Poster

## Using structural modeling to unravel complex interactions between climatic oscillators, endogenous signals and stochastic noise in population dynamics

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Time-series analysis in population ecology usually involve the use of direct and/or delayed difference equations [1], which severely restricts the ability of the modeler to structure complex multivariate relationships between climatic phenomena and ecological variables, such as population density and growth rate [2]. Here I show that this limitation can be reduced with the implementation of structural modeling with latent constructs techniques [3] to time-series analysis in ecology.

As an example, I propose a set of three phenomenological equations describing the density-dependent dynamics of diving waterfowl, with highly variable spatial ranges and population densities ultimately dependent on rainfall fluctuations, and with complex non-additive effects of large-scale climatic phenomena on *per capita* growth rate, of the form

$$N_{t} = N_{t-1} \exp\left[\alpha + \sum_{i=0}^{d} \beta X_{t-i} + \sum_{i=0}^{d} \omega W_{t-i} + \sigma_{1} \epsilon_{t1}\right], \quad (1)$$

$$X_{t-i} = \delta + \gamma W_{t-i} + \sigma_2 \varepsilon_{t2}, \qquad (2)$$

$$W_{t-i} = \mu + \eta U_{t-i} + \tau Z_{t-i} + \sigma_3 \varepsilon_{t3}, \qquad (3)$$

where  $N_t$  denote population size at time t;  $\frac{N_t}{N_{t-1}} = per \ capita$  growth rate;  $X_{t-i}$ population density (e.g., birds/Km<sup>2</sup>);  $W_{t-i}$  rainfall variability;  $U_{t-i}$ ,  $Z_{t-i}$  two large-scale climatic oscillators (e.g., the NAO and the ENSO, [2]);  $\varepsilon_t$ , random white noise  $\approx N(0, \sigma^2)$ ; and i a time-lag of order d. Finally, we can specify climatic oscillators to covary in some sense in the above model, that is

$$\rho, \operatorname{Cov}(U_{t-i}, Z_{t-i}) \neq 0.$$
(4)

Symbols  $\alpha, \beta, \omega, \delta, \gamma, \mu, \eta, \tau, \sigma_i$  and  $\rho$  are free parameters to be estimated [3]. Additionally, observation errors, process noise and other sources of uncertainty are explicitly implemented on variables  $\frac{N_t}{N_{t-1}}$ ,  $X_{t-I}$ ,  $W_{t-I}$ , which yield a latent construct model [3].

An information-theoretic approach is suggested in order to select the most parsimonious d-lags model, and bootstrap resampling [4] must be used in order to provide unbiased uncertainty estimates of parameters and associated standard errors. The central point here is, however, that the empirical covariance matrix generated by equations (1)-(4) is a statistical hypothesis directly derived from strict biological assumptions, as the above example shows, and conventional goodness-of-fit techniques can be used to suggest the degree of plausibility of the hypothesis in relation to the theoretical covariance matrix expected if the hypothesis was, in fact, correct.

Two main advantages arise from this modeling procedure: 1) complex biological assumptions take the form of a simple falsifiable empirical covariance structure that can be compared with a theoretical model to test for statistical consistence; and 2) observation errors and stochastic noise are explicitly included in parameter and goodness-of-fit estimation, in contrast to traditional techniques, which further provides unbiased estimates.

## References

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