

## Approximate Bayesian Computation

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An increasing number of models are sufficiently complicated that their likelihood functions cannot easily be evaluated numerically. This is problematic for most methods of statistical inference. An alternative approximate "likelihood-free" approach is possible when datasets can be simulated from the model. Here Datasets are simulated from many parameter values and those producing close matches to the observed data are used for inference. This talk reviews a simple and popular likelihood-free method which uses a Bayesian framework: approximate Bayesian computation (ABC).

The talk will first introduce and demonstrate a basic ABC algorithm. Then other topics will be covered including: summary statistics, post-processing output, tuning ABC, ABC versions of MCMC and SMC, model choice, and ABC software. Applications will also be reviewed, concentrating on population genetics, infectious disease epidemiology and systems biology.