

Approximate Bayesian Computation (ABC) for calibrating and evaluating Individual Based Models

Project Highlights:

- Spatially-explicit landscapes IBMs can show how populations change over time in response to management actions
- Development of new Monte Carlo techniques for calibrating IBMs using state-of-the-art statistical techniques
- Use of machine learning methods for reducing computational cost of Monte Carlo approaches

Overview:

Individual-based models (IBMs) are used to simulate the actions of individual animals as they interact with one another and the landscape in which they live. When used in spatially-explicit landscapes IBMs can show how populations change over time in response to management actions. For instance, IBMs are being used to design strategies of conservation and of the exploitation of fisheries, and for assessing the effects on populations of major construction projects and of novel agricultural chemicals.

There is urgent need to improve methods of calibrating such models: existing methods are too slow, and not always accurate. This project aims to improve the best existing method: Approximate Bayesian Computation, ABC. ABC is currently being used at Reading for statistical inference in a diverse range of applications in ecology, evolution and more widely, including for example: models of elephants in Amboseli; mackerel in the North East Atlantic; local butterfly populations; but also evolution of pathogens; social network analysis; and statistical physics (see Didelot et al. 2011; Prangle et al. 2016; van der Vaart et al. 2016). In most of these cases the challenges of parameter estimation and model comparison are both of importance, but implementation can prove computationally expensive. This project aims to improve ABC methods and to collaborate with model builders to help them in fitting models to data. Initial focus will be on IBMs developed for fisheries management by CEFAS, part of the UK government, <https://www.cefas.co.uk/>.



Figure 1: Screenshot of a spatially-explicit IBM for modelling sea bass stocks.

Methodology:

ABC compares model outputs with data and is particularly useful for statistical inference where the model is only available as a computer simulator such as an IBM. ABC is a relatively new field of research, and is a hot topic in statistics and several applied fields (Beaumont 2010). There are many open problems in this area, some of which lie at the heart of this project, including:

- ABC for high-dimensional parameter spaces. IBMs often have more than 10 parameters that have to be estimated by fitting the model to data: more than in many current applications of ABC.
- ABC for computationally expensive simulators. Some IBMs take several minutes to complete a run. This is a problem because existing ABC methods require thousands of runs to obtain reliable results.

This project will develop new methods to address these issues, driven by the need for accurate fisheries models to guide fisheries management.

Complex models in many fields (e.g. neuroscience, ecology, genetics) are not identifiable from the data that scientists wish to fit them to. In some cases, this points to a need to refine the model. However, this lack of identifiability is rarely known in advance, and is often very informative to the developers of the model. Thus, there is a need to perform accurate Bayesian inference in such cases. Recently developed *active subspace* approaches propose a means of recognising a subspace on which the parameters are identifiable, and use this to enhance the efficiency of Markov chain Monte Carlo algorithms. Further, the method may be used to inform practitioners about the suitability of their model.

Masters Project summary: Understand and use methods for inferring the parameters of individual-based models. Then focus on avoiding problems encountered due to the lack of identifiability of parameters in the model, using developing a new technique for using active subspaces together with recent Monte Carlo methods.

Further reading:

- Beaumont (2010) "ABC in Evolution and Ecology." *Annual Review of Ecology, Evolution, and Systematics* 41: 379–406.
- Constantine, P. G., Kent, C., and Bui-Thanh, T. (2016). Accelerating MCMC with active subspaces. *SIAM Journal on Scientific Computing* 38(5), A2779–A2805.
- Didelot et al. (2011) "Likelihood-Free Estimation of Model Evidence." *Bayesian Analysis* 6 (1): 49–76.
- Prangle et al. (2016) "A Rare Event Approach to High Dimensional ABC." *Arxiv*.
- van der Vaart et al. (2016) "Predicting How Many Animals Will Be Where: How to Build, Calibrate and Evaluate IBMs." *Ecological Modelling* 326: 113–23.