Unlocking ensemble ecosystem modelling for simulation of high-dimensional networks: From days to minutes

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Abstract: Conservation planning requires an analysis of the potential risks of action, including the risk that the conservation is ineffective or causes unintended consequences. In this respect, quantitative ecosystem models are a valuable decision-making tool for predicting ecosystem responses to actions. Systems of differential equations, such as the generalised Lotka-Volterra equations, can be combined with information about species interactions via food webs to model species abundances. However, parameterising these models is challenging – particularly for data-limited ecosystems.

Ensemble ecosystem modelling (EEM) is an increasingly popular method that uses expected dynamic systems constraints to parameterise ecosystem models without time-series abundance data (Baker et al., 2017). This method works by randomly sampling the parameter space to identify an ensemble of models with a stable equilibrium that has coexistence (feasibility) for all species in the ecosystem defined by the inputted food web. But this process is computationally intensive because there can be a very low probability of randomly sampling ecosystem models which meet the constraints (Peterson and Bode, 2021), limiting EEM's usefulness to highly simplified, low-dimensional ecosystem networks.

To overcome this computational burden, we connected EEM to approximate Bayesian computation techniques, allowing us to take advantage of established efficient parameterisation algorithms in the field. We develop a new algorithm called SMC-EEM, adapted from Drovandi and Pettitt's (2011) sequential Monte Carlo approximate Bayesian inference algorithm – an efficient parameterisation process for low probability constraints, given intractable likelihoods (Sisson et al., 2007).

Through simulation studies, we show that our SMC-EEM algorithm is several orders of magnitude faster than the standard-EEM method for high-dimensional ecosystem models. We show that the methods produce equivalent results though a combination of standard sample comparison methods, and a novel use of data-informed sensitivity analysis. Demonstration on a Great Barrier Reef food web (Rogers et al., 2015) reveals that SMC-EEM reduces the computation time from 46 days to 41 minutes, whilst giving similar time-series predictions and inferences.

Our new method takes the parameterisation of feasible and stable ecosystem models from impractical to practical. Consequently, more realistic, high-dimensional ecosystem models can be considered. Our SMC-EEM method allows us to forecast the potential risks of conservation actions in data-limited ecosystems within minutes, without simplifying our understanding of complex ecosystem dynamics.

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