

# Comment on Capdevila et al. (2021) “Global patterns of resilience decline in vertebrate populations”

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## Background

Capdevila *et al.* (2021) use data from the Living Planet Database (Loh *et al.* 2005), to evaluate temporal trends in what they refer to as resistance and recovery. Given a time series of counts, Capdevila et al. (2021) first calculate the change in population size from one time step to another as

$$r_t = \log \left( \frac{N_{t+1}}{N_t} \right), \quad (1)$$

such that  $r$  indicates whether a population is increasing ( $r > 0$ ), decreasing ( $r < 0$ ) or stable ( $r = 0$ ). They then refer to times when  $r > 0$  as instances of recovery, and those when  $r < 0$  as periods of resistance. Once the estimates of  $r$  have been calculated, Capdevila et al. create two different time series of recovery and resistance.

To estimate possible trends in recovery and resistance over time, Capdevila et al. use a state-space model for a biased random walk observed with error, whereby the true underlying change in population size is given by

$$r_t = r_{t-1} + \mu + E_t, \quad (2)$$

where  $\mu$  is the upward or downward bias over time and  $E_t \sim N(0, \sigma^2)$ . The observed (estimated) change in population size ( $Y_t$ ) is then given by

$$Y_t = r_t + F_t, \quad (3)$$

where  $F_t \sim N(0, \tau^2)$ <sup>1</sup>. Capdevila then claim that they can rearrange equation (3) and substitute it into equation (2), as apparently Daskalova *et al.* (2020) did, to arrive at

$$Y_t = Y_{t-1} + \mu + E_t + F_t. \quad (4)$$

However, their algebra is incorrect and the combined equations should instead be

$$Y_t = Y_{t-1} + \mu + E_t + F_t - F_{t-1}. \quad (5)$$

Here I show that this approach fails to recover the true changes in the log of population size from time step to another, and offer a different, but related, approach to do so.

## Estimating population size

There is a long history of estimating changes in population size from time series of count data, much of which is based upon a stochastic, discrete-time Gompertz model (Dennis & Taper 1994; Holmes 2001). Beginning with the deterministic version of the model,

$$n_t = n_{t-1} \exp[a + (b - 1) \log(n_{t-1})], \quad (6)$$

where  $n_t$  is the population size at time  $t$ ,  $a$  is the intrinsic rate of population growth, and  $b$  is the strength of density dependence. When  $b = 1$  the change in population size is density independent, and the strength of density dependence increased as  $b \rightarrow 0$ . On a log scale where  $x_t = \log(n_t)$ ,

$$\begin{aligned} x_t &= x_{t-1} + a + (b - 1)x_{t-1} \\ &= a + bx_{t-1}. \end{aligned} \quad (7)$$

Here the equilibrium population size is given by  $a/(1 - b)$  for  $b \neq 1$ . The stochastic version of this model is a simple, first-order autoregressive process, AR(1), given by

$$x_t = a + bx_{t-1} + e_t, \quad (8)$$

and  $e_t \sim N(0, \sigma^2)$ .

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<sup>1</sup>I note here that Capdevila et al. incorrectly refer to  $Y_t$  as the true change in population size, rather than  $r_t$ .

It is well known that sampling or observation errors will lead to an estimate of  $b$  that is biased low, suggesting the population is under greater density dependence than it is in reality. Thus, equation (8) is often combined with an explicit observation model to form a state-space model, whereby the observed log-counts ( $y_t$ ) are a function of the true population size plus some error, such that

$$y_t = x_t + v_t. \quad (9)$$

## Simulation study

```
## load libraries
library("MARSS")
```

## References

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