

Phylogenetic comparative methods in everyday typology

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Keywords: Linguistic phylogenetics, Balanced sampling, Pama-Nyungan, Phonological typology, Quantitative methods

Phylogenetic comparative methods are shrouded in a little mystery for many linguists. Yet the path that led to their development in biology is so closely paralleled by the methodological history of balanced sampling, that these methods could just as easily have been discovered first by a linguistic typologist. In this talk, we elucidate the logic of phylogenetic comparative methods and their relationship to the longstanding intellectual focus on sampling methodologies in comparative linguistics. We aim to clarify the role of these methods in modern typological research and demonstrate how they can be built into common typological workflows with a case study of the laminal contrast in Pama-Nyungan languages.

An abiding concern in typology is genealogical non-independence. Observations taken from historically related languages will lack the property of independence, which is a crucial assumption in many common statistical methods, due to their shared histories through common ancestor languages. Genealogical non-independence is an issue for comparative biology too, and in Part I of the talk, we discuss the history of addressing this challenge through sampling methodologies, which is common to both fields. We then describe the breakthrough insight that led to the progression from sampling strategies to phylogenetic comparative methods in comparative biology (Felsenstein 1985), and how this applies to other fields, including linguistics, which face the same problem in essence, of genealogical non-independence.

In Part II of the talk, we introduce concepts, methods and tools for bringing phylogenetic comparative methods into the everyday practice of typological researchers. In contrast to balanced sampling methods, which can never fully achieve statistical independence and require substantial amounts of comparative data to be discarded, phylogenetic comparative methods enable all observations to be retained. Essential notions covered include phylogenetic signal; uncertainty about trees; typological averages and proportions that are sensitive to genealogy; comparison across language families, and the effects of areality.

In Part III, we present the case study of the laminal contrast in the Pama-Nyungan family. Pama-Nyungan languages contrast between 4–6 supralaryngeal places of articulation including either one or two laminal places (Evans 1995; Round 2022). This laminal contrast has been described previously as a largely areal phenomenon (Dixon 1970; Dixon 1980; Evans 1995). In this case study, however, we show that this feature contains strong phylogenetic signal and clusters closely within internal Pama-Nyungan subgroups (Figure 1).

Lastly, we give a brief overview of accompanying hands-on tutorial materials for putting phylogenetic comparative methods into typological practice. Phylogenetic comparative methods

need not be a black box reserved for those with special expertise. They are a natural progression from balanced sampling and can be built into the workflows of any linguistic typologist.

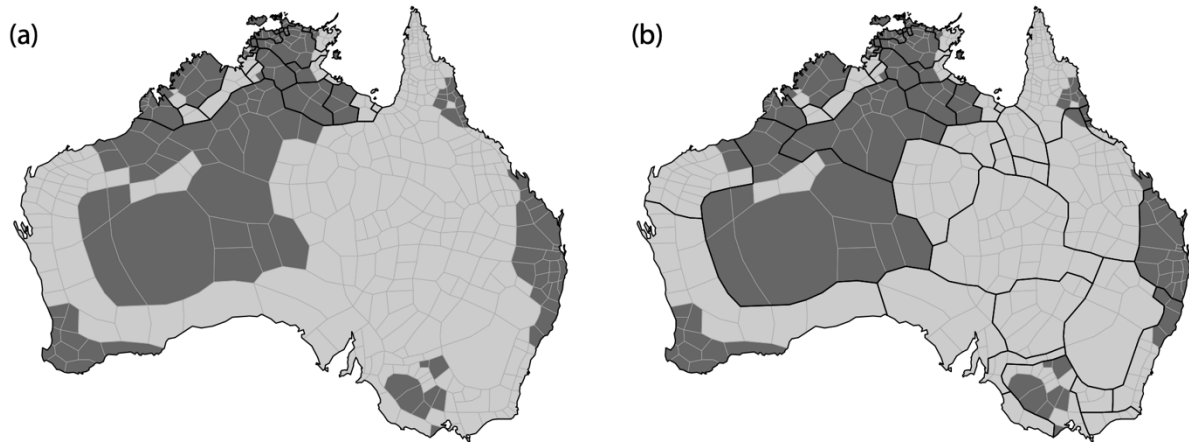


Figure 1. The distribution of the presence (light) and absence (dark) of a laminal contrast in Australian mainland languages. No pattern stands out in (a), which shows language family boundaries. A clear pattern emerges, however, when Pama-Nyungan subgroup boundaries are superimposed (b).

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