

Using pronominal syncretisms as a tool for diagnosing phylogeny in Papuan languages

Nicholas Evans & Simon Greenhill

The vast number of Papuan languages and families, and the difficulties in finding cognate vocabulary and grammatical morphemes between them, creates the necessity for developing new methods if we are to make significant advances in understanding the historical relationships between languages. In this paper we will outline a new approach we are developing, based on patterns of syncretism in pronoun paradigms, and apply it to a significant subset of Papuan clades as a heuristic trial of its usefulness, including Trans-New Guinea and half a dozen other language families.

There is growing interest in the use of typology in historical linguistics. One particularly promising approach is to investigate relationships between tightly organised subsystems of language, as fractal-like proxies for overall relationships. Here we focus on one linguistic subsystem – personal pronouns – which is found in all spoken languages and can hence be applied universally in linguistic comparison.

Our method is to compare the architecture of attested pronominal systems. We develop a diachronic typology of the stepwise pathways between them, and then harness this to a phylogeny to infer the most parsimonious historical scenarios relating pronominal systems across a series of languages.

To get the right balance between informativeness and comparability, we focus on four (potentially) distinct forms of each personal pronoun: those for the three core grammatical relationships (A, S and O) and for the possessive pronoun (of course many languages will neutralise some of these distinctions). These four values then combine with the system of person/number combinations as well as other categories such as gender to give a paradigm. Within any pair of cells in the paradigm we code a number of relationships ranging from totally distinct (e.g. *we* and *our* in English), total syncretism (e.g. A=S in English *he*, S=O for Nen *bā* 'he/she'; sg=du=pl in English *you*) to formal overlap (e.g. *me* and *my* in English) to formal increment (e.g. Nambo 1stsg ergative *yndo* from Nambo 1st sg absolutive *ynd*). Taken together, these factors then give a vast 'architectural design space' formed by the product of all featural paradigms (in terms of feature combinations) with all formal relationships between all cells within them.

Diachronic pathways between possible paradigms in the design space can then be modelled by assuming they are achieved by (a) adding or subtracting features or combinations thereof (e.g. neutralising inclusive/exclusive, or developing a distinct ergative form) (b) changing the formal relationship between any two cells (e.g. from formal increment to formal overlap, or from distinct to total syncretism). Once the set of possible pathways has been exhaustively elaborated, we can give the evolutionary distance between any two paradigms by calculating the number of transformational steps needed to get from one to another. We can then use a Bayesian phylogenetic methods to infer a set of phylogenies based on the most parsimonious set of changes across the whole population of paradigms.

The method will be tested against existing classifications of one well-known language family (Indo-European) to determine its reliability, and then trialled as a heuristic classification for Australian and Papuan languages (Trans-New Guinea and Morehead-Maró, plus selected outgroups).

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