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## **Using Mixture Density Networks to Emulate Complex Individual-Based Models in Inference**

In epidemiology, and mathematical biology in general, there are a profusion of complex computationally-costly models. Simulations of these models can take very long to run, and especially if the models require to be evaluated several times this can pose as a most crippling impediment. This introduces the idea of using emulation, where the simulation is approximated with a statistical model that is much quicker to evaluate. Indeed, there have been recent developments in deep neural networks that we can leverage for this task.

Using Tensorflow, an open-source software library for machine learning, we implemented a particular kind of neural network called a mixture density network (MDN), which allows for the fact that a single input in the model can have multiple outputs due to stochastic variation. Once the network was implemented, an individual-based model of an epidemic was used to generate data for the MDN. We then evaluated the model via cross-validation.

An application to be looked into is for Approximate Bayesian Computation (ABC). This is a technique to perform Bayesian Inference where a likelihood is computationally expensive or intractable, as is often the case with an individual-based model. The disadvantage of this technique is that it requires many model evaluations, and so it can be a very slow process, but

with emulation this can be resolved. Further, an emulator that outputs an associated probability for a given data statistic, as an MDN does, fits well for the procedure.