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Commentary

Chundra A. Cathcart*

Good enough for Galton, and much more: commentary on “Replication and methodological robustness in quantitative typology” by Becker and Guzmán Naranjo

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In recent years, the language sciences have adopted and refined philosophies and tools for data analysis employed in related fields like evolutionary anthropology (McElreath 2016) and disciplines like biology where analogous phenomena (e.g., trait evolution; Garamszegi 2014) are studied. These methodological developments have not been without controversy. In particular, the perceived encroachment upon linguistic topics by tools associated with other disciplines has led to a degree of tension within the language sciences. The conflict is often framed as one between traditional methods (e.g., stratified sampling) and phylogenetic comparative methods (PCMs; for a recent revival of this debate see e.g. Haspelmath 2020), the latter of which can be challenging and computationally intensive to implement, not to mention black box-like.

However, if computational difficulty is the main drawback of PCMs, then the key issues of this debate may be misconstrued. PCMs as we use them today are usually implemented in a Bayesian framework, which estimates posterior distributions of parameters (i.e., estimands that we do not observe and wish to infer) via iterative sampling-based procedures like Markov chain Monte Carlo (MCMC), when no analytic (i.e., paper and pencil) solution is available (for an alternative framework, see Blei et al. 2017). Frequentist statistical methods (e.g., chi-squared tests, classical regression) generally operate within a Maximum Likelihood (ML) framework and are faster to implement, but many of these models are restrictive in terms of what they allow to be analyzed and make arcane assumptions that are poorly understood. Despite their computationally intensive nature, Bayesian methods are more flexible, giving more freedom to practitioners in terms of model building. Yet the “costly/complex” (Bayesian) versus “cheap/simple” (ML) dichotomy cuts across less and more “traditional” families

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***Corresponding author: Chundra A. Cathcart [ˌt͡ʃʌndɹə ˈkæθkɑɹt]**, Institute for the Interdisciplinary Study of Language Evolution, University of Zurich, Zürich, Switzerland, E-mail: chundra.cathcart@uzh.ch. https://orcid.org/0000-0002-3066-4532

of models. One can find fast, ML implementations of PCMs (Harmon 2019), just as one finds Bayesian *t*-tests and Bayesian regression (Kruschke 2014).

The target article's (Becker and Guzmán Naranjo 2025) authors use a version of Bayesian regression that accounts for phylogenetic and spatial non-independence in a highly flexible manner. As such, this methodology is a continuation of a more familiar one (regression), but it incorporates properties of PCMs and involves a more complex parameterization and model-fitting procedure than standard regression models (even more so than mixed-effects models implemented in R packages like lme4, Bates et al. 2015). In general, I believe that the target article makes very clear the benefits of this approach. Certainly, this type of modeling strategy should be part of the methodological arsenal of anyone wishing to establish associations between linguistic variables while accounting for phylogenetic and spatial non-independence. I wish, however, to highlight how the freedom provided by this framework forces users to make a number of non-trivial decisions, and to emphasize that broadly speaking, PCMs allow practitioners to treat phylogeny not simply as a nuisance factor which must be controlled for, but as a means of shedding light on the complex scenarios underlying the associations we detect synchronically.

The flexibility of Bayesian methods is one of their major draws, and can be both beneficial and challenging. While for many frequentist methods, key assumptions are built into the model, Bayesian practitioners must make many assumptions themselves over the course of model building. Even the most standard-seeming assumptions may not be trivial. When we construct a simple model with a small number of parameters, what we may see as a fairly neutral decision can also be construed as an active choice between restrictiveness and relaxation (e.g., Lemey et al. 2010). Other choices in model building may embody highly divergent understandings of the processes giving rise to the data. One ostensibly trivial decision I wish to highlight is the authors' use of phylogenetic regression to control for phylogenetic effects. Given the scope of the paper, the authors understandably avoid technical details, but more specifically, what they assume is that linguistic features evolve according to Brownian motion (which like the spatial model they employ is a type of Gaussian process, albeit with a different kernel, i.e., the function determining the covariance between languages). Brownian motion is just one of a large suite of models of phylogenetic trait evolution (Blomberg et al. 2020; Gill et al. 2017; Landis et al. 2013), not all of which are Gaussian processes, and not all of which can be combined with a regression model in a straightforward manner. The assumptions of Brownian motion are fairly simple – the covariance between two taxa in a phylogeny with respect to some trait value is proportional to their shared history (i.e., the displacement in time between the root of the tree and the most recent common ancestor of the two taxa). Under Brownian motion, the variance in a value's displacement is proportional to the time elapsed during displacement, but the expected displacement is zero – Brownian motion does not accommodate long-term preferences or biases in change, unlike the mean-reverting Ornstein-Uhlenbeck process, a type of Gaussian process that can be included in a regression model using a kernel function similar to what the authors use to model spatial effects (Butler and King 2004; Ringen et al. 2021). As a mean-reverting process, the Ornstein-Uhlenbeck model assumes that while trait values can exhibit random walk-like behavior (as in Brownian motion), they are drawn back to some optimal value according to a parameter representing strength of selection. While it may be challenging to find exact linguistic analogs for all parameters in this process, it is conceptually not unreasonable to posit that some linguistic features may exhibit more mean-reverting behavior than others. Is it necessary to investigate this possibility when controlling for statistical biases? Perhaps not, although it is impossible to be certain that the Brownian assumption is entirely unproblematic, at least without more detailed investigation, including simulation studies. My point here is not that researchers should test all possible evolutionary scenarios – this would be unfeasible – but that even fairly trivial-seeming choices may not be so, and this issue underscores the fact that multiple modeling approaches are needed to understand the conditions under which certain associations between features obtain.

With diachronic change being as complex as it is, it is worth emphasizing that PCMs, of which phylogenetic regression is just one example, offer us more than just a means of accounting for Galton's problem, that is, the issue of phylogenetic non-independence (Narroll 1961). Indeed, many authors using more complex phylogenetic models are content to see their results as demonstrating a relationship between multiple variables while accounting for phylogenetic history (Jäger and Wahle 2021) and to leave matters there. But there is more to be explored beyond simply detecting whether there is evidence for an association – we can ask questions regarding the dynamics that led to said association (Cathcart et al. 2020; Craevschi et al. 2025; Sheehan et al. 2023). For instance, if we detect an inverse relationship between complexity in different domains of morphosyntax using phylogenetic methods, we can investigate whether one domain simplifies before the other, or whether simplification is simultaneous in both domains. Similar models probe whether linguistic migration precedes putatively environmentally driven linguistic changes (Hartmann et al. 2024). Phylogenetic models that are more explicit with respect to their assumptions about the nature of change might additionally be able to shed light on evolutionary scenarios between which regression-based approaches are unable to distinguish. And while most of the phylogenetic approaches in the literature do not explicitly model contact, they may indirectly absorb information regarding areality in an interpretable fashion (e.g., if rates of change on a branch are higher than expected). At the end of the day, it is likely impossible to incorporate all relevant dimensions of linguistic change into a single model; hence, a multi-pronged approach is needed to fully understand the processes that have given rise to what we observe synchronically. The approach outlined in the target article is an important puzzle piece, but one of many.

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