Towards Improved Prediction of Chaos in Ecology: A Model-Data Fusion Approach

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Introduction
The discovery by May in the 1970s that simple population models may generate complex chaotic dynamics triggered heated debate and caused a paradigm shift in ecology. Since May’s findings, mathematical models have shown that chaos can be generated by a plethora of ecological mechanisms, including competition for limiting resources, predator–prey interactions, and food-chain dynamics. However, experimental demonstrations of chaos in ecology have been scarce, and limited to simple laboratory systems with a short duration and artificial species combinations. In a recent Nature paper Beninca et al. (2008) presented the first experimental demonstration of chaos in a long-term experiment with a complex food web. The species abundances showed striking fluctuations over several orders of magnitude, despite constant external conditions. Predictability was limited to a time horizon of 15–30 days, only slightly longer than the local weather forecast. In this project, sponsored by a grant from the UCI-ENVIRONMENT INSTITUTE we will demonstrate that species abundances predictability can be improved considerably by merging the predictions of a commonly used dynamic population model with the available measurements. This mathematical technique, also known as data assimilation, has found widespread application and use in related fields such as hydrology, oceanography and climatology for operational forecasting, but has not yet been used in ecology. Our data assimilation project, will (a) help to close the gap between complex ecological models and observations, (b) provide important guidance on how to improve our mathematical description of ecological processes, and (c) help ecologists decide when and where to measure species compositions with a view towards a sustainable future. This project also benefits from the PIs ongoing collaboration with Dr. Beninca from the University of Amsterdam (UvA) in the Netherlands.

Data
The food web analyzed in Beninca et al. (2008) and isolated from the Baltic Sea will be used. This food web consists of bacteria, phytoplankton species, herbivorous and predatory zooplankton species, and detritivores. The food web was cultured in a laboratory mesocosm, and sampled twice a week for more than 2,300 days.

Model
We predict the time series of species abundances using the population model of Vandermeer (2004). This model involves two preys (P, phytoplankton) and two predators (Z, zooplankton), and uses a system of coupled ODEs

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\begin{align*}
\frac{dP}{dt} & = r_1 P \left( 1 - \frac{P + P_1}{K_1} \right) - \frac{g_1 P Z_1}{H_1 + P_1 + P_z} - \frac{g_2 P Z_2}{H_2 + P_1 + P_z} \\
\frac{dZ}{dt} & = r_2 Z \left( 1 - \frac{P + P_2}{K_2} \right) - \frac{g_3 P Z_1}{H_1 + P_2 + P_z} - \frac{g_4 P Z_2}{H_2 + P_2 + P_z}
\end{align*}
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Model-data fusion method
The SODA methodology of Vrugt et al. (2005) is used to merge the population model predictions with the respective observations. This should improve predictability of complex food webs.

Initial results synthetic data
To test our methodology we first illustrate our approach using synthetically (model generated) data. The top two plots of Figure 3 depict the SODA results for the phytoplankton and the bottom two panels for the zooplankton. Data is with black “+” symbols and corresponding SODA ensemble (prediction uncertainty) in cyan.

Figure 1: Overview of the model-data fusion problem

Figure 2: Data of the mesocosm experiment from Beninca et al. (2008)

Figure 3: Results of Vandermeer model using synthetic data

Literature Cited