%, respectively.

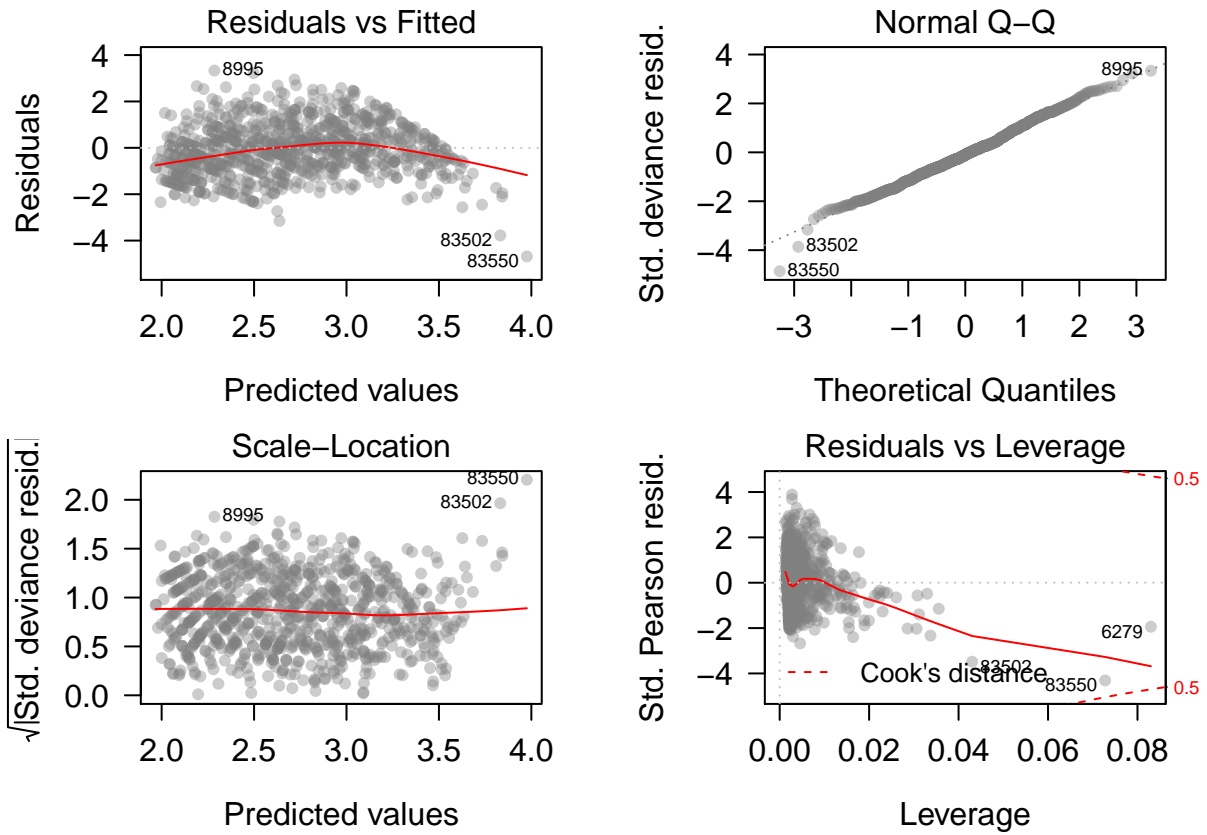


Figure A2: Output of generalized linear model with a Poisson error structure for predicting the minimum time required with explanatory variables of the absolute value of the slope coefficient (or trend strength), temporal autocorrelation, and variability in population size.

S2.2 Minimum time required and biological correlates

In the main manuscript, we examined the minimum time required to detect a significant trend in abundance over time using linear regression. As detailed in the main manuscript the minimum time required was around 15, but there was a wide distribution. Therefore, we were interested in potential explanatory variables of the minimum time required. In the main manuscript, we examined characteristics of the time series itself, like variability, autocorrelation, and the trend in abundance over time. Here, we combined our time series data with a data on life history characteristics of amniotes from Myhrvold et al. (2015). There was life history information available for 547 populations representing 315 different species, all of which were birds (Aves class).

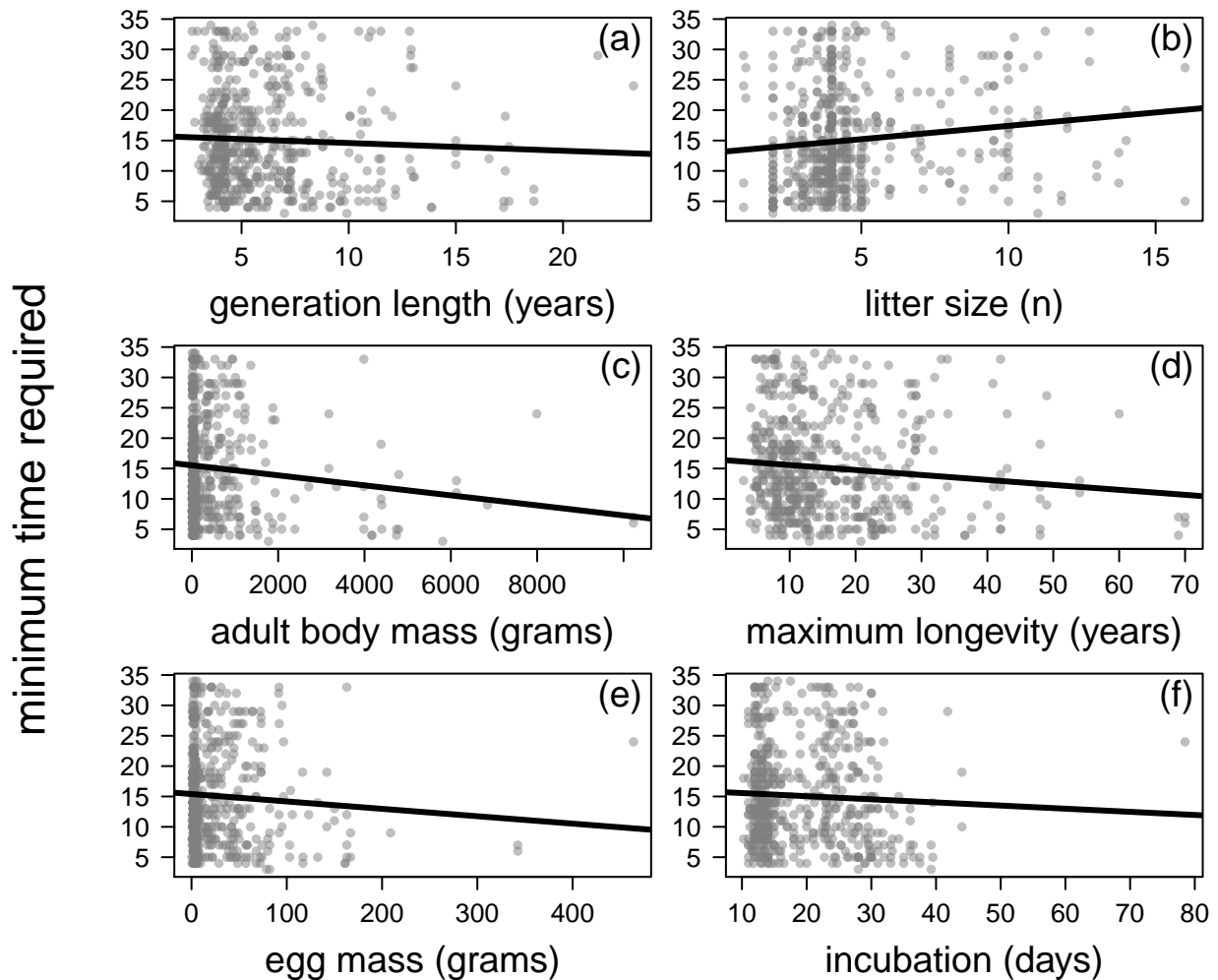


Figure A3: Minimum time required versus (a) generation length (years), (b) litter size (n), (c) adult body mass (grams), (d) maximum longevity (years), (e) egg mass (grams), and (f) incubation (days). The lines in each plot represent the best fit line from linear regression.

We then correlated minimum time required for each population with its corresponding life history characteristics. In figure A3 we examined minimum time required versus generation

length (years), litter size (n), adult body mass (grams), maximum longevity (years), egg mass (grams), and incubation (days). None of these variables had much explanatory power in accounting for the variance in the minimum time required. We ran a generalized linear model (with a Poisson error structure) and found that these six variables only accounted for 6.87% of the explained deviance in minimum time required.

S2.3 Minimum time series and biological class

Minimum time required differed for different biological classes. For instance, more time is required for species within the Actinopterygii class compared to other species (Fig. A4a). These differences between biological classes can be explained by differences in population variability, with species in the Actinopterygii class experiencing larger inter-annual variability in population size (Fig. A4c).

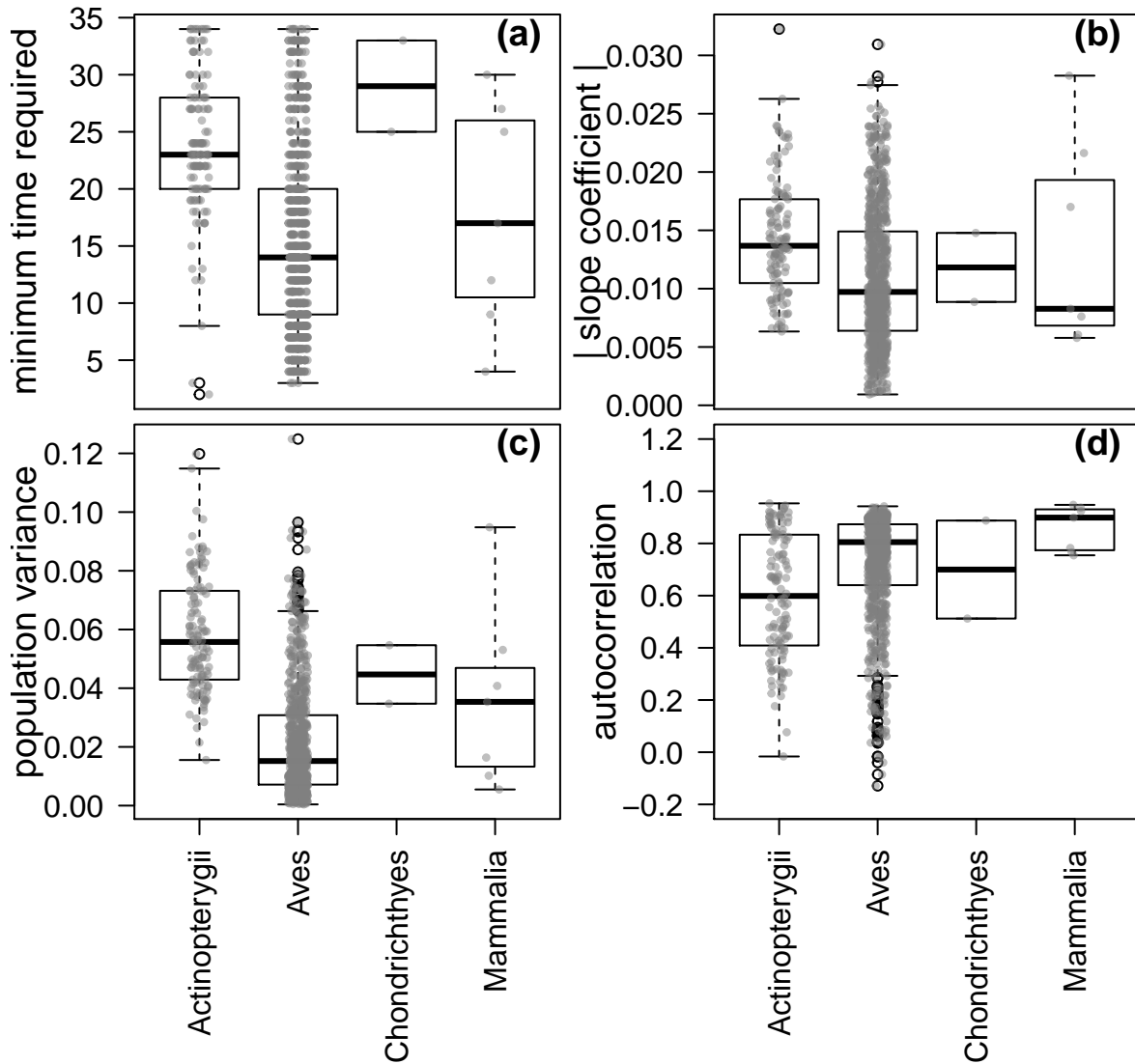


Figure A4: (a) Minimum time required to estimate change in abundance for species class, (b) long-term trend (estimated slope coefficient) by species class, (c) interannual variability in population size by species class, and (d) temporal autocorrelation by species class.

S2.4 Sensitivity analysis of significance level and power

Estimates of T_{min} depend strongly on the values used for the statistical significance level (α) and the probability of type II error (β), both of which are set by the practitioner. Again, statistical power is $1 - \beta$. Here we used simulations of the model described in the main manuscript. The model simulates linear trends in population abundance. We explored how estimates of T_{min} are affected by changes in each of these parameters. We see that the minimum time required increases with increases in statistical power or decreases with increases in the threshold for statistical significance (Fig A5).

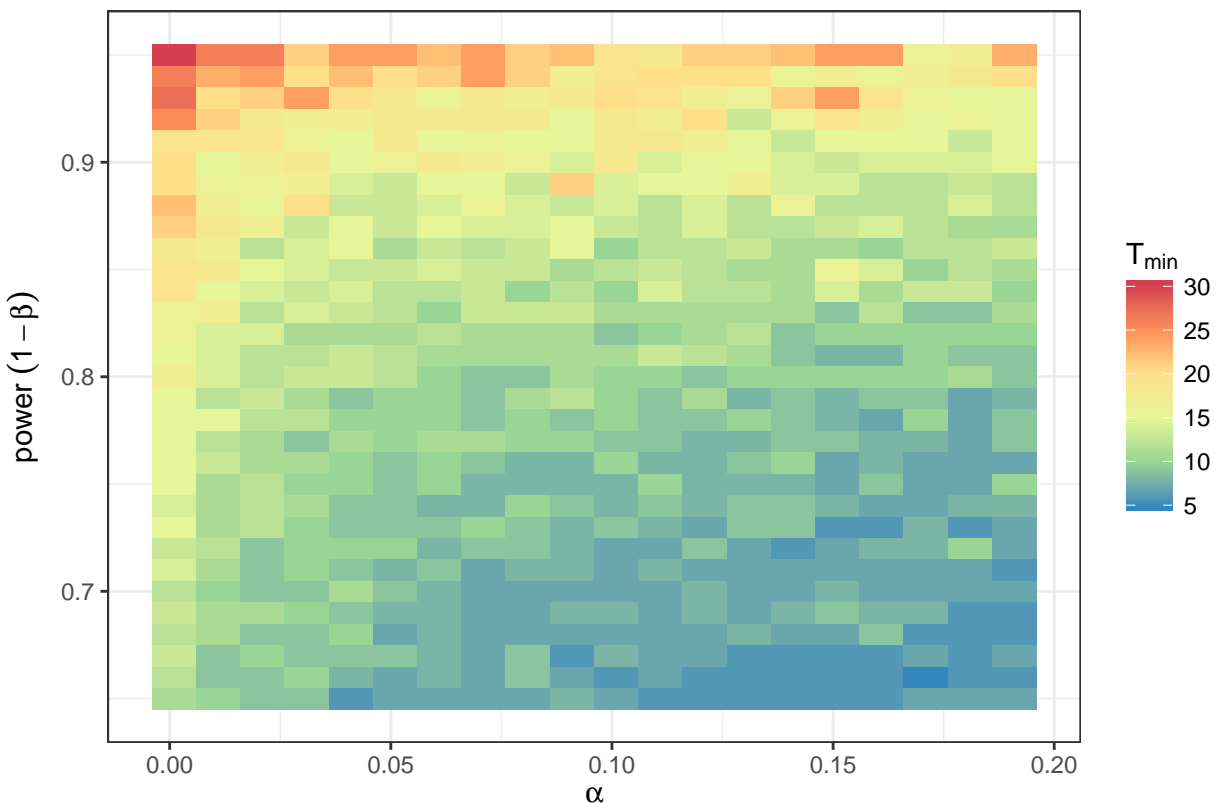


Figure A5: Minimum time required to assess long-term trends in abundance for values of statistical significance (α) and power ($1 - \beta$).

S3 Minimum time calculations testing exponential growth

In the main text, we evaluated the minimum time required to determine long-term trends in abundance via linear regression. This process examined linear trends in abundance over time. Here we examine the minimum time required to estimate long-term trends that are either exponential growth or decay. We use the same methods as described in the previous sections, but we take the \log of population density, or abundance.

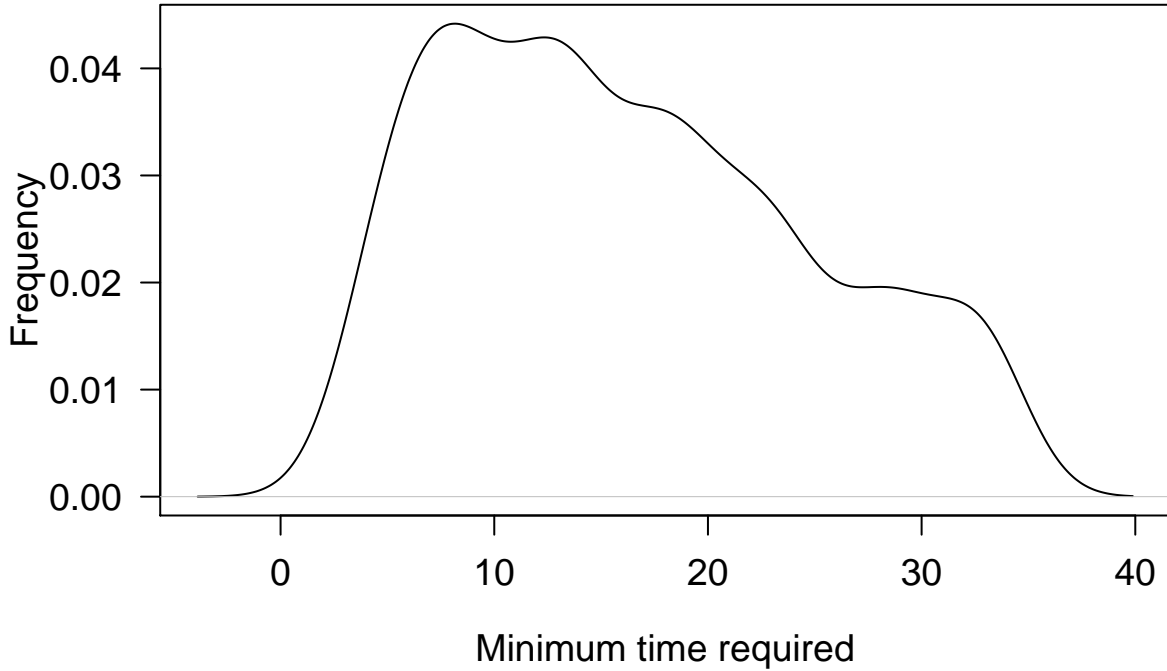


Figure A6: Distribution of the minimum time required in order to detect a significant trend (at the 0.05 level) in $\log(\text{abundance})$ given power of 0.8.

We see that the distribution of T_{min} is almost identical to that in the main manuscript (Fig. A6). This is perhaps not surprising as most time series that would significantly increase or decrease linearly would probably also significantly increase or decrease at an exponential rate. Further, the calculations here and in the main manuscript both use linear regression. Therefore both calculations estimate the same number of parameters.

S4 Simulations with more complicated population model

In the main text, we showed how a simple population model could be simulated repeatedly to estimate the power obtained with time series of increasing length (Bolker 2008; Johnson et al. 2015). The model in the main text simulated linear population growth with only a slope coefficient, y-intercept, and noise parameter required. This model is purely phenomenological and does not include any species life history. Here, we use the same routine as the main text, but simulate from a more biologically-realistic population model. We use the model described in White, Nagy, and Gruber (2014). The model is a stochastic, age-structured population model that includes density-dependence for lemon sharks (*Negaprion brevirostris*) in Bimini, Bahamas.

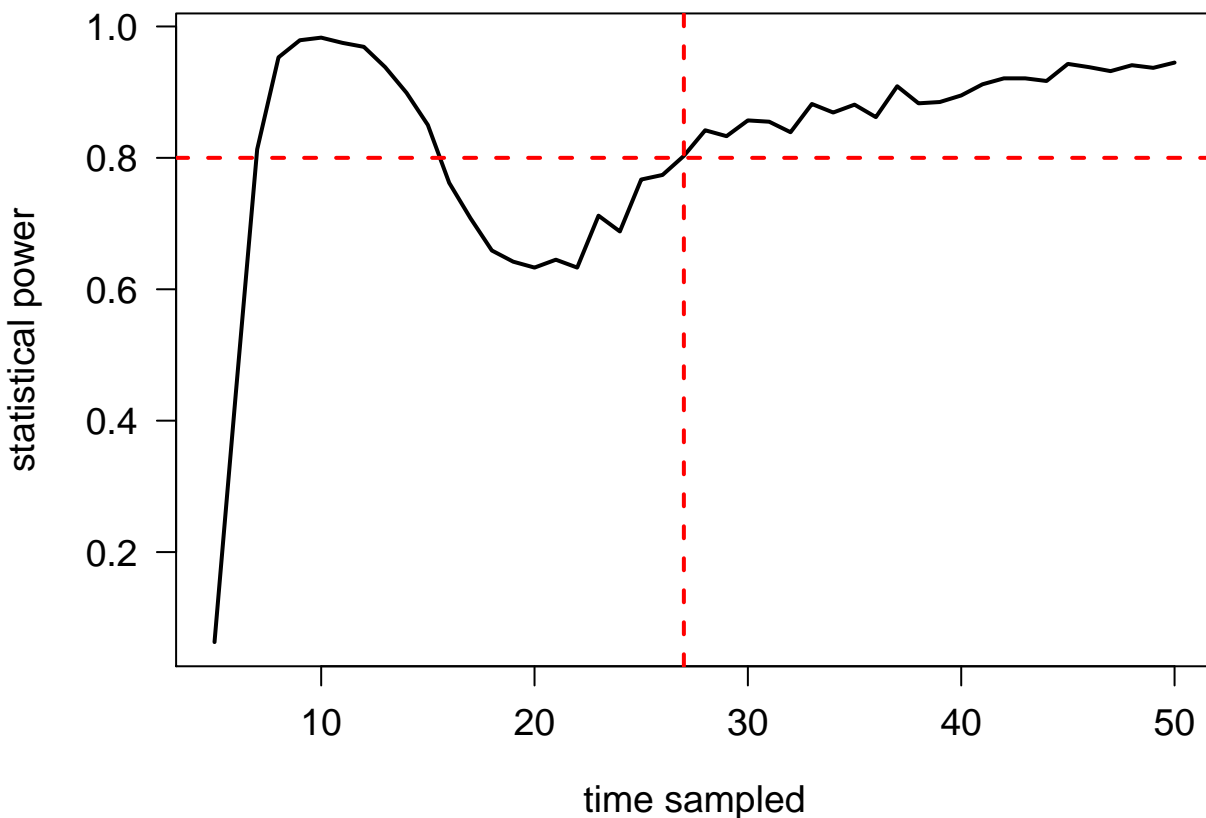


Figure A7: Statistical power for different length of time series simulations for a lemon shark population in Bimini, Bahamas.

Here, we parameterize the model for a situation where adult mortality rate is high enough to cause a population decline. In the same way we simulated models in the main text, we simulate this more biologically-realistic model for different lengths of time. For each length of time, we calculate the statistical power. Similar to results with the simpler model, statistical power generally increases with longer sampling time (Fig. A7). In this example, the minimum time required (T_{min}) to obtain at least 0.8 statistical power, given a significance level of 0.05,

is 27 years.

S5 Minimum time required to estimate geometric growth rate

Instead of detecting a trend over time with linear regression, we could also calculate the geometric growth rate of the population. In figure A8, we show how to calculate growth rates for subsamples of a time series. First, we created subsamples of each possible length from the full 35 year time series, as we did in the main next. Next, we calculated the mean and standard deviation of growth rates for each possible time series length (Fig. A8b). Lastly, we calculated the percent error $\text{percent error} = 100 \times \left| \frac{\text{observed} - \text{theoretical}}{\text{theoretical}} \right|$ between the mean of each time series length (observed) and the overall population growth rate (theoretical). In Fig. A8c), we show the percent error as a function of time series length. Here we define the minimum time required as the minimum number of years to achieve less than 20% error.

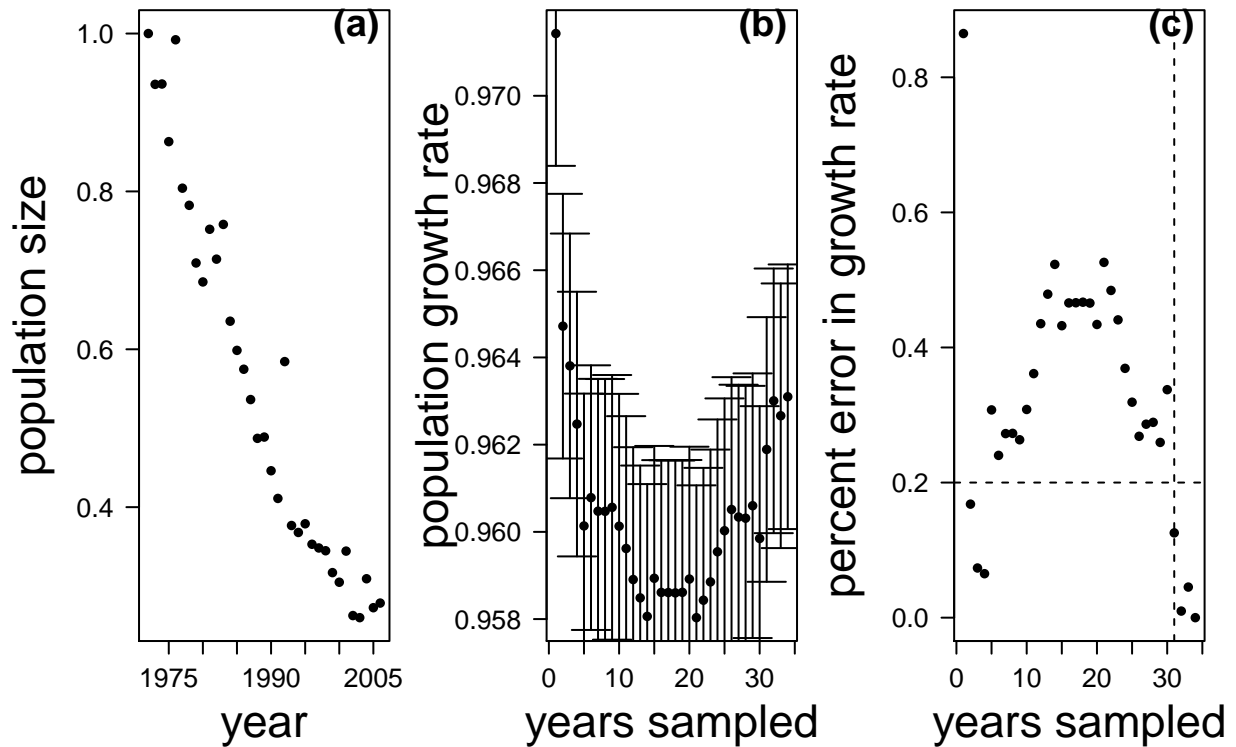


Figure A8: Example of calculating minimum time required for growth rate estimation. (a) European herring gull (*Larus argentatus*) scaled density over time, (b) mean and standard deviation of growth rate for subsamples of entire time series, and (c) the percent error between mean estimated growth rate and the true long-term growth rate. The vertical bar denotes the minimum time required to estimate growth rate within 20% error.

We applied the same calculations to 1032 population time series. We then obtain a distribution of the minimum time required to measure the “true” long-term growth rate (Fig. A9). We see

a bimodal distribution with many populations required 30+ years to estimate the long-term growth rate. The large number of short years required is due to cases where the entire time series is consistently increasing or decreasing at the same rate.

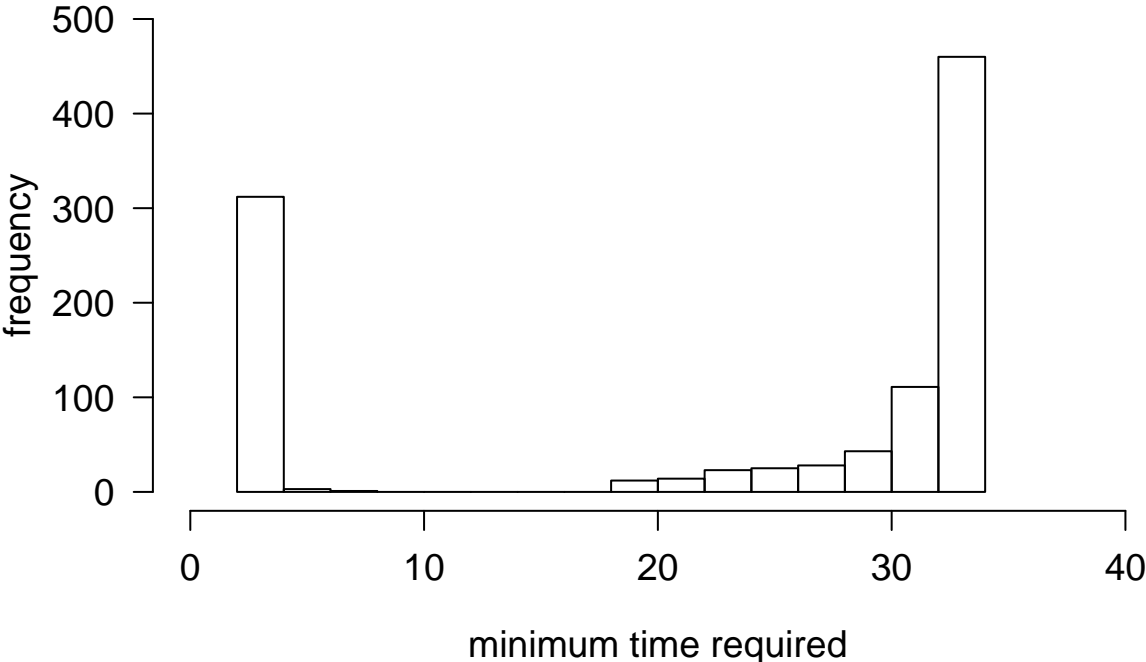


Figure A9: Histogram of the minimum time required in order to estimate the long-term growth rate within 20% error.

S6 Using Generalized additive model to identify significant trends

In the main text, we examined the minimum time required to identify a trend in abundance via linear regression. This approach allowed us to identify increases or decreases, but a linear model may not always be a good fit. Generalized additive models (GAMs) are more general than general linear models and allow more flexibility (Wood 2006). GAMs are models where a response variable depends on unknown smooth functions of explanatory variables. GAMs, therefore, can identify relationships between response variables and explanatory variables that are non-linear and perhaps more complicated. The downside of GAMs is they typically require more data and are also prone to overfitting.

Here, we conduct the same analyses in the main text, but instead calculate the minimum time series required to detect trends over time according to a GAM model. We hypothesized that GAMs should require less time to detect a trend as they are more flexible than linear regression. We provide an example that shows statistical power increases with more time sampled (Fig. A10).

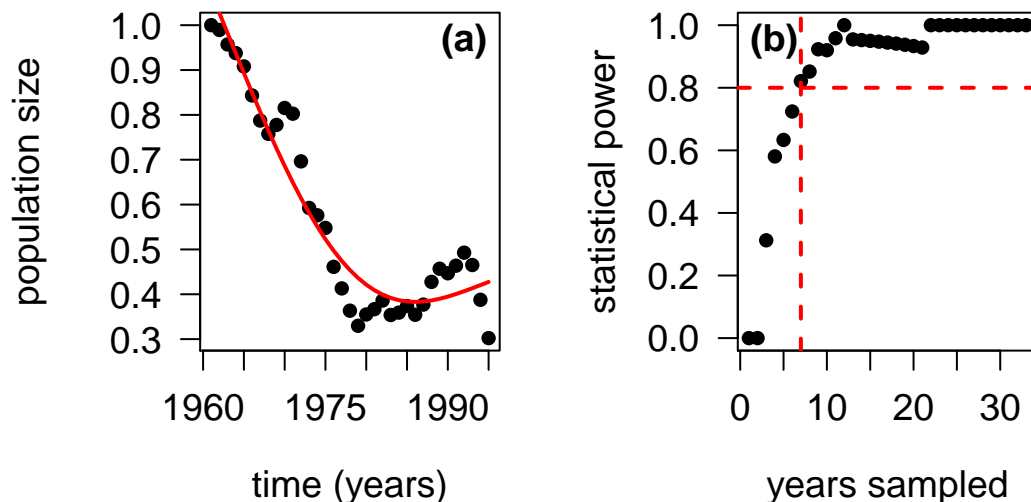


Figure A10: (a) Time series for Bigeye tuna (*Thunnus obesus*) with corresponding fitted GAM model in red and (b) statistical power as a function of the number of years sampled. The horizontal line at 0.8 indicates the minimum threshold for statistical power and the vertical line denotes the minimum time required to achieve 0.8 statistical power.

We then fit GAM models for 851 populations. We found a similar distribution of minimum time required as in the main text for linear regression (Fig. A11). However, in line with our hypothesis, the GAM models did result in a lower mean minimum time required of 14.65 years compared to the results from the main text of 16.45 years.

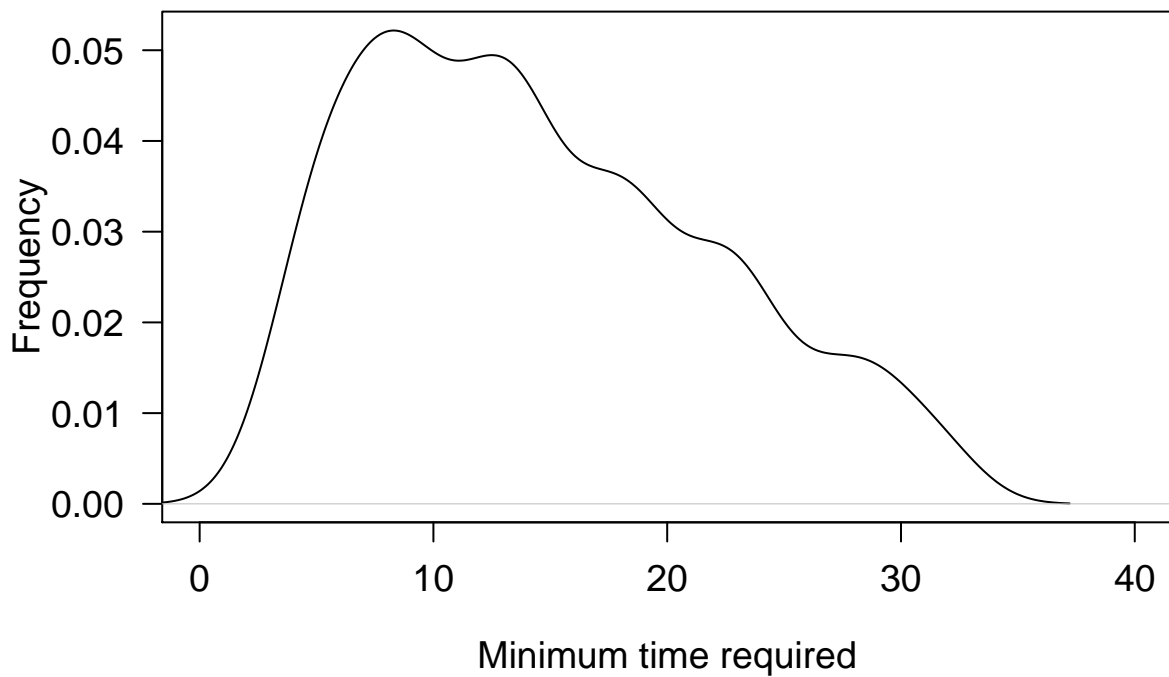


Figure A11: Distribution of the minimum time required in order to detect a significant trend (at the 0.05 level) in abundance according to a GAM model given statistical power of 0.8. The smoothing parameter was set to 3 for each population.

References

- Bolker, Benjamin M. 2008. *Ecological Models and Data in R*. 1st ed. Princeton, New Jersey: Princeton University Press.
- Gerber, L R, D P DeMaster, and P M Kareiva. 1999. “Gray whales and the value of monitoring data in implementing the U.S. endangered species act.” *Conservation Biology* 13 (5): 1215–9.
- Johnson, Paul CD, Sarah JE Barry, Heather M Ferguson, and Pie Müller. 2015. “Power analysis for generalized linear mixed models in ecology and evolution.” *Methods in Ecology and Evolution* 6 (2): 133–42. doi:10.1111/2041-210X.12306.
- Myhrvold, Nathan P., Elita Baldrige, Benjamin Chan, Dhileep Sivam, Daniel L. Freeman, and S.K. Morgan Ernest. 2015. “An amniote life-history database to perform comparative analyses with birds, mammals, and reptiles.” *Ecology* 96 (11): 3109.
- NERC Centre for Population Biology, Imperial College. 2010. “The Global Population Dynamics Database Version 2.”
- R Core Team. 2016. “R: A language and environment for statistical computing.” Vienna, Austria: R Foundation for Statistical Computing. <https://www.r-project.org/>.
- White, Easton R, John D Nagy, and Samuel H Gruber. 2014. “Modeling the population dynamics of lemon sharks.” *Biology Direct* 9 (23): 1–18.
- Wood, S.N. 2006. *Generalized Additive Models: An Introduction with R*. Chapman Hall/CRC.