

Incoherent phylogeographic inference

Templeton (1) makes a broad attack on the foundations of Bayesian statistical methods—rather than on the purely numerical technique called approximate Bayesian computation (ABC)—using incorrect arguments and selective references taken out of context. The most significant example is the argument, “The probability of the nested special case must be less than or equal to the probability of the general model within which the special case is nested. Any statistic that assigns greater probability to the special case is incoherent. An example of incoherence is shown in human evolution for ... the approximate Bayesian computation (ABC) method.” This opposes both the basis and the practice of Bayesian testing.

The confusion seems to arise from misunderstanding the difference between scientific hypotheses and their mathematical representation. Consider vaccine testing, for which in what follows we use VE to represent the vaccine efficacy measured on a scale from $-\infty$ to 100. Exploratory vaccines may be efficacious or not. Thus, a real biological model corresponds to the hypothesis “VE = 0,” that the vaccine is not efficacious. The alternative biological possibility, that the vaccine has an effect, is often stated mathematically as the alternative model “any allowed value of VE is possible,” making it seem that it contains “VE = 0.” However, Bayesian analysis assigns each model prior distributions arising from the background science; a point mass (e.g., probability $\frac{1}{2}$) is assigned to “VE = 0,” and the remaining probability mass (e.g., $\frac{1}{2}$) is distributed continuously over values of VE in the alternative model. Elementary use of Bayes’ theorem (see, e.g., ref. 2) then shows that the simpler model can indeed have a much higher posterior probability. Mathematically this is explained by the probability distributions residing in different dimensional spaces and is elementary probability theory for which use of Templeton’s “Venn diagram argument” is simply incorrect.

Templeton also argues that Bayes factors are mathematically incorrect, and he backs his claims with the notion of *coherence* of Lavine and Schervish (3). These authors do indeed criticize the use of Bayes factors as *stand-alone* criteria but point out that, when combined with prior probabilities of models (as illustrated in the vaccine example above), the result is fully coherent posterior probabilities. Furthermore, Templeton directly attacks the ABC algorithm. ABC is simply a numerical computational technique; attacking it as incoherent is similar to calling calculus incoherent if it is used to compute the wrong thing.

Finally, we note that Templeton has already published essentially identical if more guarded arguments in the ecology literature; we refer readers to a related rebuttal to Templeton’s (4) critique of the Bayesian approach by Beaumont et al. (5) that is broader in scope, because it also covers the phylogenetic aspects of nested clade vs. a model-based approach.

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Author contributions: J.O.B., S.E.F., A.E.R., and C.P.R. designed research, performed research, and wrote the paper.

The authors declare no conflict of interest.

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