

BI-CO MATHEMATICS COLLOQUIUM

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"Parameter estimation in population ecology: An approximate Bayesian computation approach for stochastic models."

Monday, November 3, 2014

Talk at 4:00 – H109

Tea at 3:30 – KINSC Math Lounge, H208

Abstract:

Many problems in biology require increasingly complex models to describe the heterogeneity present in nature. Specifically in population ecology, intraspecific variation in life history traits can create models that are impossible to fit with maximum likelihood methods. Approximate Bayesian computation (ABC) is a computational tool for parameter estimation in situations where likelihoods cannot be computed or approximated. Instead of using likelihoods, ABC methods quantify the similarities between an observed data set and repeated simulations from a model. A practical obstacle to implementing an ABC algorithm is selecting summary statistics and distance metrics that accurately capture the main features of the data. We demonstrate the application of a sequential Monte Carlo ABC sampler (ABC SMC) to parameter estimation of a general stochastic stage structured population model with ongoing reproduction and heterogeneity in life history processes. Individual variation in demographic traits has considerable consequences for population dynamics in many systems, but including it in a population model by explicitly allowing stage durations to follow a realistic distribution creates a complex model. In this project, we apply the ABC SMC framework to fit the population model to a simulated data set with known underlying parameters to evaluate the performance of the algorithm. We also introduce a systematic method for selecting summary statistics and distance metrics, using simulated data and receiver operating characteristic (ROC) curves from classification theory. Evaluations suggest that the approach is promising for model inference and parameter estimation in population ecology and could have wide applications throughout ecology.

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