

H.C. Johnson*

LONDON SCHOOL OF HYGIENE AND TROPICAL MEDICINE

e-mail: Helen.Johnson@lshtm.ac.uk

W.J. Edmunds

LONDON SCHOOL OF HYGIENE AND TROPICAL MEDICINE

e-mail: John.Edmunds@lshtm.ac.uk

R.G. White

LONDON SCHOOL OF HYGIENE AND TROPICAL MEDICINE

e-mail: Richard.White@lshtm.ac.uk

Novel ABC - Bayesian Emulation Hybrid Algorithm For Complex Model Calibration: The First Waves

Introduction. The complexity of the dynamical systems underlying epidemics has led to the use of large-scale stochastic models for prediction purposes. However, methods for robustly calibrating and analysing these simulators can be prohibitively inefficient. We propose an algorithm for fitting complex models that incorporates elements of both Approximate Bayesian Computation (ABC) and Bayesian Emulation. ABC enables inference about model parameters without the need for calculating a likelihood function, by generating approximations from repeated model runs. However, each complex model run might take hours. Emulation methods are being developed in the fields of cosmology, oceanography and meteorological modelling. The complex model function is summarised as an ‘emulator’: a stochastic function that represents the global behaviour of the complex model function as a linear regression model and local deviations from this behaviour as Gaussian processes. The emulator then becomes a cheap proxy for the complex model, allowing both calibration and probabilistic sensitivity analysis to be conducted in a fraction of the computational time.

Methods. We report the initial application of an emulation-based calibration algorithm to an individual-based stochastic model of STI transmission in Uganda. Starting with uninformative priors for 19 behavioural and biological input parameters, we ‘trained’ an emulator with 200 sampled parameter sets and their corresponding complex model output (point estimates of HIV prevalence). Sampling a further 10,000 parameter sets from the priors, we used the emulator to make output predictions over a large area of input parameter space. Weighting each parameter set according to goodness of fit to observed data, we identified promising areas of parameter space to evaluate using the complex model. A more accurate emulator was then trained, incorporating this additional complex model output. This process was repeated in ‘waves’ as per sequential ABC methods.

Results. The use of emulators allowed an evaluation of large areas of parameter space due to increased computational efficiency. Processing time for one prevalence point estimate was reduced from over 15 minutes on an HPC cluster to less than 0.1 second on a PC. Even the first two waves of such an algorithm provided helpful insight into the most influential parameters and identified promising regions of parameter space.

Conclusions. The development of an ABC - Bayesian Emulation hybrid approach to complex model calibration is promising, with emulators offering large advantages in computational efficiency. However, further research is needed regarding weighting, tolerance levels and covariance.