A tenth crucial question regarding model use in phylogenetics

John Gatesy

Department of Biology, University of California – Riverside, Spieth Hall 2314, Riverside, CA 92521, USA

‘Unfortunately, in most phylogenetic analyses, even if a log-likelihood is calculated, it is never compared with the best log-likelihood value to see if the models being considered are adequate. In fact, the fit is almost invariably awful, which may explain why such comparisons are not often made.’

J. Reeves, 1992 [1]

Kelchner and Thomas addressed nine key questions regarding the use of stochastic models in phylogenetics [2]. A tenth crucial question was not explored in detail in their TREE review: ‘In modern systematic studies, how often is the fit between model and data absolutely poor? At their best, models should provide adequate explanations of complex biological patterns. Yet until now, systematists have been preoccupied primarily with the relative fit of competing models to DNA datasets [3]. Simple methods for detecting an absolutely poor fit between DNA sequence data and a particular model have existed for some time [1,4–6], but, unfortunately, these tests have been implemented in relatively few cases [7]. Perhaps either buoyed by studies that asserted the robustness of model-based methods [8] or daunted by computational demands, systematists have hidden their heads in the sand for ~15 years.

In most published studies, statistical criteria are applied to determine which model, among a set of competing models, fits the empirical data best [3]. From the initial set, a particular model can be chosen as ‘optimal,’ but might simply represent the best of several extremely poor choices, none of which fit the empirical data well. Given the simplicity of most models, it is possible that model selection in modern systematics is analogous to an overweight man shopping in the petites department of a women’s clothing store. A particular garment might fit the portly man best, but this does not imply a good overall fit. Likewise, to assume that any of the simple molecular models commonly utilized by systematists [3] provide a good fit to the data is a leap of faith, especially considering that the most parameter-rich model (i.e. the largest dress in the store) often is chosen as the best for published data matrices [2].

Adequate models of molecular evolution are a prerequisite for successful interpretation of data in the model-based approach to systematics [1–10]. For example, statistical consistency (touted as a hallmark of this framework [9]) and accuracy of branch support values are not guaranteed given a mismatch of model to data [8,10]. The fact that the goodness of fit between DNA data and current models is unknown is a disturbing aspect of phylogenetic analysis in the 21st century. Are molecular models poor fits to the highly complex datasets compiled by modern systematists? Unfortunately, and a bit embarrassingly, we still do not know the answer to this tenth crucial question for the great majority of published datasets [7].

References


7 Wernegreen, J.J. (2005) For better or worse: genomic consequences of their best, models should provide adequate explanations of complex biological patterns. Yet until now, systematists have hidden their heads in the sand for years.


0168-9547/$ – see front matter © 2007 Elsevier Ltd. All rights reserved.
doi:10.1016/j.tree.2007.08.007
A recent paper by Lindenmayer and Fischer [1] attempts to refine definitions within the ‘panchestron’ of habitat fragmentation research. Ironically, in their pursuit of one panchestron they open another, that of ‘story-telling’ in science.

In the scientific literature the term ‘story-telling’ was originally used as a critique of a purely adaptationist approach to the study of evolution. In their ‘Spandrels panchestron’, Gould and Lewontin [2] criticized those evolutionary biologists who assumed the operation of natural selection rather than demonstrated it. As a consequence, ‘story-telling’ has become more or less synonymous with bad science. This emotive connotation persists today with the debate over approaches to the study of natural selection as relevant as ever [3,4].

Despite the negative connotations of the term ‘story-telling’, we suggest that the story-telling step in scientific investigation (in the colloquial sense of being creative) is in fact ubiquitous but too often taken for granted. Although the process of using ideas to generate an hypothesis is less structured than the rule-based methodological testing of that hypothesis it is nonetheless integral to the scientific process. Darwin spent decades assembling careful and detailed observations that led to the formulation of his hypothesis of natural selection, though he was never in a position to test it. The generation of an hypothesis is analogous to the search for ‘truth’ in history. Historians examine and compare narratives to synthesize an accepted version of truth, and after scrutiny such stories might become accepted as fact.

The bad science criticized by Gould and Lewontin lies not in the generation of an hypothesis or the story-telling step, but in acceptance of the untested, or indeed untestable, hypothesis as fact, such that it becomes dogma. Lindenmayer and Fischer [1], who highlight ‘story-telling’ as a problem that ‘contributes to unproductive debates’ in the habitat fragmentation literature, fail to distinguish between the studies that generate hypotheses [5] and those that test them [6].

We suggest the emotive connotations that have become associated with the term ‘story-telling’ be saved for the bad science itself and that the creative story-telling step in the scientific process is a necessary part of embracing complexity. Furthermore, any use of the term in the literature must be properly referenced to avoid ambiguity.

References

Story-telling: an essential part of science
Janet Gardner1, Peter Marsack1, John Trueman1, Brett Calcott1 and Robert Heinsohn2

1 School of Botany & Zoology, Australian National University, Canberra, ACT 0200, Australia
2 Fenner School for Environment and Society, Australian National University, Canberra, ACT 0200, Australia

A recent paper by Lindenmayer and Fischer [1] attempts to refine definitions within the ‘panchestron’ of habitat fragmentation research. Ironically, in their pursuit of one panchestron they open another, that of ‘story-telling’ in science.

In the scientific literature the term ‘story-telling’ was originally used as a critique of a purely adaptationist approach to the study of evolution. In their ‘Spandrels paper’, Gould and Lewontin [2] criticized those evolutionary biologists who assumed the operation of natural selection rather than demonstrated it. As a consequence, ‘story-telling’ has become more or less synonymous with bad science. This emotive connotation persists today with the debate over approaches to the study of natural selection as relevant as ever [3,4].

Despite the negative connotations of the term ‘story-telling’, we suggest that the story-telling step in scientific investigation (in the colloquial sense of being creative) is in fact ubiquitous but too often taken for granted. Although the process of using ideas to generate an hypothesis is less structured than the rule-based methodological testing of that hypothesis it is nonetheless integral to the scientific process. Darwin spent decades assembling careful and detailed observations that led to the formulation of his hypothesis of natural selection, though he was never in a position to test it. The generation of an hypothesis is analogous to the search for ‘truth’ in history. Historians examine and compare narratives to synthesize an accepted version of truth, and after scrutiny such stories might become accepted as fact.

The bad science criticized by Gould and Lewontin lies not in the generation of an hypothesis or the story-telling