Developing Bayesian approaches to understand the role of observation error in mechanistic population dynamic models.

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Aims
1) Develop a robust methodology to deduce the underlying deterministic and stochastic components of population dynamics from sample time series.
2) Use biological understanding to constrain the parameterisation, and to interpret the numerical results in terms of stability and susceptibility to stochastic extinction.
3) Draw general conclusions about types of interaction associated with groups of organisms

Background. Understanding the dynamics of populations over time is a contemporary ecological challenge. Population biologists use time series data to infer the processes and mechanisms that regulate natural populations and to determine risks of extinction. However, time series of population abundance come from counts, photographs, trapping etc. and typically incorporate observation error: Observed abundance is rarely equal to the true size of the population and ignoring observation error can lead to inaccurate estimates of population parameters.

We have recently developed a Bayesian state-space model, incorporating a simple (Ricker) density-dependent population model, using the open source R platform. This performs well when fitted to time series of insect populations from laboratory cultures, where observation error is small and easily quantifiable (Bull *et al.*, 2008). The core objective of the miniproject is to extend this model to explore the dynamics of natural populations.

Methodology. In general the dynamics of an ecological population can be represented by a function of lagged historical information, $x_{t+1} = F(x_t, x_{t-1}, \ldots, x_{t-n}) + \zeta(x_t, x_{t-1}, \ldots, x_{t-n})$, where x_t is the population size at time *t*, *F* is the underlying deterministic component of the dynamics and ζ is the stochastic component. Here a discrete time function is used to correspond to the discrete sampling that generally occurs for biological populations. In addition to population dynamics, the observed number of organisms can generally be considered as a binomial sample of the true number.

The keys to this proposal are three-fold: firstly to determine suitable functional forms for the discrete time function *F* based on a mechanistic understanding of ecological population dynamics; secondly to determine how the noise ζ is related to the deterministic component, *F,* based on a mechanistic model of the population interactions; finally to further develop existing statistical tools to parameterise such models from the available time-series data.

Models will be fitted to time series from the Global Population Dynamics Database (http://www3.imperial.ac.uk/cpb/research/patternsandprocesses/gpdd) – an unparalleled, open access database, which combines abundance data with metadata on the ecology and life histories of animals as well as an index of data 'reliability'.

Interpretation and Challenges. It is important to realise that simply obtaining a good fit to time-series data is meaningless without a biological interpretation of the results. It is therefore vitally important that the results are interpreted with reference to known factors about the organism's natural history. It will also be important to test the predictive power of the parameterised models. This will be done by parameterising models using part of the available data, and then determining the model's ability to predict the remaining data.

PhD project. This project is highly suitable for development into a PhD project. Future direction could follow mathematical or ecological routes, depending on the interests and aptitude of the student. In addition, we are currently in discussion with EPSRC over future funding opportunities for this line of research.

Bull, J. C. & Bonsall, M. B. (2008) Overcompensatory population dynamic responses to environmental stochasticity. *J. Anim. Ecol.,* **77**, 1296-1305.