



abc: an R package for Approximate Bayesian Computation (ABC)

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Many recent statistical applications involve inference under complex models, where it is computationally prohibitive to calculate likelihoods but possible to simulate data. Approximate Bayesian Computation (ABC) is devoted to these complex models because it bypasses evaluations of the likelihood function using comparisons between observed and simulated summary statistics. We introduce the R abc package that implements several ABC algorithms for performing parameter estimation and model selection. In particular, the recently developed non-linear heteroscedastic regression methods for ABC are implemented. The abc package also includes a cross-validation tool for measuring the accuracy of ABC estimates, and to calculate the misclassification probabilities when performing model selection. The main functions are accompanied by appropriate summary and plotting tools. Considering an example of demographic inference with population genetics data, we show the potential of the R package.

R is already widely used in bioinformatics and several fields of biology. The R abc package will make the ABC algorithms available to the large number of R users. abc is a freely available R package under the GPL license, and it can be downloaded at [this http URL](#)

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