

Conceptual issues in phylogeny and conservation: a reply to Faith and Baker

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Abstract: We trace the history of using systematics as a surrogate for phylogeny and that of 'phylogenetic diversity' and show that criticisms by Faith and Baker (2006) of our paper (Crozier, Dunnett, and Agapow 2005) are without foundation.

Keywords: evolutionary history, phylogenetic diversity, genetic diversity, systematic nomenclature, phylogeny, biodiversity

History of using systematics as a surrogate for phylogeny

We regret missing, in our brief historical introduction, Faith (1994) and associated papers by the same author alluded to by Faith and Baker (2006) and asserted by them to take the use of phylogenetic branch lengths inferred from systematics to the “proof of concept” stage. However, the idea of using systematics in biodiversity assessment has a long history prior to these publications, e.g., Strahan (1989) reviews earlier approaches which do not involve branch lengths.

The concept of inferring branch lengths from systematics has been independently derived several times (e.g., Warwick and Clarke (1995), and Cattin et al. (2004)), and hence is well established. What constitutes “proof of concept” is subjective, but at a minimum it should include an examination of the general properties of a measure and of its statistical sufficiency and go beyond just providing examples as Faith (1994) did. “The unexamined metric is not worth using”, as Plato might have attributed to Socrates. Faith (1994) did none of these deeper examinations and therefore we stand by our claim to have provided the first detailed examination of such a metric, while recognizing that the work can still be taken further. Clark and Warwick (1998) examined the statistical sufficiency of their measure and for it indeed gave a “proof of concept”, but as we stated (Crozier, Dunnett and Agapow 2005) their measure was not intended to assess sets of localities together (as we did) but rather to compare the structure of communities.

Referring to MeSA, Faith and Baker (2006) allege that ‘it appears that this software might incorrectly calculate’ PD, GD, and EH in terms of whether the root of the tree is included or not. Actual recourse to the software or its manual (and also implied in our text) would have shown Faith and Baker that users are required to specify whether or not to include the root, a requirement which is clearly a good idea as these discussions show. We take this opportunity to note that MeSA performs many other biodiversity calculations and has been used elsewhere (e.g., Sechrest et al. (2002)), and that our program CONSERVE IV (Agapow and Crozier, in prep., see also Crozier, Agapow and Pedersen (1999)) offers users the ability to take account of phylogenetic uncertainty, and to find optimum reserve sets under constraints such as the costs of reserves.

Meanings of PD

A number of phylogenetic distance-based approaches to biodiversity assessment have been proposed such as those of Altschul et al. (1989), Altschul and Lipman (1990), Pamilo (1990), Crozier (1992), Faith (1992), Weitzman (1993), Crozier and Kusmierski (1994), May (1994), Witting et al. (1995), Witting and Loeschcke (1994), and Nee and May (1997) (see Crozier (1997)). Faith’s original formulation (1992) clearly defined PD (“Phylogenetic diversity”) as including just the surviving species in a set, and did not include the root of the complete tree in this calculation (“The *phylogenetic diversity* (‘PD’) of [a set of taxa] is equal to the sum of the

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lengths of all those branches that are members of the corresponding minimum spanning path“ a definition reflected graphically in his figures 2 and 4 (Faith 1992)). Faith kindly read the review of Crozier (1997) in which this definition was clearly formalized (see Eq. 1 of Crozier et al (2005) and Eq. 2 of Crozier (1997)) and had not objected to this usage until the Faith and Baker (2006) paper. Thus, contrary to Faith and Baker (2006) PD was defined by Faith (1992) as not including the root, an approach which causes underestimation of biodiversity loss when there is massive extinction, as modelled by Nee and May (1997), but that nonetheless is appropriately applied in cases where there is no rational root to a tree, as in a study of microbes from all kingdoms of life. It was May (1994) and Nee and May (1997) [see also Witting et al. (1994)] who defined a measure which does include the root of the tree (Evolutionary History, EH). It is always risky trying to change the definition of a widely-used term, but in 1998 Moritz and Faith redefined PD as including the root of the tree (Moritz and Faith 1998), i.e., taking on the exact meaning of the previously defined EH. Authors have been divided on the meaning of PD since then, with a good clarifying discussion given by Rodrigues and Gaston (2002), who give PD the rootless definition but accept (as does the field generally) that the root should be included in most calculations, whatever the metric is called. PD has thus become a panchreston, e.g., Sechrest et al. (2002) use “PD” as a generic term but use EH for technical definitions. Others simply use EH, e.g., Avise (2005). Does it matter? As long as authors say exactly what they are using they could use any name, but we think that the two concepts, with root and without, should be kept separate nomenclaturally and that the original definitions should stand. Of course, as long as authors make explicit which calculation they are doing confusion will be minimized, but given the availability of the terms it seems simpler to call the phylogenetic estimation of biodiversity including the root EH – after all, this term does have priority.

Conclusions

It seems that there are no disagreements between us and Faith & Baker (2006) about the kind of calcula-

tions that are appropriate for biodiversity assessment. What are at issue are claims of priority and definition, and apart from our missing a reference we have shown that these are without substance.

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