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Biogeography Off the Tracks

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We write to convey our concerns that some mainstream evolutionary journals continue to publish articles that, in our view, present misleading accounts of biological evolution. Speci“cally, we argue that •panbiogeographicŽ studies of spatiotemporal biological history (e.g., Craw 1988; Heads 2010a, 2010b, 2011, 2012 our conc rg 0 01(e)11.9(v)39.9(ogeography as a discipline. The panbiogeographic pproach usually ignores long-distance dispersal nd considers alternative hypotheses only within e narrow con“nes of assumed ancient vicariance. though previous commentators have already penned pitaphs for the panbiogeographic paradigm (e.g., Cox 998; McDowall 2004; McGlone 2005; Briggs 2007), some ditorial and review processes continue to allow this isleading approach to be promulgated as a useful cienti“c method. Despite the approach being termed noribundŽ (Briggs 2007), recent years have seen an pparent upswing in the number of panbiogeographic udies published (e.g., Kutschker and Morrone 2012; ercado-Salas et al. 2012; Silva et al. 2012).

Panbiogeography represents a worldview of biology eemingly “xated on ancient earth history and evaluates ternative biological hypotheses only within the limited on“nes of assumed ancient vicariance. The lack of cope for considering alternative hypotheses makes anbiogeography of dubious utility, especially relative the far more developed biogeographic methods at are increasingly available (see Crisp et al. 2011). s presented in recent studies, the panbiogeographic pproach involves little more than mapping species stributions and drawing lines (tracks) connecting em. As early as 1989, when the approach was being eveloped by New York and New Zealand systematists Briggs 2007), there were calls for panbiogeography become more quantitative (Craw 1989; Page 1989), ut the approach has remained broadly qualitative and cking in reproducibility (Cox 1998) (although we note recent attempt by Echeverría-Londoño and Miranda-squivel 2011 to systematize the approach).

The methods of panbiogeography and their shortcomings are best illustrated with an example, for which we use ratite birds (Fig. 1). Using a map of current distributions, the following features are drawn: •tracks,Ž which connect all distribution points to form a minimal spanning tree; •nodes,Ž which are intersection points of tracks; •main massings,Ž which identify more diverse regions of the distribution; and •baselines,Ž which represent major landscape features traversed by tracks. First, as a general criticism, the meaning of a track is ill de“ned. Speci“cally, Craw et al. (1999) (p. 20) state that tracks •… give shape or expression to the space and time that necessarily intervenes between disjunct localities,Ž a hazy description underpinning a mysterious approach. If tracks are meant to indicate paths of dispersal or vicariant events, there is also no apparent reason why they should take the minimal distance (although indeed they are rarely depicted as great circle distances). Second, it is not always clear how the tracks are arrived at. Although they purport to be minimal spanning acyclic graphs, the speci“c tracks drawn are sometimes not the shortest available, but are seemingly swayed by locations of main massings within distributions. For example, it is not clear why Australasian ratites are linked by a track through an Indian Ocean baseline, rather than by a track from China to Papua New Guinea to create a shorter network (Fig. 1a). Third, the main massings are said to represent: •the greatest concentration of biological diversity …,Ž including taxonomic, genetic, phenotypic, or behavioral characteristics (Craw et al. 1999; p. 21), but it is unclear how this diversity is objectively quanti“ed. Fourth, track analysis and ancient vicariant scenarios are often discordant with respect to phylogenetic reconstructions (e.g., track analysis suggests a closer relationship of moa and kiwi [Fig. 1a], yet moa is more closely related to rhea [Fig. 1b]). Fifth, as with many methods, accumulating fossil data (e.g., new Montana record; Fig. 1a) and consideration of extinction events (which will be common over geological timeframes; van

(Campbell 2008; Heenan et al. 2010). Corroborating these geological “ndings, molecular data from numerous species independently indicate that biotic relationships between the Chathams and mainland New Zealand are far too young for the panbiogeographic conclusions to be considered plausible (Paterson et al. 2006; Goldberg et al. 2008; Wallis and Trewick 2009; Heenan et al. 2010; Goldberg and Trewick 2011). For example, the oldest estimated divergence of contemporary Chathams and mainland sister taxa known to date is 14 Ma for the Chatham Island forget-me-not (*Myositidium hortensium*), whereas most other Chathams…mainland species divergences appear < 3 Ma (Heenan et al. 2010). Overall, multiple independent lines of evidence clearly indicate that the modern Chathams biota was established by transoceanic dispersal, and not by ancient vicariance.

Practitioners of the panbiogeographic approach

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