Abstract

Computational Phylogenetic Reconstruction of Pama-Nyungan Verb Conjugation Classes

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The Pama-Nyungan language family comprises some 300 Indigenous languages, spanning the majority of the Australian continent. The varied verb conjugation class systems of the modern Pama-Nyungan languages have been the object of continued interest among researchers seeking to understand how these systems may have changed over time and to reconstruct the verb conjugation class system of the common ancestor of Pama-Nyungan. This dissertation offers a new approach to this task, namely the application of Bayesian phylogenetic reconstruction models, which are employed in both testing existing hypotheses and proposing new trajectories for the change over time of the organization of the verbal lexicon into inflection classes. Data from 111 Pama-Nyungan languages was collected based on features of the verb conjugation class systems, including the number of distinct inflectional patterns and how conjugation class membership is determined. Results favor reconstructing a restricted set of conjugation classes in the prehistory of Pama-Nyungan. Moreover, I show evidence that the evolution of different parts of the conjugation class sytem are highly correlated. The dissertation concludes with an excursus into the utility of closed-class morphological data in resolving areas of uncertainty in the continuing stochastic reconstruction of the internal structure of Pama-Nyungan.

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Thank you Mom and Dad and the rest of my family, and also to my many mentors, especially Claire Bowern.

Chapter 1

Introduction

1.1 Preliminaries

Within the domain of morphological theory, recent decades have seen a growing focus on accounting for the typological diversity we observe among the world's languages with respect to the organization of certain classes of words (i.e., nouns, verbs) into smaller subgroups within the lexicon. These substrata are of interest to morphologists, as they often represent a purely morphological function – what Aronoff (1994: 25) terms MORPHOMIC – in that there may be no syntactic or semantic justification for the existence of these subdivisions of a particular word class. The presence of these subgroupings often manifests itself in the shape of inflectional material, be it stems or affixes, such that membership in a given subgroup is observable from part or all of a lexeme's inflectional paradigm. As such, I will henceforth refer to CONJUGATION CLASSES, which the reader may assume are parallel to Aronoff's (1994: 64) INFLECTION CLASSES, which he similarly defines as "... a set of lexemes whose members each select the same set of inflectional realizations." This thesis explores the nature and historical development of verb conjugation classes in the Pama-Nyungan language family of Australia, using computational phylogenetic methods to evaluate testable hypotheses about how the organization of the lexicon into these conjugation classes have changed over time.

1.1.1 Conjugation classes

Many accounts of the properties of conjugation class systems come from the study of European languages – examples include Anderson's (1992: 136-156) analysis of Georgian, Corbett's (2009) work on Russian noun classes, and Stump's (2015) assessment of theoretical issues related to inflectional classes drawing especially on Icelandic. A straightforward example of verb conjugation classes comes from Spanish:

	*habl**a**r* 'to talk'		*com**e**r* 'to eat'		*viv**i**r* 'to live'	
	SG	PL	SG	PL	SG	PL
1	hablo	habl**a**mos	como	com**e**mos	vivo	viv**i**mos
2	habl**a**s	habl**á**is	com**e**s	com**é**is	viv**e**s	viv**í**s
3	habl**a**	habl**a**n	com**e**	com**e**n	viv**e**	viv**e**n

Table 1.1: Present tense indicative forms of three Spanish verbs belonging to three different conjugation classes

In Spanish, regular verbs fall into one of three major conjugations, while class membership is clearly discernible from the quality of the vowel that follows the stem (shown in bold in inflected forms in Table 1.1). Verbs take the infinitive as their citation form, which clearly demonstrates this conjugation class marker. Studies based on European language families like Romance (e.g., Maiden 2005) conclude that conjugation class systems are both explicit in their overt marking of membership and very stable over time.

1.1.2 Verb conjugation classes in Pama-Nyungan

The Pama-Nyungan language family comprises some 300 Indigenous languages spoken across the majority of the Australian continent. Examination of verb conjugation classes across the Pama-Nyungan languages leads to quite different conclusions about the nature of such systems. Pama-Nyungan languages exhibit a wide range of typological diversity with respect to verb conjugation classes, which is commonly taken (Merlan 1979; Dixon 1980, 2002; McGregor 2002, among others) to represent language change and divergence from a common ancestor of the modern languages. This typological variance is detailed in Chapter 3 and briefly summarized here.

Some modern Pama-Nyungan languages lack verb conjugation classes entirely, while others may have five or more. While common conjugation classes are identifiable across the language family, individual languages may vary with respect to which conjugation classes they contain. Thus two languages with three conjugation classes each may exhibit some, all, or none of the specific classes in common with one another. Moreover, cognate verbs often belong to different conjugation classes in different languages.

Building on these typological observations, Dixon (1980, 2002) proposes a maximal set of seven conjugation classes present in the proto-language, which have been partially or completely lost over time in the historical development of the individual modern languages. In other words, it is assumed that from a superset of conjugation classes present at an early stage, different offshoots of the language family collapsed distinctions between certain classes in different ways over time. Moreover, Dixon stipulates that languages lose conjugation classes but do not gain them. Most Pama-Nyungan languages are described as showing a strong correlation between valence and conjugation class membership, with certain classes containing mostly transitive or intransitive verbs. Others determine conjugation class membership by grouping verbs with similar phonological properties; Wakaya (Breen 1974) is described as having four conjugation classes, with membership determined by the phonological properties of the stem-final segment.

Illustrative of the conjugation class system found in many Pama-Nyungan languages is that of Guugu Yimidhirr (Haviland 1979). Guugu Yimidhirr contains three major conjugation classes, which are named for the conjugation class marker that appears between the stem and any suffixes in certain cells in the paradigm. For Guugu Yimidhirr, as with many PN languages, this is maximally visible in the nonpast forms:

Class	L	R	V
Verb	'hit'	'shut, close'	'go'
Nonpast	gunda-l	ngalbu-rr	dhada-a
Past	gunda-y	ngalbu-rrin	dhada-y
Imperative	gunda-la	ngalbu-rru	dhad-ii
Purposive	gunda-nhu	ngalbu-nhu	dhada-nhu

Table 1.2: Nonpast forms of three Guugu Yimidhirr verbs belonging to three different conjugation classes

Note that unlike Spanish (Table 1.1), Guugu Yimidhirr (Table 1.2) verbs do not obligatorily include the conjugation class marker in all cells of the paradigm. The purposive inflection is identical across the conjugations, while the past tense form of *gunda* 'hit' lacks the *-l* marker found in the nonpast and imperative forms. V conjugation verbs mark the nonpast by lengthening the final vowel of the stem and replaces the final vowel with *-ii* in the imperative mood, in addition to sharing the *-y* suffix of the L conjugation in the past tense. Conjugation class membership in Guugu Yimidhirr appears to be correlated with valence. The L and R classes are between 60-80% transitive, while the smaller V class is mostly intransitive.

The language also contains a small number of monosyllabic irregular verbs that take nonpast *-maa* (e.g., *nhaa-maa* 'see.NPST') or *-naa* (e.g., *wu-naa* 'exist.NPST'). These irregular verbs perhaps indicate reflexes of older more stable conjugation classes that have subsequently been lost over time. As evidence of this, Haviland (1979: 85) notes that at the time of his study, younger speakers of the language commonly produced inflected forms of these irregular verbs as belonging to one of the regular classes, typically into the V class as maintenance of the transitivity distinction (the irregulars in question are intransitive). An example of this is the aforementioned irregular *wu-naa*, the nonpast form of *wu-* 'lie, exist', which younger speakers have reanalyzed as being part of the mostly intransitive V conjugation. Thus they give the imperative form as *wunaa-ii*.

Moreover, Haviland (1979: 85) found that younger speakers showed evidence of reassigning regular verbs to the L and V classes to resolve mismatches of the statistical tendency for L class verbs to be transitive and V class verbs to be intransitive. This is illustrated with the reassignment of the transitive verb *banydyi-* 'wait for' from the predominantly intransitive V conjugation to the mostly transitive L conjugation; older speakers give *banydyii* for both the nonpast and imperative, while younger speakers use L conjugation morphology in producing *banydyil* 'wait.NPST' and *banydyila* 'wait.IMP'. This is complemented by reassignment of the intransitive *biili-* 'paddle' from the L conjugation to the V conjugation, thus the imperative is traditionally *biilila*, but was given as *biilii* by younger speakers.

1.1.3 Overview of the chapter

The remainder of this introductory chapter is structured as follows: §1.2 discusses the long documentary tradition in Australia responsible for the cataloging of the Pama-Nyungan languages as well as discussing the important typological studies and diachronic analyses that helped to shape current understanding of the Pama-Nyungan verb conjugation class system. §1.3 offers an exploration of the role of conjugation classes in morphological theory and provides typological generalizations about the nature of the different verb conjugation class systems found across the Pama-Nyungan family. Finally, §1.4 provides an outline and summary of the thesis, introducing key research goals and looking ahead to the results of computational phylogenetic reconstruction modeling and their implications for the current understanding of the evolution of verb conjugation classes in Pama-Nyungan.

1.2 The documentary tradition in Australia

From the time of European contact in the late 18th century, languages of the Pama-Nyungan family have been described to varying levels of completeness by documentarians with wide-ranging backgrounds, motivations, and amounts of formal training in linguistics/language documentation. The one common thread that can be found is that, continuing to present day, documentation of the PN languages has almost entirely been done by non-native (but sometimes fluent) speakers. As such, while we must appreciate the contributions of these documentarians, especially in the face of accelerated language loss and death across the Australian continent, we should also recognize the implications for the type of data recorded and reliability of forms and phonetic descriptions that come as a result of a dearth of direct native speaker influence. Stockigt (2017) provides a comprehensive overview of the documentary tradition in Australia over the last century, a summary of which is provided in §1.2.1.

In addition to description and analysis of individual languages and language subgroups, there are three foundational works that must be mentioned in any discussion of Pama-Nyungan verb conjugation classes. Merlan's (1979) proposal that modern Pama-Nyungan verb conjugation class markers are reflexes of older compound verb constructions is briefly discussed in §1.2.2. McGregor (2002, §1.2.3) provides a number of generalizations about the size, typological profile, and geographical distribution of Pama-Nyungan verb conjugation class inventories and their exponents based on an extensive survey of the modern languages. Finally, Dixon (2002), which serves as a revision/restatement of his earlier (1980) account, offers important typological information on verb conjugation classes, ultimately putting forth a reconstruction hypothesis which is by no means universally agreed upon, but has nonetheless proven immeasurably influential in continued research on the subject. Dixon's findings are presented in §1.2.4 and dicussed throughout the thesis.

1.2.1 Three periods of documentation

In her historiographic account of descriptions of PN morphology and syntax, Stockigt (2017) identifies three major periods of documentation of Australian languages between the mid-19th century and present day. The first of these ranged from the 1840s until the turn of the century and was dominated by descriptions of individual languages of South Australia authored by Lutheran missionaries. While these missionaries were primarily focused on proselytization, Stockigt (2017: 38-9) notes that their efforts at linguistic description and documentation were in many cases comprehensive. The data contained in these early works is still often cited and reanalyzed in the modern grammars which have supplanted them in the documentary record of PN. Here we include Reverend Nicholas Hey's (1903) description of Ntrangith and the large body of work produced by R. H. Mathews, including descriptions and analyses of Bunganditj (1903) and Ganai (1907). Descriptions of verbal morphology present in the writings of this era are often present if not somewhat lacking in development. Often a partial paradigm of a single verb is given as an illustration of the tense, aspect, and modality (TAM) system with comparisons to English, a practice which obscures investigation into the possible presence of multiple verb conjugations.

Stockigt (2017: 30) describes the second descriptive era (1930-1960) as being characterized by a focus on typology, gathering together earlier publications in order to provide a more comprehensive understanding of the grammatical structures found in the PN languages. The third, so-called ‘modern period’ (Stockigt 2017: 29) began in the 1960s, when Australian universities began to recognize linguistics as an independent research enterprise. Descriptions and analyses from the 1960s and later form the majority of the sources from which data for the current study were compiled, supplemented as necessary with lexical and conjugation data from overviews of verb conjugation class information for a large set of PN languages compiled by Harold Koch and Pascal Jacq (n.d.), as well as the CHIRILA database (Bowern 2016). In the published material from this era, we see a turn towards more complete descriptions of the verbal morphology, with some degree of attention to conjugation classes. Some grammars from the late 1960s and early 1970s, such as Platt’s (1972) description of Kuktaja, provide basic evidence of verb conjugation classes with illustrative partial verbal paradigms, but lack discussion of the classes themselves beyond the way they are realized via affixation. Others, such as Alpher’s (1973) grammatical description of Yir Yoront, feature a full breakdown of the number of verbs attested in each conjugation and attempt to define conjugations in terms of their size, openness, and the identity of their members. This latter practice has since become the standard for many documentarians, likely due in part to the influence of Dixon (1980). Additional notable examples include Thompson’s (1988) grammar of closely related Kuuku Ya’u and Umpila and Patz’ (2002) description of Kuku Yalanji.

1.2.2 Merlan’s (1979) diachronic account

While thorough explorations of the nature of verb conjugation classes and their historical development are somewhat uncommon in the literature on the typology of Australian languages, they are by no means absent. An early account from Merlan (1979) argues for a historical development scenario in which compound verb structures at an older stage of the language gave rise to modern conjugation class markers. This is in contrast with the assumption that PN verbs were historically monomorphemic (e.g., Dixon 1980: 378-430). Beginning with the observation that in language after language, verbs which take *-l-* as a conjugation marker are predominantly transitive while verbs which take *-y-* as a conjugation marker are predominantly intransitive, Merlan (1979: 40-1) argues that these conjugation markers are likely to have a grammatical origin, perhaps being reflexes of older auxiliaries or derivational affixes. She notes that while many modern PN languages contain a small number of monosyllabic verb roots, earlier stages of PN must have had more monosyllabic roots, which were subsequently lengthened to two or more syllables. A case in point (Merlan 1979: 41) is the ubiquitous root *bu* 'hit', which is monosyllabic *bu-* in Nyawaygi and *pu-* in Walmatjari, but polysyllabic *buma-* in Ngiyambaa. For Merlan, many of these disyllabic roots go back to compound verb constructions at an older stage of PN. To illustrate (Merlan 1979: 52-8), consider the verb *baga-*∼*paka-* 'spear, hit', which is found in a large number of PN languages. Evidence for *baga-* being derived from an earlier compound comes from the fact that the verbal lexica of many modern PN languages contain numerous roots with second syllable *ga* which are semantically related to the concepts of hitting, stabbing, etc. For example, Dyirbal has the following 'ga' verbs: *baga-* 'pierce, spear', *balga-* 'hit, kill', *dalŋga-* 'cut', and *ŋalga-* 'poke with stick', all of which belong to the *l*-conjugation and are transitive. Merlan notes that cognate verbs with second syllable *ga* are found in Guugu Yimidhirr, Ngiyambaa, Yidiny, and Pitta Pitta, among many other PN languages. Merlan (1979: 62-5) further identifies *Da*[1] as a common second syllable in modern PN verbs related to eating and other actions involving the mouth which may have originally been compound constructions as well. Examples include Ngayimbaa *ḑiːnḑa-* 'lick' and the widespread *baḑa-* 'eat'. In terms

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[1] Where *D* represents a dental stop. Merlan gives this as lamino-dental d̪ or lamino-palatal ḑ, though she notes it may have alternative spellings in some languages.

of conjugation class markers having come from a similar source, Merlan (1979: 65-71) proposes -$n(a)$ as an auxiliary attaching to intransitive verbs of motion or stance at an older stage of PN, which subsequently was reanalyzed as the conjugation marker -n found in a number of modern PN languages.[2]

1.2.3 McGregor's (2002) typological generalizations

McGregor (2002: 207-13) provides a brief but detailed overview of verb conjugation classes in the Pama-Nyungan languages. At the outset, he gives six generalizations that encapsulate the typological characteristics of the Pama-Nyungan verb conjugation class apparatus. These are summarized below, with additional comments on their general applicability where appropriate:

- A small number of verb classes are distinguished in languages that have conjugation classes, generally between two and five are identifiable. It should be noted that while many Pama-Nyungan languages fit this generalization, a few outliers may have more than five, while others lack verb conjugation classes entirely.

- Conjugation classes are normally signaled by bound dedicated markers that are usually fused to the root. Here McGregor is referring to stem formatives, but encoding of conjugation class membership via allomorphy of inflectional affixes (i.e., material which is not typically analyzable as being fused with the root) is a common strategy employed by a number of Pama-Nyungan languages.

- Conjugation classes markers are usually obligatory in all environments (including non-finite verbs). As we saw in Table 1.2, Guugu Yimidhirr does not follow this generalization; many of the inflectional endings do not include any sort

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[2] cf. Dixon (1980: 378-430) who takes the origin of conjugation markers to be reanalysis of consonant-final verb roots.

of identifiable conjugation marker. In fact, the current survey finds that segmentable conjugation class markers are less common than asserted by McGregor, at least for the 111 Pama-Nyungan languages investigated. Instead conjugation class membership is generally identifiable from patterns of inflection in the realization of tense, aspect, and modality features. Moreover, syncretism is rampant across the paradigms of different verb conjugation classes across the Pama-Nyungan family.

- Conjugation classes typically exhaust the verbal lexicon, though some languages do contain a number of irregular verbs that do not seem to belong to any identifiable conjugation class. Most descriptions do make mention of a small number of irregular verbs which defy inclusion in the definable conjugation classes based on patterns of inflection. The Yolngu languages also contain a number of loan verbs from English and Austronesian that do not host any inflection.

- A relatively small proportion of lexical verb roots can belong to more than one conjugation class. While this is not explicitly referenced in some descriptive grammars, we do see evidence from a number of Pama-Nyungan languages that a small subset of verbs can belong to multiple classes. In languages with a strong correlation between verb class membership and transitivity, some ambivalent verbs may belong to more than one conjugation class as a way of mediating their variable argument structure.

- The number of conjugation classes a single verb root can belong to is typically less than or equal to two. Only rarely does a given verb belong to more than two conjugation classes.

Based on evidence from descriptive grammars and discussion from Dixon (1980), McGregor (2002: 209-12) also identifies four general patterns related to the size and productivity of conjugation classes. For some languages, especially those to the Northern extremum of the Pama-Nyungan geographical extent, conjugation classes all feature closed membership. Many of these languages are members of the Marrngu, Nyumpin-Yapa, and Yolngu subgroups. These languages contain ∼30-100 monomorphemic verb roots, which are subdivided into four or more conjugation classes. Moreover, the individual classes are of disparate size, often consisting of two classes that are large relative to the remaining smaller classes. Here McGregor cites Morphy's (1983) description of Djapu (among other examples), which has around 75 monomorphemic verb roots comprising four major conjugation classes. Of these, two classes are somewhat larger, containing 21 and 25 members, while the remaining two are smaller, with 8 and 13 members.

The second group in McGregor's typology contains languages that feature a single open conjugation class and some number (around three) of smaller, closed classes. He identifies the Western Desert languages and Nyangumarta as exemplars. Some Marrngu languages also fit this profile. In the Western Desert language Ngaanyatjara, McGregor (2002: 211) identifies a single open class with hundreds of members, with an additional three closed classes. Two of these have roughly 20 members, while the third is notably smaller.

A third possibility is to have two open classes, with or without additional closed membership conjugations. McGregor (2002: 211) notes that this type of system is quite common in the Pama-Nyungan context, including languages from the south and central parts of Western and Eastern Australia. Here there is some variation with respect to how many additional closed classes a given language may contain, though the number generally ranges from zero to four. As an example of the two extremes, McGregor (2002: 211) cites Yingkarta as having two open classes and no closed classes (plus a handful of irregular verbs that are not identifiable as belonging to a specific class) and Nyawaygi as having two open classes and three or four closed classes, each of which has less than thirteen members.

Finally, a small number of Pama-Nyungan languages lack variable conjugation classes entirely, instead containing lexical items which take a single, regular set of inflectional affixes. McGregor (2002: 211) notes that these languages are variably referred to as containing no conjugation classes or a single class. The current study adopts the latter of these, though the distinction may be based on preference rather than any theoretical concern or prediction. Examples of this are Arabana, Diyari, and Pitta Pitta, among others, most of which belong to the Karnic and Arandic subgroups. Interestingly, these languages all contain a large number of verb roots. As McGregor (2002: 212) describes, the typology does not contain languages with a small, closed class of verbs that does not also contain conjugation classes. Moreover, McGregor (2002: 212) also provides a short discussion of the distinctive property of conjugation classes in Pama-Nyungan (and Australian languages more generally) that there is often a correlation between class membership and transitivity.

1.2.4 Dixon's (1980, 2002) typology and reconstruction

Dixon (2002: 215-34), which itself builds on earlier work (Dixon 1980: 378-430), advances an account of verb conjugation classes in Australian languages that attempts to provide a scenario of historical development and loss of conjugations that reflects and is informed by typological factors. In addition to the state of the modern languages with respect to conjugation classes, Dixon (2002: 215) also draws on two foundational assumptions.

The first of these is morphological. Dixon contends by hypothesis that Australian languages by and large become more synthetic and fusional over time in terms of their inflection. This claim seems have its origin in the notion (Dixon 2002: 109) that Australian verb stems do not surface in isolation, without some degree of suffixation, which is loosely asserted to lead to a predisposition for development of fusion of the root and immediately adjacent suffix(es). Further evidence of this directional change in the morphological structure of Australian languages is argued (Dixon 2002: 26, 55, 215) to come from languages of the north-central part of the Australian continent[3], where the development of bound pronominal prefixes has interacted with the tense, aspect, and modality marking system to give rise to fusional prefixes that simultaneously realize disparate morphosyntactic functions. As a consequent, he assumes that this fusional morphology likely developed from a more agglutinative system, where the realization of distinct morphosyntactic properties was discernible from independently segmentable pieces of word/phonological structure.

Dixon's second claim is purely phonological, that verb roots at this earlier agglutinative stage featured a root-final vowel, nasal, liquid or semivowel. This second point is crucial to Dixon's thesis, as it is these final segments that are later recruited as exponents marking conjugation class membership. This is contra analysis by other Australianists (Dixon cites Alpher, Evans & Harvey 2003 as an example), who reconstruct vowel-final verb roots and take overt morphological expression of conjugation class membership as an innovative phenomenon within Pama-Nyungan. Ultimately, Dixon (2002: 222) reconstructs seven distinct conjugation classes for some earlier stage of proto-Australian, each indexed by what he analyzes as the historic final segment of the verb roots belonging to a given class. As individual daughter languages developed, certain conjugation classes were lost, resulting in the typological diversity observable in the modern languages. Comparative evidence from cognate forms in closely related languages demonstrates that there is typological variance not only in the number of conjugation classes, but also which of the original classes have been maintained/lost. A case in point can be seen in the comparison of Walmajarri and Warlpiri, both of which show evidence of five distinct conjugation classes (partial

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[3] Here Dixon is referring to what are generally termed the non-Pama-Nyungan languages and some of their Pama-Nyungan neighbors.

paradigm examples are from Dixon 2002: 217-218, chosen for forms that demonstrate overt conjugation class membership for all five roots):

(1) a. Walmajarri future tense forms for five conjugation classes

Class	n	ŋ	l	rr	∅
Verb	‘go’	‘give’	‘eat’	‘bite,chop’	‘cook’
Form	ya-**n**-ku	yu-**ŋ**-ku	ŋa-**l**-ku	patja-**rr**-ku	kampa-[∅]-wu

b. Warlpiri future forms for five conjugation classes

Class	n	ŋ	l	y	∅
Verb	‘go’	‘give’	‘eat’	‘burn’	‘excrete’
Form	ya-**n**-ku	yu-**ŋ**-ku	ŋa-**l**-ku	kampa-[**y**]-tju	natja-[∅]-ku

In (1), we see the future tense forms of five verbs belonging to five different conjugation classes in Walmatjarri (1a) and Warlpiri (1b). The overt marker of class membership is separated as a distinct element of word structure for visibility, while exponents that are elided (such as medial *-y-* in Warlpiri *kampa-tju*) or otherwise not realized overtly (∅) are indicated with square brackets [ ]. There are two important conclusions we can draw from the data in (1). First, Walmatjarri has an ‘rr’ class and lacks the ‘y’ class of Warlpiri, while the converse is true of Warlpiri. Moreover, note that the verb root *kampa-* ‘cook’ belongs to distinct classes in the two languages, though it is clearly cognate otherwise. According to Dixon, this is evidence that the older ‘y’ class, which has been preserved in Warlpiri, was lost and its members folded into the ‘∅’ class in Walmatjarri. Drawing on further comparative evidence, Dixon (2002: 219) has a similar account of the ‘rr’ class in Warlpiri, which he claims must have been lost and its members now part of the ‘∅’ class (consider for example Warlpiri *ŋatja-*[∅] ∼ Walmatjarri *ŋatja-rr* ‘excrete’).

Much like McGregor (2002), Dixon also finds typological generalizations that can be drawn about conjugation classes in the modern languages, though many of these relate to class membership across languages. These generalizations go somewhat beyond what is mentioned in typical descriptive grammars of individual languages, and as such they are important to the extent they can be clearly substantiated. Dixon's (2002: 227) typology of what he considers to be the seven strongly supported verb conjugation classes is outlined below:

- The 'n' class typically includes both mono- and disyllabic roots, most of which are transitive. Taking the putative marker of conjugation class to be analyzable as a distinct morphological element or part of the inflectional marker, verb roots in this class typically end in *a* (*u* and *i*-final roots are uncommon).

- The 'm' class is generally small and typically consists of transitive, monosyllabic roots which end in *a* or *u*.

- Verb roots in the 'ŋ' class are mostly transitive, both mono- and disyllabic, and often end in *a* or *u*.

- Membership in the 'l' class is more variable in different languages. In Warlpiri, this is arguably no longer an identifiable class, consisting of a single monosyllabic root. In other languges, the 'l' class is open, containing hundreds of members. As an open class, the 'l' conjugation lacks a clear pattern with respect to final vowel, though most members are polysyllabic and transitive.

- The 'rr' class is another small to medium sized class, consisting of less than 50 members, most of which are intransitive, polysyllabic, and have final *u* or *a*.

- The 'y' class is typically the large open class for polysyllabic intransitives with final *a* or *i*.

- Finally, the '$\emptyset$' class is often a large open class, though transitivity varies depending on language (either mostly transitive or mostly intransitive). The final vowel for members of this class is usually *a* or *i*.

While the influence of Dixon's account on subsequent research cannot be overstated, his endeavor highlights several facets of the development of conjugation classes that remain unsatisfactorily accounted for. Each of these corresponds to the aforementioned generalizations about class membership in the modern languages. I outline here three of these which are potentially relevant to the research questions proposed in §1.4. The first of these deals with the correlation between class membership and transitivity. Dixon notes that most Australian languages have more transitive verb roots than intransitive, sometimes twice as many. Intransitive roots tend to congregate in the '∅' and 'y' classes, often comprising the majority of these classes, while they are less common in other conjugations. The second relates to the question of whether there is a phonological or prosodic basis for determining class membership. Specifically, certain classes ('rr', 'y', and '∅') do not appear to allow monosyllabic roots, while others feature a mix of mono- and polysyllables. Finally, though Dixon thoroughly considers ways in which conjugation classes may be lost or conflated over time due to a variety of factors, as well as provides evidence of this loss having taken place, a more complete understanding of which classes tend to undergo these changes is left wanting. Moreover, Dixon assumes that conjugation classes can only be lost, i.e. that the conjugations found in the modern languages are a subset of the original classes. This precludes the possibility that conjugation classes could have been gained or regained once lost, a prediction which is testable under the proposed study.

1.3 Conjugation classes in morphological theory

In §1.1, I introduced a descriptive view of conjugation classes as the stratification of a language's nouns or verbs (or some other class of lexemes) into subgroups. This division into conjugations classes is often reflected in the morphology of a language, giving rise to observable patterns with respect to the shape of inflectional material employed in the exponence of morphosyntactic properties. As Aronoff (1994: 64) cogently describes, an inflection or conjugation class is "... a set of lexemes whose members each select the same set of inflectional realizations." This section provides a formal discussion of conjugation classes, drawing on evidence from the verb conjugation systems found across the Pama-Nyungan language family. Moreover, components of Corbett's (2009) proposed 'canonical' approach to categorizing conjugation class systems is employed as intended – as an idealized baseline against which the typological variation found in the Pama-Nyungan verb conjugation class apparatus can be highlighted.

1.3.1 Formal considerations

An inflected wordform can be thought of as resulting from the association of a lexeme ℓ with a set of morphosyntactic features or properties σ, following notions present in e.g., Matthews (1974), Anderson (1992), Stump (2001, 2015), and Round (2015). Paradigm Function Morphology (Stump 2001, 2015), assumes that the inflectional morphology of a language supplies the exponents needed to realize this association between ℓ and σ, for all such morphosyntactic property sets σ for which ℓ may inflect. This set of morphosyntactic property sets we will denote as $\mathcal{M}$. Stump (2015: 2-3) defines two relevant structures resulting from the process of inflection. The CONTENT PARADIGM of a lexeme ℓ is defined as the set of pairs $\langle \ell, \sigma \rangle$, for all σ in $\mathcal{M}$. Each individual pairing is a CELL in the content paradigm of ℓ. The FORM PARADIGM of ℓ consists of the appropriate morphological realizations of the cells in ℓ's content paradigm, resulting in the look-up table of inflected wordforms that make up the familiar notion of a lexeme's inflectional paradigm. The distinction between content and form paradigms is a useful one for the current discussion, as it affords a straightforward way to distinguish conjugation class systems. We may observe that there are many languages for which lexemes belonging to a coherent syntactic category (i.e., nouns, verbs) are divided into various subgroupings, such that the form paradigms of disparate subgroupings differ (in terms of the set of inflectional material associated with a given subgrouping), while the content paradigms are generally consistent with one another.

In Table 1.2, I introduced the notion of verb conjugation classes in the Pama-Nyungan languages by providing a partial form paradigm of the three major verb conjugations found in Guugu Yimidhirr. A more complete representation of the verb conjugation system of Guugu Yimidhirr (Haviland 1979: 80-81) provides a clear example of the preceding discussion. Most verbs in Guugu Yimidhirr belong to one of three major conjugations. Verbs in the language are inflected for eleven tense or aspectual distinctions via suffixation. Moreover, five of these morphosyntactic properties may also be expressed through reduplicated forms, in which reduplication appears to target either the stem or suffix. According to Haviland's description, each of the eleven cells in each verb's paradigm contains an inflected wordform. Thus the cells of the content paradigm of a Guugu Yimidhirr verb, regardless of conjugation class, consist of the pairing of the relevant verb lexeme with the following morphosyntactic property sets:[4]

(2) Morphosyntactic property sets for inflectional content paradigms of Guugu Yimidhirr verbs

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[4] On notation: Following Anderson (1994) and Stump (2001, 2015), morphosyntactic properties are given as unordered sets with no punctuation or delineation. In essence, the order in which the properties are listed may reflect the observed pattern of phonological realization of inflected forms, but is not required to do so. Instead the association between morphosyntactic properties and their exponents is many-to-many. In Guugu Yimidhirr, the theoretical distinction outlined here is less relevant, as the relevant inflectional categories cannot co-occur with one another – verbs in this language take a single tense or aspectual suffix.

{ nonpast } { past } { imperfective }

{ purposive } { contrafactual } { past negative }

{ cautionary } { anticipatory } { precautionary }

{ subordinate$_1$ } { subordinate$_2$ }

Thus while the Guugu Yimhidirr verbs *gunda-* 'hit', *ngalbu-* 'shut, close', and *dhada-* 'go' each belongs to a different major conjugation class, their content paradigms similarly consist of the full range of morphosyntactic property sets outlined in (2). It is in the form paradigms of these three verbs where differences between the major conjugation classes of the language may be observed:

Class	‘L’	‘R’	‘V’
Verb	‘hit’	‘shut, close’	‘go’
Nonpast	*gunda-l*	*ngalbu-rr*	*dhada-a*
	gundaarnda-l	*ngalbuurbu-rr*	*dhadaara*
Past	*gunda-y*	*ngalbu-rrin*	*dhada-y*
	dundaarnda-y	*ngalbuurrbu-rrin*	*dhadaara-y*
Imperative	*gunda-la*	*ngalbu-rru*	*dhad-ii*
	gundaarnda-la	*ngalbuurbu-rru*	*dhadiiri*
Purposive	*gunda-nhu*	*ngalbu-nhu*	*dhada-nhu*
	gundaarnda-nhu/	*ngalbuurbu-nhu/*	*dhadaara-nhu/*
	gundaa-nhu	*ngalbuu-nhu*	*dhadaa-nhu*
Contrafactual	*gunda-nda*	*ngalbu-nda*	*dhada-nda*
	gundaarnda-nda	*ngalbuurrbu-nda*	*dhadaara-nda*
Past neg.	*gunda-almugu*	*ngalbu-almugu*	*dhada-urrmugu*
Cautionary	*gunda-ya*	*ngalbu-urr-baga*	*dhada-ya*
Anticipatory	*gunda-yigu*	*ngalbu-rrigu*	*dhada-yigu*
Precautionary	*gunda-aygamu*	*ngalbu-rrin.gamu*	*dhada-aygamu*
Subordinate$_1$	*gunda-ayga*	*ngalbu-rrin.ga*	*dhada-ayga*
	gundaarnda-yga/	*ngalbuurbu-rrin.ga*	*dhadaara-yga/*
	dunaarndiga		*dhadaariga*
Subordinate$_2$	*gunda-nhun*	*ngalbu-nhun*	*dhada-nhun*

Table 1.3: Form paradigms for three Guugu Yimidhirr verbs belonging to three different major conjugation classes

Note that in addition to the nonpast endings, from which the descriptive names of the classes are taken, the conjugations are distinguished from one another in a number of cells in the form paradigm in Table 1.3, though the inflectional suffixes for the L and V classes are more similar to one another in form than either are to the R class. Moreover, individual conjugations are not fully differentiated, in that the purposive, contrafactual, and subordinate$_2$ categories are realized by a single suffix across all of the classes. This is a pattern commonly found in the verbal paradigms of Pama-Nyungan languages – conjugation class differences are commonly found in the nonpast, imperative, and/or purposive affixes, while a high degree of syncretism is found throughout the rest of the paradigm.

Stump (2015: 37) points out that while conjugation classes provide a useful way to describe the patterns we observe in the form paradigms a given word class, we are left with the issue of how best to represent them in our formal theories. Ultimately, he outlines two possible solutions to this question of representation. First, assuming a rule-based approach to morphological realization, we may simply stipulate conjugation class membership in the rules themselves, where it is relevant to do so. Thus for the Guugu Yimidhirr past tense forms in Table 1.3, we might posit rules like the following:

(3) a. Verbs take a *-y* suffix in the past tense

b. Verbs belonging to the R class take a *-rrin* in the past tense

The rules in (3) leverage the syncretic inflectional suffixes in the L and V conjugations, with a single rule (3a) that represents the 'default' past tense suffix *-y*. Rule (3b) applies whenever a verb belonging to the R class is encountered, as competition between rules is always decided in favor of the more specific or more narrow rule (Stump 2001; Panini's Principle).

A second approach to formally accounting for the patterns we observe as inherent to conjugation class systems relies on the notion that speakers may make use of implicative relations between the cells of a lexeme's form paradigm in order to infer the full paradigm based on knowledge of the form of one or more forms that define a given conjugation class (Wurzel 1989; Blevins 2006; Finkel & Stump 2007; Stump

2015). The relevant form paradigm cells a speaker needs to know varies from system to system, but in general forms for which the realization of a given category is fully differentiated across conjugation classes are ideal. Returning to the Guugu Yimidhirr forms in Table 1.3, we see that the conjugation class membership of a given verb, and thus the set of inflectional suffixes that make up its form paradigm, can be inferred from either the nonpast or imperative forms.

1.3.2 Canonicity and distinctiveness

Corbett (2009) introduces two important principles based on his notion of an idealized, or CANONICAL, conjugation class system. The subject of this section is the first of these principles, namely DISTINCTIVENESS, which is quite similar in its formulation to the analysis offered in §1.2.1. Specifically, Corbett explains that in a canonical conjugation class system, disparate classes share equivalent function (i.e., similar content paradigms) and differ in their form (i.e., distinct form paradigms).[5] This principle of distinctiveness can be further broken down into a set of four criteria (Corbett 2009: 4-5), each of which targets a different consequence of the principle that may or may not be adhered to by a given language.

The first criterion deals with the notion of differences in the form paradigms of lexemes belonging to different conjugation classes, with the canonical system being maximally distinct, in that each cell-to-cell comparison between conjugation classes reveals a difference in the realization of inflectional material. In reality, we find that many languages show varying degrees of non-canonicity in this regard. In Guugu Yimidhirr (Tables 1.2 and 1.3), there is a moderate degree of syncretism between the

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[5] Content here refers to the set of morphosyntactic properties that are encoded in a verb's paradigm. In the Pama-Nyungan context, this generally covers the tense, aspect, and modality system. Previewing the finding that verb valence patterns with conjugation class membership in a large number of Pama-Nyungan languages, we may also want to consider valence or transitivity as a property encoded in the inflectional endings that differ across conjugation classes in a given language. On this notion, many Pama-Nyungan languages are non-canonical with respect to Corbett's second distinctiveness criterion (see §1.3.2 for further discussion of this criterion).

L and V classes, with respect to their inflectional endings. Moreover, while the R class inflectional endings are more distinct from the other two classes, it is not fully distinct for all tense/aspectual distinctions.

Syncretism across verb conjugation classes in at least some forms is exceedingly common in the Pama-Nyungan context. In fact, nearly every language with conjugation classes included in the current study shows evidence of a single inflectional suffix for at least one morphosyntactic property across disparate conjugation classes. Yingkarta, which has two conjugation classes, provides an example of a Pama-Nyungan language with minimal overlap between inflectional endings in different conjugations. Dench (1998: 41) provides the following summary of the Yingkarta system:

Class	∅-conjugation	L-conjugation
Imperative	*-ya*	*-ka*
Future	*-wu/-ku*	*-lku*
Past	*-purru*	*-lpurru*
Imperfective	*-npa*	*-npa*
Present	*-nyi*	*-lanyi*
Relative_1	*-nhuru*	*-rnuru*
Relative_2	*-tha(nu)*	*-rarnu*
Purposive	*-wura*	*-lkura*
Apprehensional	*-warangu*	*-lkarangu*

Table 1.4: Inflectional endings for Yingkarta verbs

Note that while many of the inflectional endings in the two Yingkarta verb conjugation classes are similar, the L conjugation endings in almost all cases begin with an initial *l/lk* or *r/rn*, resulting in forms that are distinct from those of the ∅ conjugation. The only part of the system which does not adhere to the independence of forms is in the imperfective, which is marked with *-npa* in both conjugations.

The second criterion relates to the stipulation that the content paradigms of conjugation classes have the same basic structure (i.e., they contain the same morphosyntactic or morphosemantic distinctions). Corbett (2009: 4) discusses interpretations of this criterion mainly in relation to noun declensions, but we may apply the same approach to the study of verb conjugations. In general, verbs in individual Pama-Nyungan languages inflect for the same set of morphosyntactic properties, regardless of conjugation class. This is the case for Guugu Yimidhirr verbs – as we saw in Table 1.3, all verbs in the language are inflected for the full range of tense and aspectual distinctions, regardless of conjugation class membership. Instances of verb conjugations that lack certain cells of the full inflectional paradigm are infrequent in Pama-Nyungan, although a potential example comes from Nygangumarta (Sharp 2004).

In Nyangumarta, verbs are separated into four conjugation classes and obligatorily inflect for a one of a range of tense and aspectual distinctions as well as indexing the person feature of the subject. Sharp (2004a) notes that verbs belonging to the open NY and RN conjugations only differentiate nonfuture and simple present tenses with third person singular subjects, but not with first person subjects.[6] Consider the following illustrative examples (Sharp 2004a: 167):[7]

(4) a. RN conjugation

Paji-rna-rni
bite-NFUT-1SG.SUBJ
'I'm biting it. / I bit it.'

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[6] Note though that Sharp does mention the occasional maintenance of a present/nonfuture distinction with first person subjects for some younger Nyangumarta speakers.

[7] Sharp (2004a: 167-168) further illustrates dialectal differences in the quality of the vowel in certain tense suffixes, e.g. the RN conjugation nonfuture marker can surface as *-rna*∼*-rni* in different dialects. In either case, the surface realization of the nonfuture form for this conjugation is clearly not the same as the present tense marker *-ninyi*, which only appears in conjunction with a third person singular subjects.

Paji-ninyi
bite-PRES
'He is biting it.'

Paji-rni
bite-NFUT
'He bit it.'

b. NY conjugation

Janpa-nya-rni
bathe-NFUT-1SG.SUBJ
'I'm bathing. / I bathed.'

Janpa-yinyi
bathe-PRES
'He is bathing.'

Janpa-nya
bite-NFUT
'He bathed.'

In (4), we see that in the presence of a first person singular subject, the nonfuture suffix is used to convey either present or past meaning, even though a present tense suffix is available elsewhere in the paradigm. Contrast this with the N and NG classes, both of which distinguish present and nonfuture tenses for all subjects. We may want to follow an analysis which describes the present as being syncretic with the nonfuture in the RN and NY conjugations, as the morphosemantic expressiveness of the verbs in these classes is not diminished in any way by the impossibility of using the present tense suffix with a first person subject. Regardless, this imbalance in the paradigm structure of the RN and NY classes is not shared by the N and NG classes.

Sharp (2004a: 164) observes a pattern in the form paradigms of Nyangumarta inflectional endings for three of the conjugation class in which certain suffixes begin with or contain the same phonological content as the nonfuture suffix, while a smaller set of suffixes (imperative, anticipatory, potential, and future) show a different pattern. Sharp's suggestion based on this pattern is that the nonfuture may also contribute imperfective aspectual meaning. She further notes that this analysis runs into issues in the NG conjugation, which has initial /ny/ in the nonfuture inflection and /ng/-initial realization across the rest of the paradigm. An alternative analysis is that these initial segments of the inflectional suffixes represent realization of a verb's conjugation class membership.

Third, a canonical conjugation class system lacks intra-conjugation variation. In other words, lexemes belonging to a given conjugation class all inflect in the same way, avoiding regular or lexically specified morphonological alternation and/or alternate realizations of stems or inflectional material.[8] This criterion also precludes the existence of subclasses within larger classes. Potentially included here (Corbett 2009: 4) are phonological processes that lead to fully predictable differences among members of a conjugation.

Numerous Pama-Nyungan languages are analyzed as having subconjugations based on regular (often phonological) patterns that subset the members of a given conjugation. Examples include Dhuwal (Heath 1980), Djambarrpuyngu (Wilkinson 1991), Dhangu (MacLellan 1992), and Ngiyambaa (Donaldson 1980).[9]

Mbakwithi (Crowley 1981) is described as having four conjugation classes, each of which can be broken into two subclasses based on phonological properties of the stems and minor differences in inflectional endings in some cells of the paradigm. The relevant inflectional endings are given in Table 1.5 (Crowley 1981: 174), note that a *V* indicates a vowel that participates in vowel harmony based on the final vowel of the stem to which it attaches:

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[8] Guugu Yimidhirr reduplicated stem alternation (Table 1.3) provides a clear example

[9] Note that some languages feature subdivisions within a single conjugation class, while the other conjugations lack subclasses. As Corbett's criteria are meant to describe the complexity of the overall inflectional class system of a language, we may entertain the notion that multiple distinct form patterns within a single inflectional class does not increase the complexity of the system in relation to the remaining classes. Examples include Wangkajunga (Jones 2012) and Ritharrngu (Heath 1980).

Class	Ia	Ib	IIa	IIb	IIIa	IIIb	IVa	IVb
Present	*-nV*	*-nu*	*-nV*	*-nV*	*-y*	*-y*	∅	∅
Past	*-ɣV*	*-ɣu*	*-nV*	*-nV*	*-ni*	*-ni*	*-nV*	*-nV*
Future	*-yV*	*-yü*	*-yV*	*-yV*	*-yi*	*-yi*	*-tV*	*-tV*
Imperative	*-ʔV*	*-ʔu*	*-ʔV*	*-ʔV*	*-ʔi*	*-ʔi*	*-ʔV*	*-ʔV*
Consecutive	*-nVkumu*	*-nukumu*	*-nVkumu*	*-nama*	*-nikumu*	*-nama*	*-nVkumu*	*-nama*

Table 1.5: Inflectional endings for Mbakwithi verbs

There are various patterns of alternation that underlie the division of Mbakwithi conjugation classes into subclasses. For Class I, the two subclasses differ in the quality of the vowel; the vowel of Class Ia suffixes depend on the quality of the final vowel of the stem, while class Ib suffix vowels are always *u* or ü. For the rest of the Mbakwithi conjugation classes, the form of the consecutive suffix is the only signal of subclass membership. Here we see that Class I is the most divergent from the other classes, in that Class Ib suffixes do not participate in the same morphonological processes as Class Ia. Moreover, note that class II lacks a clear distinction between the form of the present and past tense markers, which is reminiscent of the discussion of Nyangumarta above.

Finally, in a canonical system, each cell in a lexeme's form paradigm is equally predictive of every other cell for a given class. In other words, each inflected form allows the inference of the conjugation class of the lexeme and of every other inflected form. This criterion has a parallel in the concept of MAXIMAL TRANSPARENCY outlined by Finkel & Stump (2007). The idea is that in the idealized case where all inflectional affix forms are distinct from one another, knowing any cell in a lexeme's form paradigm allows the prediction of the conjugation class membership of the lexeme, as well as the realization of the additional cells of the form paradigm itself. Stump & Finkel (2013) extend this idea to quantifying the transparency of individual inflectional classes with respect to one another within the same language.

Returning to the discussion of Mbakwithi verb conjugation classes and subclasses (Table 1.5), note that the divergent Class Ib is highly transparent, as knowing any of the inflected forms of one of its members allows you to identify its class membership unequivocally, as well as the realization of the rest of the reference verb's paradigm. Class Ia and Class IIIa allow prediction of the full form of the paradigm given the past tense and consecutive forms, respectively. The rest of the subclasses are more OPAQUE, as each of their inflectional endings is shared by at least one other cell in another classes' paradigm. For these, we need to know at least two cells in the paradigm in order to predict the other three.

Some Pama-Nyungan languages (e.g., Yolngu languages) have large number of distinct patterns of inflection, which can be grouped together into conjugation classes and subclasses. Subclasses are generally defined on the basis of similarity in these inflectional patterns, such that subclasses of a single conjugation class are usually somewhat opaque with respect to one another, while there is more distinctiveness between subclasses of different conjugations. In Dhuwal (Heath 1980a), distinction betweeen subclasses of the same conjugation class is typically only visible a single cell of the paradigm, though note that inflectional suffixes for the three subclasses of the sixth conjugation class are identical. Subclasses of this conjugation are instead determined by phonological properties of the stem; one subclass has /a/-final stems that preserve the final vowel in all contexts, another has /u/-final stems, while the third has /ka/-final stems that undergo final /a/ > /u/ in most cells of the paradigm (e.g., *kurruka-* 'carry' > *kurruku-ngal* 'carry-PAST).

Note that the situation where subclasses of a single conjugation feature a high degree of opacity, as in Dhuwal, is not a requirement of such an inflectional system. In the closely related Djapu (Morphy 1983: 66), subclasses have more distinctiveness in their inflectional paradigms, though they are still similar enough in their patterns of inflection to warrant their description as subclasses of a single conjugation. To illustrate this, partial suffix paradigms are given in Table 1.6:

Class	NG		N		L		∅			
Subclass	NG1	NG2	N1	N2	L1	L2	∅1	∅2	∅3	∅4
Unmarked	*-m*	*-ma*	*-n*	*-n*	*-n*	*-rn*	∅	∅	*-rr*	-rr
Potential	*-ng*	*-ngu*	*-rr*	*-rr*	*-l*	*-l*	∅	∅	∅	*-rr*
Perfect	*-ng*	*-ngal*	*-r*	*-nan*	*-r*	*-r*	*-n*	*-n*	*-n*	*-n*
Past	*-nha*	*-nha*	*-na*	*-na*	*-na*	*-na*	*-nya*	*-nya*	*-nya*	*-nya*

Table 1.6: Inflectional suffixes for four Djapu conjugation classes and their subclasses

We see in Table 1.6 that Djapu conjugation classes show differing amounts of distinctiveness in their subclasses; the NG class is only syncretic in the Past tense suffix form, while the ∅1 and ∅2 suffixes are fully opaque. Morphy (1983: 68) demonstrates that these two subclasses are distinguished only by a change in the stem-final vowel to /u/ in the ∅1 potential forms (e.g., *luka-* 'eat' > *luki* 'eat.POT'; cf. *lukan* 'eat.PAST'). Comparing the situation in Djapu with that of Dhuwal, note that languages belonging to the same subgroup may show differing levels of distinctiveness in their patterns of suffixation.

1.3.3 Morphomics and the principle of independence

Corbett's second principle addresses the extent to which the existence of conjugation classes is relevant or visible to components of the grammar beyond morphology, including, but not limited to, syntax, phonology, and semantics. This is formulated as the principle of INDEPENDENCE, in which Corbett (2009: 5) argues that the distribution of lexemes into classes in canonical conjugation systems is not due to the syntax, phonology, etc. of the language in question. In essence, this principle may be thought of as a less strong version of Aronoff's (1994) notion that certain morphological processes are MORPHOMIC – that is they are purely morphological in function, rather than being motivated by forces exterior to the morphology. Following Aronoff, a number of linguists have categorized the presence of morphomic phenomena, including stem and affix allomorphy in Romance (Maiden 2005; Maiden et al. 2011; Cruschina et al. 2013). O'Neill (2014) provides a succinct overview of the status of the morphome in prevailing theoretical approaches to inflectional morphology, including Paradigm Function Morphology (Stump 2001) and Distributed Morphology (Halle & Marantz 1993). Round's (2013, 2015) work on Kayardild (non-Pama-Nyungan) identifies distinct categories of morphomic phenomena based on which level of morphological representation they play a role in.

The existence of a purely morphological level of structure is by no means accepted across the discipline, many instead categorize morphology as phonological material stored in the lexical entry of a wordform along with stipulations about how this phonological material may be used by the syntax (Bermúdez-Otero 2012; Haugen & Siddiqi 2016, among others). Bermúdez-Otero & Luís (2016) provide a useful overview of the debate over the existence of morphomic phenomena, in addition to arguing for a phonological account of the patterns observed in the inflection of Spanish nouns and adjectives. Steriade (2016) argues for phonological and semantic motivations underpinning certain stem alternations in Latin verb declensions.

In Distributed Morphology (DM; Halle & Marantz 1993, 1994), the relevant assumption is that there is a level of morphological structure that exists between the syntax and phonology of a language. This morphological component provides the interface for realizing morphosyntactic features (provided by the syntax) with phonological forms. DM seeks to leverage regularity in the paradigm by proposing that inflectional affixes are specified for various morphosyntactic features, and that syncretism represents the consequence of underspecification of some feature. In other words, an affix belonging to class C, with permissible features α, β, and τ, might not have a feature specification for τ. This underspecified affix thus serves as a 'default', over which fully-specified affixes may take precedence if their feature settings agree with those required by the morphological structure. If a more narrowly applicable affix is not appropriate based on the requirements of the syntax, the default is used, leading to realization of the same phonological form in different morphosyntactic contexts.

Illustrative of the DM approach to inflection classes is Arregi's (2000) account of Spanish verb conjugation classes, the basics of which were introduced in Table 1.1 (§1.1.1).[10] In essence, verbs in languages with verb conjugation classes are assumed to have a 'theme' (Th) position in all syntactic functional heads, which may be filled by binary-valued (i.e., $+/-$) class features, with the number of distinct class features being dependent on how many inflection classes there are in the language and what the patterns of inflection look like. Thus for Spanish, Arregi (2000: 4) posits two class features for three conjugation classes. Regularities in the conjugation class marker (i.e., 'theme vowel') within verb classes and in inflectional suffixes are taken to be the realization of identical Th features. Irregularities in the expected patterns are explained as the result of morphonological processes or the elimination of some expected structure by the syntax before the insertion of feature-matched affixes takes place.

As formulated by Corbett (2009), the idea of independence provides a way to approach the patterns we observe in conjugation class systems, taking the purely morphomic extreme as a sort of 'default' against which we can make comparisons. Corbett again defines a number of criteria, the first several of which refer to the inability of various components of the language (i.e., syntax, semantics, phonology) to motivate the distribution of lexemes into classes. An additional criterion addresses the size of conjugation classes, stating that a larger conjugation class (in terms of

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[10] See also Oltra Massuet's (1999) DM analysis of Catalan verb conjugation classes.

number of members) is more canonical than a very small one, the latter of which could just as easily be represented in the lexicon without the need for an additional class.

In the Pama-Nyungan languages, it is common to find both large and small classes in the verb conjugation system of a single language, especially for languages with four or more classes. Nyawaygi (Dixon 1983) has seven conjugation classes; 3 classes are open and contain 57, 25, and 12 members, while the remaining four have closed membership of four or fewer roots. Karajarri (Sharp 2004b: 160) has four conjugations; the two large classes have 129 and 36 verb roots, while the two smaller classes have 5 and 3. Yir Yoront has four verb conjugation classes of size 45, 15, 4, and 2.[11] Moreover, verb inventory sizes vary widely among the Pama-Nyungan languages, such that small and large conjugation class membership size are relative terms based on the overall scale of the verbal lexicon. In other words, a small class in a language with 500 attested verbs is possibly different from a small class in a language with 50 attested verbs in terms of number of members.

Stump (2015) highlights the prevalence of correlation between a lexeme's conjugation class and other (syntactic, semantic, phonological) properties, which more accurately describes the situation found across the Pama-Nyungan languages. On this view, while a correlation between conjugation class membership and stem phonology or morphosyntactic considerations may exist, the membership of any given lexeme is not necessarily predictable by knowing its stem phonology or syntactic requirements. As detailed throughout this thesis, verb conjugations in Pama-Nyungan languages commonly show correlations with verb valence and/or phonological properties of the stem, but the division of the verbal lexicon along these lines is by no means comprehensive or clear-cut. Returning to Guugu Yimidhirr, we see an example of a system in

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[11] Alpher further posits a fifth conjugation class, consisting of a single ditransitive root *waqa* 'give'.

which conjugation class membership correlates imperfectly with verb valence. Specifically, we find that the L and R classes consist of mostly transitive roots, while most of the members of the V conjugation are intransitive, while exceptions exist for both of these categorizations.[12] Yingkarta (source) has two conjugation classes, whose membership again roughly correlates with verb valence. Specifically, one class contains 82% intransitive roots, while the other is 87.5% transitive. We find this same imperfect correlation with verb valence in languages with a larger number of conjugation classes as well. Yir Yoront is described as having four conjugation classes which divide 123 verb roots as follows:

Class	% Transitive	% Intransitive
l	**61**	39
r	**71**	29
n̪	19	**81**
l̪	25	**75**

Table 1.7: Proportion of transitive and intransitive members of four Yir Yoront verb conjugation classes

Additional examples are numerous, a majority of the languages sampled in the current exploration of Pama-Nyungan verb conjugation classes show some degree of correlation between class membership and verb valence. In these cases it would be an oversimplification to claim that conjugation class membership is determined by or a function of the syntax or argument structure, nor can we predict the membership of any individual root based on the number of arguments it takes.

In the Warluwaric languages Warluwarra (Breen 1971), Wakaya (Breen 1974), and Bularnu (Breen n.d.), conjugation class membership is determined by phonological

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[12] See the subsequent section (§1.3.4) for a brief discussion of differing interpretations of the term ‘transitivity’ in linguistic theory and how they relate to the way terminology is used in the documentation of the Pama-Nyungan languages

properties of the stem, rather than valence or argument structure. Each language has four conjugation classes, though the determining criteria for membership differs slightly from language to language. The Warluwarra and Bularnu conjugation class systems are somewhat similar in this regard; the TH and ∅ conjugations contain verbs with stem-final /a/, while verbs with stem-final /i/ fall into the J conjugation, and the RR class verbs have stem-final /rra/. Further distinction is drawn between the TH and ∅ classes, the latter of which has stems that end in sequences of an oral stop + /a/, while the former consists of all other /a/-final stems. The patterns of membership in Wakaya are more complex, but are similarly described as having membership defined by stem-final segments. It should be noted though that many of these distinctions are more descriptive generalizations about class membership, rather than being strict rules. Breen (n.d.: 604) finds that the membership of many Bularnu stems ending in /a/ is not predictable, citing the TH conjugation *gaga* 'to cry' and ∅ conjugation *baga* 'to walk'. By contrast, membership in the J and RR conjugations is predictable from the stem. Thus we might analyze the relationship between the conjugation class system and the phonology in the Warluwaric languages goes beyond a simple correlation in certain places.

A third possibility found in the Pama-Nyungan languages is a 'hybrid' conjugation class system, where both verb valence and stem phonology appear to be correlated with conjugation class membership. A case in point is Ngiyambaa (Donaldson 1980), which is described as having three conjugation classes, whose membership is correlated with transitivity; the R conjugation consists only of transitive verbs, L conjugation verbs are mostly transitive, with a few intransitives, and Y conjugation verbs are mostly intransitive, with some transitive verbs. Subclasses within Y and L conjugations appear to break along the stem-final vowel, though there are exceptions to the observed patterns rather than them being absolute.

These three distinct possibilities highlight useful patterns that can be further investigated using computational methods. As with the typological variance in terms of number of conjugations discussed in §1.2, the profiles of individual languages with respect to tendencies for how verbs are grouped into classes provide a parameter for the reconstruction model. In essence, description of the number of conjugation classes a language contains and their makeup is imbued with the notion distinctiveness, in that the patterns of variance in the conjugations of individual verbs belie the existence of the classes themselves. Regarding independence, it should be noted that the computational phylogenetic approach to linguistic reconstruction often involves categorizing features of a linguistic system in absolute terms. If the way verbs are organized into classes is taken to be a reconstruction parameter, we must make decisions about whether the tendencies we observe are strong enough to categorize a language as having a valence-based or phonology-based system, or both.

1.3.4 Transitivity and valence

So far, I have used terms like 'transitivity' and 'valence' somewhat interchangeably, though it should be noted that 'transitivity' as a linguistic concept has different usage in different theoretical approaches to analyzing argument structure. This section offers a synopsis of the different ways these terms have come to be understood in the literature before turning to a brief discussion of the way terms like 'transitive' and 'intransitive' are used in descriptions of Pama-Nyungan verb conjugation classes. Grossman's (2019) exploration of the susceptibility for transitivity and valence-related phenomena to undergo contact-induced change additionally includes a clear overview of this topic.

In the most general sense, 'valence' refers to the argument structure of a verb (or some other word) directly, including information about how many arguments are required or allowed and how/whether those arguments signal their role as such overtly via morphological marking (e.g., case on argument nouns or noun phrases). Here it is useful to describe verbs in terms of the number of arguments they subcategorize for; MONOVALENT verbs take a single argument, while terms like BIVALENT, TRIVALENT, and POLYVALENT refer to verbs that require multiple arguments, though note that the nature of these arguments may differ.

The notion of 'transitivity' is used in various ways the literature. In some approaches to understanding argument structure, transitivity involves a specific type of subcategorization, namely the requirement of a(n agent-like) subject and a (patient-like) direct object argument. Here Grossman (2019: 4) cites Huddleston & Pullum's (2005) grammar of English as an example of this line of thinking. Huddleston & Pullum (2005: 78) define transitivity in terms of the number of objects a verb takes; an intransitive verb is one which takes no objects, monotransitive verbs require a single (direct) object, and ditransitives require two objects (direct and indirect).

A second conception of transitivity (exemplified by Comrie 1989; and in Grossman 2019) attempts to provide a more general definition that can apply cross-linguistically. On this approach, a prototypically transitive verb is used as an exemplar against which other verbs are compared. If the argument structure and/or morphosyntactic properties of a given verb align with those of the transitive exemplar, the verb in question is considered transitive.

While the first two definitions center on the morphosyntactic requirements of a verb, a third approach places transitivity on a spectrum based on the semantics of entire clauses, rather than verbs themselves. Hopper & Thompson (1980: 252) outline a set of metrics for quantifying the amount of transitivity in a clause, including considerations of the number of participants (2 or more participants are more transitive than 1), inherent action (transferrable action > states of being), aspectual information (telic, completed action > atelic, partially completed action), punctuality (instant actions > inherently on-going actions), intentionality (intentional > unintentional action), mode (realis > irrealis), level of affectedness of the patient or object, and several others.

Turning now to descriptions of the Pama-Nyungan languages, we observe that most do not explicitly explain their assumptions about transitivity when discussing whether a specific verb is transitive or intransitive. Instead, verbs, their roots or stems, etc. are asserted as being transitive or intransitive (or both in different contexts). At a descriptive level, the usage most closely lines up with the morphosyntactic approaches, specifically the treatment of transitivity as a direct correlate of valence, i.e., that a verb that only takes a subject or agent argument is intransitive, while all other verbs that take multiple arguments are transitive. Moreover, it is often not clear whether transitivity is taken to be a property of a stem, a root, a clause, or some combination of the three, nor is there extended discussion of the semantics of transitivity as a cline. As the phylogenetic analysis on offer here is subject to the description of verbs and conjugation classes in the available Pama-Nyungan grammars and wordlists, we will similarly take the transitivity of a verb to be mostly determined by the number of arguments it subcategorizes for, though it should be emphasized that a closer examination of the notion of transitivity and its interaction with more formal theoretical approaches and the verb conjugation class systems of the Pama-Nyungan languages should be a *desideratum* of continued scholarship on this topic.

1.4 Overview of the thesis

1.4.1 Key research questions

While the typological characteristics of a large number of the modern PN languages are moderately well-described, there are several facets of the modern and proto-PN verb conjugation class apparatus that remain to be well understood. The current study will address many of these, which are summarized below:

1. What was the verb conjugation class system like at older, unattested stages of Pama-Nyungan? Is Dixon (1980, 2002) likely correct in assuming the proto-language contained all of the conjugation classes that can be found in at least one modern language? If not, how many conjugation classes were there likely to have been? Which of the modern reflexes are reconstructable at what depth in the diachrony of the PN tree? Ultimately, phylogenetic reconstruction models center on a two or three conjugation class system in the prehistory of Pama-Nyungan, while larger inventories, such as the seven proposed by Dixon, are not supported (§§4.3-4.4).

2. Related to 1, Dixon and others assume conjugation classes can only be lost via the collapsing of distinctions between two separate classes. Do we find evidence that conjugation classes may also be gained via dissimilation of subsets of a single class (or by other means)? Once lost, can distinctions between specific lexical substrata be regained? Results show (§§4.3-4.4) that conjugation classes were likely to have been both lost and gained over the evolution of the modern Pama-Nyungan languages. Moreover, innovation of conjugation classes from a previous stage of not having them as a feature is less likely to occur than adding to an existing inventory.

3. How was conjugation class membership determined at older, unattested stages of Pama-Nyungan? Were transitive and intransitive verbs separated into different classes, or was there a phonological or prosodic basis for determining class membership? Or, is neither of these likely to have been a determining factor for conjugation class distinctions? Findings of the current study suggest a strong correlation between the membership of conjugation classes and verb valence, while phonology becomes a relevant conditioning factor for languages with four or more conjugation classes (§4.5).

1.4.2 Chapter summary

This introductory chapter has provided a comprehensive overview of the history of descriptive documentation of the Pama-Nyungan languages, including foundational literature on the evolution of verb conjugation classes, discussion of verb conjugation class membership and typology and their relation to modern morphological theory, and the key research goals of the current project. What follows is an extended summary of the chapters that comprise the remainder of the thesis, with attention to the methods employed, results obtained, and conclusions drawn therein.

We begin with an exploration of PHYLOGENETIC METHODS FOR LINGUISTIC RESEARCH in Chapter 2. In its nascent stages as a research enterprise in linguistics, computational phylogenetics has been brought to bear on a variety of historical reconstruction data, both in determining the internal genealogy of a given language family (e.g., Bowern & Atkinson 2012; Dunn et al. 2015; Bouckaert, Bowern & Atkinson 2018, among others), as well as tracking the diachronic development of specific linguistic features based on these inferred phylogenies (e.g., Nunn 2011). The former of these involves using linguistic (often lexical) data to infer relationships between languages and across language families. Bowern (2018) notes that Bayesian tree construction models involve a number of parameters representing explicit assumptions about the nature of language evolution being modeled. These include assumptions about time-scale or -depth, rate and/or permissibility of the gain or loss of a feature, prior knowledge about the structure of subgroups within the larger language family, and so on. The latter task involves investigation of how a linguistic feature or set of features evolved over time. Given a single tree or a set of trees representing plausible internal relationships among members of a language family and observed data about the modern languages that comprise the family in question, one can probe the tree or trees to explore how and when a given feature was innovated, changed, or lost.

This often takes the form of ancestral state reconstruction – the inference of the state of the ancestor(s) of modern languages with respect to some linguistic feature. This can involve reconstruction of the state of the root node in the phylogeny (representing the common ancestor of the entire family) or for any of the intermediate nodes (representing where subgroups or individual languages would have diverged from one another).

The core proposition of this thesis involves the latter of these two possibilities – that is reconstruction and analysis of the verb conjugation class system of an earlier, unattested stage of Pama-Nyungan, based on a typological features of the modern languages and making use of existing reconstructions of the Pama-Nyungan family tree (Bowern & Atkinson 2012; Bouckaert, Bowern & Atkinson 2018). To accomplish this task, I make use of the ancestral state reconstruction method developed by Pagel & Meade (2004), which computes the probability of a given state or typological characteristic at a given node as a function of the rate(s) of transition between members of the set of possible states for a given feature. Ancestral state reconstructions using Pagel & Meade's method are performed using the BayesTraits (version 3.0.1)[13] software package.

Moreover, this chapter provides a more detailed exploration of the computational phylogenetic methods employed in subsequent chapters. This includes discussion of the mathematics behind these methods and their applicability to the task of linguistic reconstruction. Relevant methods include tests for phylogenetic signal, as well as models of tree inference and ancestral state reconstruction (Bayesian evolutionary models, especially Markov chain Monte Carlo models).

Following this discussion of the core concepts and methods of phylogenetic reconstruction in linguistics, Chapter 3, MORPHOLOGICAL TYPOLOGY, introduces the representative Pama-Nyungan verb conjugation class data which form the basis for

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[13] Available from http://www.evolution.rdg.ac.uk/BayesTraitsV3.0.1/BayesTraitsV3.0.1.html

the current study. The language sample consists of data from 111 Pama-Nyungan languages, specifically chosen for inclusion based on the notions of achieving sufficient heterogeneity of genetic (language subgroup) affiliation and geographical distribution. In other words, curation of the language sample was meant to avoid privileging any of the numerous Pama-Nyungan subgroups or including too many languages from a single geographic region. Moreover, coverage of the sample is limited by the availability, accessibility, and completeness of the existing documentation and description of the Pama-Nyungan languages. Languages were coded (assigned a discrete feature value) for three features of their verbal morphology, specifically with respect to verb conjugation classes. These features are summarized as follows, with specific reference to the key research question (§1.3.1) they address:

1. CHARACTER 1: PRESENCE OR ABSENCE OF VERB CONJUGATION CLASSES. The first character addresses parts of key research questions 1 and 2 by seeking to reconstruct whether or not the ancestor of the modern Pama-Nyungan languages was likely to have had verb conjugation classes as a defining characteristic, which were subsequently lost over time as the languages diverged from one another, or whether multiple innovations of verb conjugation classes are better supported by the data. For traditional approaches to linguistic reconstruction, the former of these is generally preferred over the latter, although Warnow et al. (2005) provide a number of examples of observed parallel innovation of phonological and morphological features, and to a lesser extent properties of the lexicon.

2. CHARACTER 2: NUMBER OF VERB CONJUGATION CLASSES. The second character rounds out the analysis of key research questions 1 and 2. Languages were coded based on how many verb conjugation classes they contain, with permissible values ranging from zero (for languages that lack verb conjugations) to four

(representing languages with four or more conjugation classes).[14] The choice of four as an upper bound was motivated by the desire to reduce model complexity in terms of the rates that need to be estimated by the reconstruction models, as well as the observation that many of the languages with more than four productive verb conjugations fall into a small subset of the linguistic sub-families of Pama-Nyungan. Importantly, this choice serves as a digression between traditional reconstruction analyses, which assume that the ancestor language necessarily contained all of the conjugation classes for which a reflex is found in the modern languages. With this in mind, research proceeded with the caveat that a result indicating a high probability of four or more conjugations would necessitate an expansion of the feature coding for this character.

3. Character 3: Conjugation class membership features. The final character addresses the third key research question by focusing on the generalizations that can be drawn about the membership of the verb conjugation classes in each of the languages in the sample. As described in §1.2, membership in verb conjugation classes in the Pama-Nyungan languages can generally be defined based on either morphosyntactic (i.e., argument structure) or phonological properties of the verb stems. Noting that many of the languages are described as having both a morphological and phonological basis for determining class membership, this character was further split into two features, one for each possibility. Thus languages were coded according to four logical possibilities, representing the independent or combined presence or absence of either membership feature.

A discussion of character coding and decisions plus the full set of coding profiles

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[14] In order to avoid confusion in description of the coding values for this character, "0" was chosen over "1" for languages that lack conjugation classes. "1" is not a permissible value for this character.

provides insight into the assumptions of the research, as well as encouraging replicability and modification. In the interest of extending the description presented in part in §1.2, this chapter further discusses the typology of the verb conjugation class systems in various Pama-Nyungan subgroups. This chapter begins to address the main research goal of the dissertation, namely computational phylogenetic analysis of the diachronic development of the Pama-Nyungan verb conjugation class system.

Model setup and the results of Ancestral state reconstruction comprise Chapter 4. Tests of phylogenetic signal, including Fritz & Purvis' (2010) D statistic for binary traits and Blomberg, Garland & Ives' (2003) K test for multistate traits reveals strong evidence of phylogenetic signal in the coded data for all three characters. The presence of phylogenetic signal in the data further validates the use of the Pagel & Meade model for reconstruction of these features. A discussion of model setup and parameter optimization is followed by a detailed introduction to model comparison via marginal likelihood estimation. Varying the input to the model in terms of which paramaters are estimated and what restrictions are placed on the parameters themselves represent different hypothesis about the nature of the evolution of the linguistic features we want to reconstruct. Model comparison attempts to quantify evidence in favor of one or more distinct models.

The remainder of Chapter four provides an extended presentation of the results of a multiple reconstruction models for each character as well as an interim discussion of the implications of these results. Ancestral state reconstruction modeling, like any stochastic research endeavor, is limited by the quality of the data and the assumptions introduced into the model. We can get around some of these limitations by building datasets of sufficient size and breadth and ensuring the hypotheses we are testing are specific and faithfully implemented. Moreover, the language of Bayesian phylogenetic reconstruction is of probabilities rather than absolutes. With that in mind, results of reconstruction of the Pama-Nyungan verb conjugation class system do provide several interesting points of discussion.

First, we find strong support in favor of reconstructing presence of conjugation classes for the ancestor of the modern languages across a number of models, while the model that stipulates absence of conjugation classes in the prehistory of Pama-Nyungan importantly fails to provide a good explanation of the data. We can liken this result to a weak version of Dixon's (1980, 2002) reconstruction hypotheses, in that they categorically assume the existence of verb conjugations as a defining characteristic of the proto-language. To be more exact, this finding adheres to the hypothesis that once verb conjugations are lost as a feature of a language, they are unlikely to be regained in the descendants of that language.

Reconstruction also favors the hypothesis that the ancestor of the modern Pama-Nyungan languages had two (possibly three) verb conjugation classes, a finding which is in direct opposition to Dixon's reconstruction of seven. Modeling this character leads to additional important details beyond the ultimate number of reconstructed conjugation classes. Specifically, we find that the best fitting models were those that 1) allowed both gain and loss of conjugation classes to occur (cf. Dixon, and certain parsimony-based traditional reconstruction methods more generally, which eschew parallel or multiple independent innovations) and 2) disallowed the gain or loss of more than one conjugation class in a single evolutionary step. In other words, a language with three or four conjugation classes cannot undergo catastrophic collapse of the entire conjugation class system all at once, nor can languages with zero or two conjugations undergo rapid proliferation of the system. Moreover, as confirmation of the findings of the models of the first character (and perhaps vindicating the traditional arguments-from-parsimony), the best fit to the data was found in the model that disallowed innovation of conjugation classes as a typological feature, i.e. going from zero to two conjugation classes.

Finally, while the results of reconstructing the conjugation class membership character were not strongly conclusive, we do find support for the hypothesis that the ancestral language had conjugation classes with membership based on verb valence, and against phonology as a determining factor. Moreover, we find evidence that these two features were likely to have coevolved, rather than being two independent systems that evolved side by side without any influence of one over the other.

Ultimately, we do not find support the strongest version of Dixon's hypothesis of a maximal set of seven conjugation classes, though the weaker claim that parallel innovation of conjugation classes as a feature is unlikely is supported.

Building on the evidence for the coevolution of valence- and phonology-based conjugation classes, Chapter 5 investigates the possibility of CORRELATED EVOLUTION BETWEEN TRAITS. Here I specifically look at the relationship between the number of conjugation classes and the generalizations that can be drawn about class membership in the first of two focused extensions of the phylogenetic analysis offered in Chapter 4. Correlation between traits may be positive or negative in polarity. In other words, two traits may show evidence of evolving together, or they may move in opposite directions, with the prevalence of one trait coming at the cost of the loss of another.

An independent model (assuming no correlated evolution) and a dependent coevolution model were fitted for each of the six possible combinations of conjugation class system size (2, 3, or 4 or more classes) and membership features (valence or phonology), and the resulting pairwise model comparisons for each combination quantify the evidence in favor of either hypothesis. Results indicate evidence of correlated evolution between valence-based conjugations and all three of the class system sizes, as well as between phonology-based conjugations and four conjugation classes. Further examination of the relative size of the estimated transition rates in the fitted models reveals interesting conclusions about the predicted evolutionary pathway of Pama-Nyungan verb conjugation classes.

Specifically, we see support for the notion that the presence of valence-based conjugation classes coincides with the gain and loss of conjugation classes, as well as the converse, that stability in the conjugation class system is unlikely to cause loss of valence as a defining characteristic of membership. Moreover, we find support for the most common situation for languages with two conjugation classes is to have valence-based membership. Finally, the gain of phonology as a membership characteristic is strongly associated with the presence of four or more conjugations. This leads to the inference of an evolutionary pathway whereby a small number of conjugation classes with valence-based membership may undergo proliferation of the number of conjugation classes it contains and the correlated introduction of phonology as a determining factor for membership in conjugation classes with the same valence-based feature value. In other words, phonological properties of the stem are used to further disambiguate the existence of multiple conjugation classes that contain either mostly transitive or intransitive verbs.

Chapter 6 explores the EFFECTS OF TREE TOPOLOGY ON RECONSTRUCTION, noting both the amount of uncertainty about certain facets of the internal structure of Pama-Nyungan based on previous analyses (Bowern & Atkinson 2012; Bouckaert, Bowern & Atkinson 2018) and the relative lack of investigation into the status of tree topology as a free parameter of ancestral state reconstruction models in the literature. This chapter proposes two preliminary approaches to understanding how varying the input tree may influence reconstruction and model likelihood. As a preliminary step, four distinct Pama-Nyungan phylogenies were identified that vary with respect to their placement of a specific subgroup, namely the Karnic languages.

In the first proposed study, strength of phylogenetic signal in the verb conjugation class character data given each of the candidate topologies is compared. Ultimately, this was uninformative for discerning between the specific trees under consideration, as the morphological traits are highly conserved, and phylogenetic signal is strong across the board.

An extension of this idea of comparison of topologies involves using various measures of homoplasy, multiple appearances of a feature state in its evolutionary history. The basic idea is that while an exact quantification of what constitutes a 'good' amount of homoplasy for a given character is not straightforward to resolve, comparison of relative homoplasy metric scores for the same data on different trees may provide some insight into which we may want to privilege in our analysis of the set of trees. Results showed similar outcomes for each of the four candidate topologies, though the tree that assumes a direct common ancestor between Karnic and the Central Pama-Nyungan macro-group slightly outperformed the alternatives for all but the phonology-based membership character, where all topologies showed identical amounts of homoplasy.

Having confirmed the presence of phylogenetic signal for all characters and all four candidate topologies, the second proposed study uses the set of four reference trees as input to ancestral state reconstruction models and explores the effect of tree topology choice on the posterior likelihood of the model, as well as on the interaction between estimated transition rates and posterior likelihood. Results of this mini-study again indicate a slight preference for the tree that includes Karnic and Central Pama-Nyungan as a clade, while the tree which proposes that Karnic and Central Pama-Nyungan do not share a common ancestor before the root node also finds some support for Characters 1 and 2. While these results may be somewhat specific to the trees and morphological characters in question, the exercise presented in Chapter 7 serves as a proof of concept for using closed-class morphological data to explore larger questions about how to resolve uncertainty in a tree sample.

Finally, Chapter 7 offers a brief SUMMATION AND DISCUSSION of the main research goals and findings of the thesis, with attention to the implications for 1) our understanding of the utility of computational phylogenetic methods to reconstruct closed-class morphological systems, 2) the relationship between the specific reconstruction findings of the current research and existing traditional reconstructions of the Pama-Nyungan verb conjugation class apparatus, and 3) contributions to the ongoing stochastic resolution of the internal structure of the Pama-Nyungan language family.

Chapter 2

Phylogenetic methods for linguistic research

This chapter offers a detailed exploration of computational phylogenetics and its application to linguistic reconstruction. Core concepts of computational phylogenetics, including network- and tree-based approaches to representing genetic relationships and various methods for computing these relationships from observed features of a group of entities are discussed in §2.1. In §2.2, computational phylogenetic approaches to linguistic reconstruction are detailed, including both language family tree inference and ancestral state reconstruction. The latter of these two tasks being the goal of the current study, §2.3 outlines the integral components of ancestral state reconstruction, including feature types and coding, tests for tree-like signal in the dataset, and Pagel & Meade's (2004) Bayesian inference model for ancestral state reconstruction. Included in this is a discussion of the BayesTraits software implementation of the Pagel & Meade model.

2.1 Core concepts of computational phylogenetics

In biology, a PHYLOGENY is the evolutionary history of an organism or a genetically related group of organisms. The study of PHYLOGENETICS seeks to reconstruct these evolutionary histories based on observable features of the modern members of a genetically related group of organisms, including biomolecular sequences (DNA, RNA, amino acids) in addition to other molecular level traits, such as morphology (shape) and metabolic pathways (Moret, Wang & Warnow 2002: 1-3). The phylogeny itself is sometimes represented as a binary branching TREE structure, where the leaf nodes or tips of the tree represent the modern organisms (TAXA) and the edges or branches of the tree indicate the relationship each organism has to the overall group:

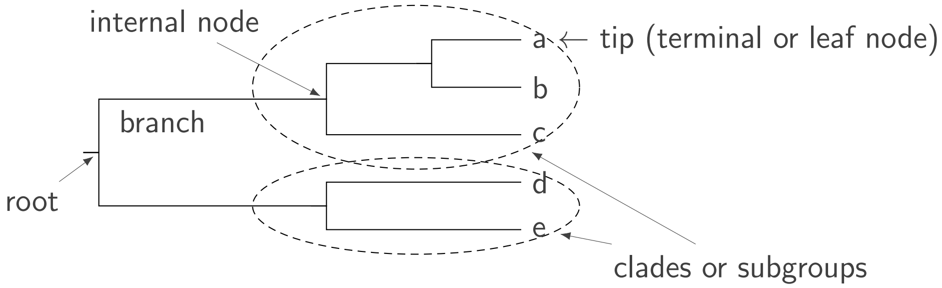

Figure 2.1: The anatomy of a simple phylogenetic tree

The tree in Figure 2.1 depicts the historical internal relationship between five hypothetical species (or cultures or languages for our purposes). The relationships between taxa in a phylogeny are typically described according to familiar kinship terms. Sisters (those taxa that descend from a common internal node) are more closely related to one another than they are to other taxa in the tree. In Figure 2.1, note that *a* and *b* are sisters, as are *d* and *e*. Moving inward from the taxa at the tips, internal nodes convey additional information about the evolutionary history in question. Specifically, internal nodes represent the MOST RECENT COMMON ANCESTOR (MRCA) of the internal nodes and tips they dominate. Taxa which share an MRCA are more closely related to one another than they are to other taxa. In Figure 2.1, we see that *a*, *b*, and *c* share a common ancestor that is not shared with *d* and *e*, while the same can be said for the latter pair. These groupings of taxa based on their shared common ancestry are referred to as CLADES or SUBGROUPS (indicated with dashed circles in Figure 2.1). The root node represents the common ancestor of all the taxa in the phylogeny. We can thus recover the evolutionary history of the modern organisms as a series of evolutionary splits from the common ancestor at the root node. Moreover, trees depicting real-world phylogenies often additionally use branch length to indicate time-scale.

Moret, Wang & Warnow (2002: 4) note that there are three major approaches to computing a phylogeny, namely DISTANCE-BASED, MAXIMUM PARSIMONY, and MAXIMUM LIKELIHOOD methods. In addition, it is important to consider BAYESIAN methods, which build on maximum likelihood approaches by incorporating prior probability and relative strength of evidence for proposed groupings.

2.1.1 Distance-based methods

In distance-based models of phylogenetics (Pardi & Gascuel 2016), the evolutionary distance between each pair of taxa is estimated based, for example, on the number of substitutions that have occurred in DNA or RNA sequences over the course of the evolution of the relevant organisms. These distances are then used to infer a phylogenetic tree that accounts for the data. To illustrate, consider the following DNA sequence data for four related taxa:[1]

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[1] Adapted from Geer et al. (2003)

DNA site / Taxon	1	2	3	4	5	6	7	8	9	10
a	A	T	A	T	A	C	G	T	A	T
b	A	T	G	T	A	C	G	T	A	T
c	G	T	A	-	A	C	G	T	G	C
d	G	C	G	T	A	T	G	C	A	C

Table 2.1: Aligned DNA sequences for 4 taxa at 10 sites

In order to determine the optimal phylogeny based on the data in Table 2.1 according to the distance-based approach, we must first decide on the appropriate metric of evolutionary distance. Pardi & Gascuel (2016: 5) note that due to the possibility of complicating factors such as multiple substitutions at the same site, taking the raw count of the number of substitutions between aligned sequences is not generally considered tractable as a valid measure of distance. However, we will assume for current purposes that correcting for such complications is unnecessary. We can thus create a matrix of proportional evolutionary distances (d) between sequences (Table 2.2) according to the raw count of substitutions between them and the number of DNA sites (equation 2.1):

$$d = \frac{\#\ \text{substitutions}}{\#\ \text{sites}} \tag{2.1}$$

	a	b	c	d
a	–	0.1	0.4	0.6
b		–	0.5	0.5
c			–	0.6
d				–

Table 2.2: Uncorrected pairwise distances for 4 taxa in Table 2.1

Given the uncorrected pairwise distances for the 4 taxa in Table 2.2, the phylogeny can be constructed according to a number of algorithms, including Neighbor Joining (Saitou & Nei 1987), UPGMA (Sokal & Michener 1958), and WPGMA (Sokal & Sneath 1963). In the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method, these pairwise distances are used to group the taxa in order of increasing distance, such that the pair with the shortest distance between them forms an immediate subgroup, which is then joined with the next nearest taxon, and so on. From Table 2.2 we see that *a* and *b* have the shortest pairwise distance, thus they form a subgroup and the distances from *c* and *d* to *ab* are recalculated. Ultimately, we arrive at the full phylogeny:

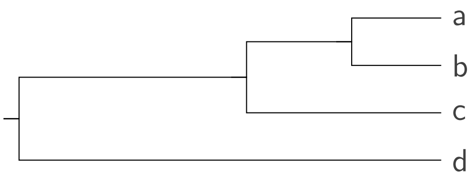

Figure 2.2: UPGMA tree for phylogeny in Table 2.1

2.1.2 Maximum parsimony

Maximum parsimony takes as its measure of relatedness the number of substitutions themselves, rather than estimating a matrix of evolutionary distances. In this approach, the optimal phylogenetic tree is the one which requires the fewest amount of substitutions. Returning to the data in Table 1, note that the phylogeny of a set of four taxa can be represented by three distinct unrooted trees:

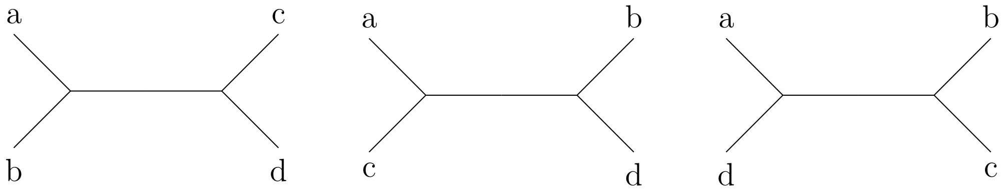

Figure 2.3: Three unrooted trees representing phylogeny in Table 2.1

In Figure 2.3 the three possible pairwise combinations of the phylogeny are depicted. In order to determine the most parsimonious option, a simple count of the necessary substitutions is tallied. The guiding principle behind this approach is that losing trees will contain extraneous substitutions that could be better explained by proposing the winning tree. Based on the data in Table 1, the left-hand in Figure 2.3 requires 9 substitutions, the middle tree requires 10 substitutions, and the right-hand requires 11 substitutions, thus the left-hand tree is the most parsimonious.

2.1.3 Likelihood methods

Likelihood methods (Dunn 2015: 197) attempt to calculate the likelihood L of observing the given data D given a specific evolutionary model θ (a phylogeny, consisting of a tree, its branch lengths, etc.), i.e. $L = p(D|\theta)$. In the maximum likelihood (ML) approach, the goal is finding the value of the model parameters θ such that L is maximized. Dunn (2015: 197-8) notes that for phylogenetic applications of ML, while finding the optimal values of most model parameters (i.e., branch lengths, transition rates) is generally possible, finding the best tree topology is a much harder problem. This is due to the number of possible trees, which can quickly grow to an astronomical count as the size of the set of taxa increases. Put simply, there is currently no known approach which will produce the optimal tree from a large set of trees consistently within a measurable amount of time using the ML approach. Enumerating the possibilities is clearly unworkable, and random sampling is similarly unable to reliably pick out the optimal tree. Fortunately, there is a solution to this daunting problem, namely Bayesian inference.

2.1.4 Bayesian methods

In phylogenetics, one common approach to efficiently searching a large tree space is through complex sampling methods, such as Bayesian Markov Chain Monte Carlo (MCMC; Metropolis et al. 1953). MCMC sampling is initialized at a random tree in the set of possibilities, and parameter values are modified randomly, resulting in a jump to a new part of the search space. At each iteration, the likelihood of the current tree given the current parameter settings is evaluated in comparison to the likelihood of the previous tree given the previous settings. The higher likelihood solution is accepted, though the algorithm occasionally accepts lower likelihood solutions based on how much less likely it is. As Dunn (2015: 198) notes, this random acceptance of lower likelihood trees as the starting point for the subsequent iteration accomplishes two important things. First, avoiding accepting only relatively high likelihood solutions avoids the issue of getting stuck in local maxima – areas of the search space containing trees which are relatively high probability compared to their neighbors, but which are not the optimal tree. Moreover, accepting lower probability solutions in proportion to how much less likely they are avoids the original issue of spending too much time in very low probability areas of the search space. This sampling method continues for a generally large number of iterations, often in the tens or hundreds of thousands or even millions. After an initialization period (termed ‘burn-in’), in which the algorithm is searching broad areas of the search space, a set of trees called the posterior sample is recorded by storing the current tree and other parameter settings at set intervals (usually more than 1000 to avoid oversampling statistically non-independent trees). The resulting set of trees and parameter settings will have been sampled in proportion to their likelihood (Dunn 2015: 198). This posterior distribution of trees can then be further distilled into a single consensus tree that demonstrates the general levels of support for the various levels of internal structure (i.e., subgroups) present in the sample. Beyond the inference of phylogenies themselves, a popular Bayesian MCMC method developed for ancestral state reconstruction (Pagel & Meade 2004) estimates the transition rates between states for a (set of) character(s) along a given phylogeny. A detailed introduction to Pagel & Meade’s approach and its BayesTraits software implementation is provided in §2.3 of this chapter.

2.2 Phylogenetic methods beyond biology

The past two decades have seen a growing interest in the application of stochastic phylogenetic methods beyond genetics, especially in investigations of the evolution of human culture and language. The development and application of phylogenetic comparative methods to linguistic and anthropological research affords the benefit of building robust hypotheses about the evolution of language and culture, as well as support or refute existing claims about the ways in which our languages and populations have changed over time.

2.2.1 Cultural phylogenetics

Within the realm of evolutionary anthropology, researchers seek to track patterns of historical change among human populations with respect to biological characteristics, ethnographic or cultural features, or a combination of the two (Jordan 2013: 46). Holden & Mace (1997, supplemented by Mace 2009) uses phylogenetic comparative methods, specifically maximum likelihood, to investigate a number of previous hypotheses related to an observed geographic disparity in adult human populations' relative ability to digest lactose from dairy animal milk. The authors collected data from previous surveys consisting of around 8000 individuals belonging to 62 distinct culture groups (Holden & Mace 1997: 616). The culture groups were coded based on various previous hypotheses about determining factors in the evolution of lactose digestion in humans, including percentage of adults that demonstrated ability to digest lactose, percentage of cultural dependence on pastoralism, amount of solar radiation based on the geographical location of a culture's territory, and number of dry months and/or average rainfall (Holden & Mace 1997: 617). Using existing cultural and linguistic phylogenies of the culture groups under investigation, the authors (1997: 624) confirmed the assumption that adult ability to digest lactose evolved in cultures which had previously adopted pastoralism as a cultural practice, while other factors such as geographical location or climate were not supported as contributing to lactose digestion.

Watts et al. (2015) use phylogenetic comparative methods to investigate the evolution of the relationship between religious/supernatural beliefs and political complexity among Austronesian cultures. More precisely, the authors applied Bayesian phylogenetic modeling to test competing claims that a general threat of supernatural punishment for immoral or socially uncooperative behavior and the more specific presence of religious deities related to moral behavior lead to the evolution of more complex political stratification among culture groups. A sample of 96 Austronesian cultures was coded based on relevant cultural features, including presence or absence of 'belief in supernatural punishment' and 'moralizing high gods' and relative level (high or low) of political complexity. The evolution of the cultural traits in question was then compared along an existing linguistic phylogeny, resulting in the conclusion that belief in supernatural punishment gave rise to political complexity, while moralizing deities are likely to have arisen subsequent to the development of political stratification.

2.2.2 Linguistic phylogenetics

Stochastic phylogenetic methods have been brought to bear on a variety of historical linguistic reconstruction data as well. One primary task in historical linguistics is determining the internal genealogy of a given language family or set of languages. Traditionally, this involves comparison of sets of cognate lexemes, along with assumptions about specific, regular sound changes. Phylogenetic approaches to this task often (though not always) also take lexical cognates as comparative data. This data is coded or labeled such that each of the languages under consideration can be represented by an alphanumeric sequence akin to genotypical representations of biological organisms. Coded data is then used as input to any number of phylogenetic models in order to infer genealogies.

Tree inference

Noting that traditional methods have failed for various reasons to come to a consensus over the internal structure of the Pama-Nyungan (PN) language family of Australia beyond low-level subgroups, Bowern & Atkinson (2012) leverage Bayesian phylogenetic methods to generate a probabilistic model of the full phylogeny of the family. Lexical cognate data from a sample of 194 PN languages were coded according to phonological and semantic similarity, as in traditional reconstruction, which was then converted to binary coding representing the presence or absence of specific cognate groups for each of the languages in the sample (Bowern & Atkinson 2012: 826-828). This presence/absence data was subsequently used to infer a probabilistically weighted set of trees representing the internal structure of the PN family based on the gain and/or loss of specific cognate groups in its evolutionary history (Bowern & Atkinson 2012: 828). Interestingly, not only was the model able to infer higher-level structure in the PN family (Bowern & Atkinson 2012: 831), it also provided evidence for more precise lower-level subgrouping than previous analyses (Bowern & Atkinson 2012: 836). Building on this line of research, Bouckaert, Bowern & Atkinson (2018) expand the lexical cognate sample to 306 PN languages (see Figure 3.1 in Chapter 3) in an investigation into the temporal and geographic spread of Pama-Nyungan across the Australian continent.

In instances where lexical cognate data is unavailable or uninformative, features related to phonology, morphology, and/or syntax may provide sufficient character data for phylogenetic comparative methodologies. A case in point is Dunn et al.'s (2008) exploration of a collection of languages spoken in Island Melanesia. The authors note that in addition to around 100 Austronesian languages, Island Melanesia is also home to 23 so-called Papuan languages, for which the phylogenetic relatedness was unknown, and for which lexical cognates were scant enough to eliminate lexical data as a source of comparative evidence. Instead, the Papuan languages were coded based on shared grammatical features, the result of which was then modeled using maximum parsimony methods in order to determine a possible genealogy (Dunn et al. 2005: 2073).

Ancestral state reconstruction

Another important avenue of research for linguistic phylogenetics is in tracking the diachronic development of specific linguistic features. Given a phylogeny resulting from tree construction models and observed data about the modern languages that comprise the family in question, one can probe the phylogeny to explore how and when a given feature was innovated, changed, or lost. This often takes the form of ANCESTRAL STATE RECONSTRUCTION (ASR) – the inference of the state of the ancestor(s) of modern languages with respect to some linguistic feature.[2] This can involve reconstruction of the state of the root node in the phylogeny (representing the common ancestor of the entire family) or for any of the intermediate nodes (representing where subgroups or individual languages would have diverged from one another). While the application of ASR methods in answering linguistic and anthropological questions is relatively underrepresented in comparison to the aforementioned task of tree inference, a number of recent projects demonstrate its utility.

Bouchard-Côté et al. (2013) use Bayesian phylogenetic methods to model sound change at the phonemic level in order to accurately generate automated lexical reconstructions based on cognate data from a large set of Austronesian languages and existing phylogenies. Results demonstrate the importance of choosing informative parameters and sufficient data size. Specifically, notable improvement in the fidelity of automated reconstructions as compared with existing lexical reconstructions was observed as both the size of the language sample (in terms of number of modern languages) and refinement of tree topology (from uninformative/flat) increased. In a second experiment, the model was provided raw lexical forms and their meanings and asked to infer information about cognates. The resulting automatically generated cognate sets were in turn used as input to the reconstruction model. Results of cognate set inference boasted a roughly 90% accuracy rate in terms of correctly grouping lexical items. The authors indicate (2013: 4227) that while the second model leads to an increase in the number of errors in reconstruction as compared with the initial baseline where cognate data was provided to the model, it comes with the benefit of reducing the initialization cost of manual preparation of cognate set information.

Hruschka et al. (2015) model sound change in 26 Turkic languages using lexical

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[2] This method is also often referred to as ANCESTRAL CHARACTER ESTIMATION (ACE). See, e.g., Revell (2013), Paradis & Schliep (2019).

cognate data which was coded based on the phonetic realizations of the cognates, while simultaneously inferring the phylogenetic tree and its time-depth. Comparison of two models representing sporadic and regular sound change showed preference for the latter, which the authors (2015: 3) note corresponds to linguistic theoretic notions of how sound changes proceed over time. In addition to reconstructing a phylogeny that closely resembles the accepted internal structure of the Turkic language family, the model also showed an ability to reconstruct chain-shift sound changes.

Zhou & Bowern (2015) use Bayesian phylogenetic methods to model the evolution of numeral systems in the Pama-Nyungan language family. Noting that Pama-Nyungan languages vary with respect to how many numerals are encoded as discrete units, as well as whether or not larger numbers are represented compositionally as combinations of smaller numbers, the authors model the evolution of the numeral system in the language family using Reversible Jump MCMC. Choice of algorithm in this case allows for abstraction over the set of model parameters, such that different settings, restrictions, and omissions of various parameters can be tested within the same model run. The authors note (2015: 2) that Reversible Jump MCMC is appropriate when the number of parameters is high and where specific decisions by the researcher about which rates to restrict and/or omit cannot be straightforwardly motivated. The model was evaluated against a number of hypotheses about the evolution of the numeral system in Pama-Nyungan related to the possibility of gain and loss of numerals over time, restrictions on upper limits of the numeral systems, and the influence of horizontal transfer (borrowing) on the system. The study found that languages can both gain and lose numerals over time, as well as a clear effect of horizontal transfer in the Pama-Nyungan numeral system.

Haynie & Bowern (2016) investigate the evolution of color-term related lexical inventories in the Pama-Nyungan language family in an exploration of both linguistic and cognitive/perceptual significance. Taking the seminal work on the evolution of color terms by Berlin & Kay (1969) and Kay & Maffi (1999) as a baseline, Haynie & Bowern evaluate the predictions of existing theories of color-term evolution against the findings of Bayesian phylogenetic reconstruction. A sample of 189 Pama-Nyungan languages were coded based on the presence or absence of seven discrete color categories. An MCMC algorithm and an existing phylogeny of the language family were used to model the evolution of color terminology in Pama-Nyungan with respect to two hypotheses related to 1) whether languages gain and/or lose color terms and 2) whether elaboration of the color term lexicon proceeds according to a universal pattern. For the latter research question, a Reversible Jump MCMC algorithm was employed. Results demonstrate that both gain and loss of color terms is likely to have occurred in the prehistory of Pama-Nyungan, a finding which contradicts earlier theories that terms may be gained but rarely or never lost. Moreover, the trajectory of growth of the color term lexicon was shown to not be uniform across the family, with different subgroups showing evidence of distinct patterns of elaboration not shared by their neighbors. This also conflicts with earlier theories, which hold that increased division of the color space into distinctly named categories follows a universal pattern cross-linguistically.

In each of the above examples, we see that the Bayesian phylogenetic methods have been employed in investigations into the evolutionary history of a variety of linguistic features. This research has in many cases added a new dimension to our understanding of how properties inherent to our communicative systems change over time. In the case of Hruschka et al. (2015), we see evidence of the robust nature of constrained, data-driven phylogenetic modeling, in that the results obtained closely mirrored the evolutionary history of the Turkic family obtained from traditional methods. Zhou & Bowern (2015) and Haynie & Bowern (2016) demonstrate that probabilistic reconstruction methods can be used to test the predictions of earlier theories, as well as providing evidence for the bidirectionality of change in closed-class linguistic systems, a sentiment which is echoed by the findings of the current study.

2.3 Anatomy of an ancestral state reconstruction analysis

This section provides an exploration of the goals of and methods involved in linguistic phylogenetic analysis, with a focus on the task of Ancestral State Reconstruction (ASR). As noted in §2.2, ASR involves the inference of the state of internal nodes in a language phylogeny with respect to some number of typological features that show observable variance among the modern languages in the family. In practice, ASR analyses consist of a number of interrelated components, including feature identification and coding, tests for tree-like signal in the dataset, and choice of model type/algorithm.

2.3.1 Feature identification and coding

Initial effort involved in any ASR study necessarily takes the form of identification of suitable typological features based on research goals and observable details about a set of languages and developing a schema for representing these features. Recall that ASR typically assumes a given phylogeny, though this is not always the case, as highlighted in §2.2 for Hruschka et al. (2015). Common sources of linguistic features include phonological, morphosyntactic, and/or lexical data for which there is observable variation in the state of the languages in the sample. After appropriate features have been selected, a coding schema is determined based on the permissible state values of the features in question. This schema is based on the language data and can be described generally as being of one of two types, namely CONTINUOUS or DISCRETE. Continuous trait measures are appropriate when the degree of variation between languages for a given feature are not categorizable in terms of discrete units.

Instead, these are features where a scalar interpretation better captures the observed data. Straightforward examples of continuous traits from biology include quantitative factors such as height or blood pressure. In linguistics, continuous features similarly involve variation that exists on a scale, such as phonetic measures of pitch or vowel formant values. Discrete traits, by contrast, are used when the typological variation for some feature can be described in terms of alternations between a constrained number of distinct, non-overlapping possibilities. Discrete traits can be further subdivided into BINARY traits, which capture variation between two possible observations, and MULTISTATE traits, for which three or more possibilities exist. In linguistics, binary traits are most commonly used for, but not restricted to, encoding the presence or absence of some feature. Multistate traits often represent variation in terms of discernible categories, such as the number of distinct noun or verb declensions, numerals (Zhou & Bowern 2015), or some other linguistically relevant category. It should be noted that although continuous measures do involve labeling a given taxon/language as having a discrete feature value along a continuum, there is some risk of obscuring categorical patterns in the data in the interest of obtaining fine-grained distinctions. A possible remedy for this is to use clustering methods to create discrete categories from continuous features. Table 2.2 summarizes these general feature categories and representative examples:

Type	Description	Example	Values
Continuous	Variation along a scale or continuum	Vowel formants	Frequency (Hz)
Binary	Variation between two possible values	Presence/absence of a cognate set	1 (presence) 0 (absence)
Multistate	Variation between a constrained number of distinct values	Number of verb declensions	0, 2, 3, 4 ...

Table 2.3: Variable types in phylogenetic modeling

Once a suitable coding type and schema is designed for each of the relevant features under investigation, each of the taxa (languages) in the dataset is coded accordingly. The resulting pairings of languages with their code profiles are used as input data to the inference model alongside the phylogeny if one is specified. For an extended discussion of the features and coding schema employed in the current study, refer to Chapter 3.

2.3.2 Phylogenetic signal

Given a phylogenetic language tree and a characteristic such as presence/absence of lexical cognates or a grammatical or phonetic feature, there are a variety of methods for discerning whether or not the distribution of character states at the leaf (modern language) nodes of the tree is likely to have arisen as the result of language evolution that measurably corresponds to well-known types of biological evolution. This evidence of our ability to characterize historical development of this character as a correlate of biological evolution is termed PHYLOGENETIC SIGNAL. Prior to computing the ancestral state of some grammatical (or lexical, etc.) feature with respect to a phylogeny, it is important to investigate whether there is sufficient phylogenetic signal in the data. This section discusses metrics for measuring phylogenetic signal in binary and multistate data. As the characters used in the current study are all discrete, detailed discussion of phylogenetic signal in continuous data is not further elaborated here. It should be noted that several measures of phylogenetic signal in continuous data exist, including Pagel's (1999a) λ measure.

For binary data, Fritz & Purvis (2010) propose a method for evaluation of the strength of the phylogenetic signal for binary (0 or 1) characters, namely the statistic D, which compares the distribution of character states to a known model of biological evolution, as well as to randomly distributed character states. More specifically, Fritz & Purvis' D statistic is evaluated relative to two null hypotheses; 1) the expected historical development given a Brownian evolutionary model and 2) the expected historical development given random assignment of feature values to the tips of the phylogeny. In practice, calculation of D involves comparison of the number of state changes required from the root node to result in the observed character data (Δ_{Obs}) with the number of state changes required for both null hypotheses. For the first null hypothesis, a simulated continuous trait is evolved along the phylogeny, with the resulting tip values clustered such that the resulting categories maintain an equivalent distribution of values as found in the observed data. The resulting number of state changes proposed in the simulation is recorded. Similarly, the second null hypothesis is evaluated by determining the number of state changes necessary to account for randomized character data, where the overall proportion of observed features is maintained but specific feature values are randomly assigned to the tips of the phylogeny. Each simulation is repeated for a given number of iterations (generally greater than 1,000), with the mean values for each hypothesis (Δ_{Brn} and Δ_{Rdm}, respectively) used as input to equation (2.2):

$$D = (\Delta_{Obs} - \Delta_{Brn})/(\Delta_{Rdm} - \Delta_{Brn}) \tag{2.2}$$

A *D* statistic value near 0 indicates that the observed distribution of the of the character is similar to what would be expected from Brownian evolution, which is interpreted as reasonable evidence of phylogenetic signal in the data. Conversely, a value near 1 indicates overdispersion, i.e., greater variation than would be expected by chance. In the context of language evolution, overdispersion is generally thought to arise from language contact or environmental conditioning. Note also that *D* values below 0 indicate the character is more conserved than expected given Brownian evolution, which can be interpreted as strong evidence of phylogenetic signal in the data. Fritz & Purvis (2010: 1044) illustrate the relationship betweeen trait variation and *D* statistic relative to four possible distributions of trait values:

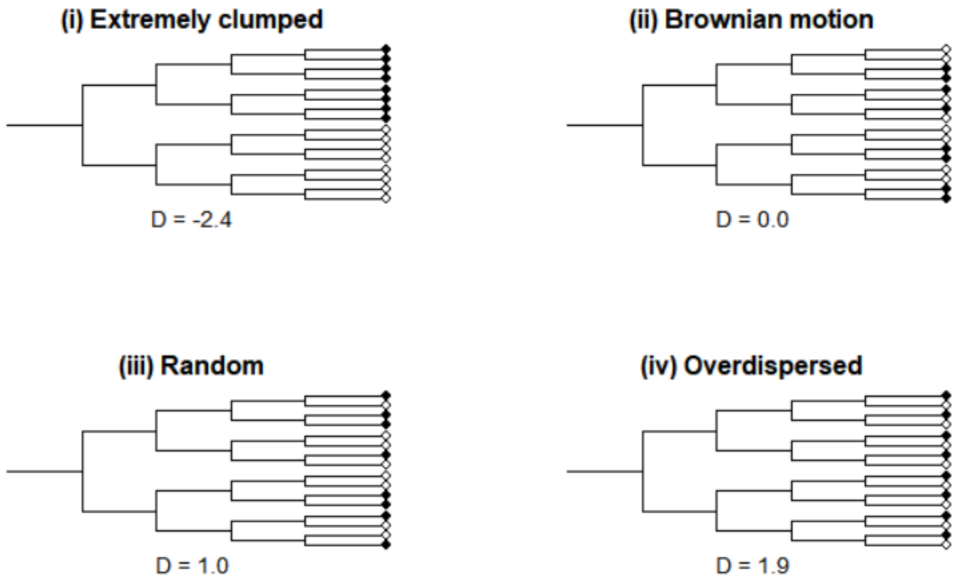

Figure 2.4: Trait variation and *D* statistic for four distinct distributions of a binary trait

In Figure 2.4, a binary trait represented by black and white dots varies over a toy phylogeny according to four different distributions. *D* is evaluated relative to the Brownian tree (ii).

In addition to phylogenetic signal, *D* statistic is sensitive to the size of the language sample and the relative frequency of each character state in the data itself. As the phylogenetic sample increases in size and distribution of character states, the influence of these factors is diminished. In practice, a sample size of greater than 50 taxa is taken to be sufficient to ensure accurate results.

While Fritz & Purvis' D statistic is specific to binary characters, there are a number of statistical tests that are appropriate for multistate characters, i.e. those that involve more than two diametrically opposed possible values. One such measure is K (Blomberg, Garland & Ives 2003), which like the aforementioned D statistic assumes a Brownian model of evolution as a comparative factor. Computation of K (Blomberg, Garland & Ives 2003: 722) involves the calculation of the mean standard error of the tip data measured from the phylogenetically compared mean (MSE_0) divided by the mean standard error of the data calculated using a variance-covariance matrix derived from the tree (MSE). The authors (2003: 722) explain that, in essence, if the data is well-explained by the tree, values of MSE will be low, leading to higher values of $\mathrm{MSE}_0/\mathrm{MSE}$. Conversely, lower values of MSE_0 are obtained when the tree does not explain the variation in the data, resulting in lower values of $\mathrm{MSE}_0/\mathrm{MSE}$. This ratio is calculated for the observed data and the expected values of MSE_0 and MSE given Brownian evolution that resulted in the observed data distribution, with the expression of K given as the ratio of these ratios, as in equation (2.3):

$$K = observed\frac{MSE_0}{MSE}\bigg/expected\frac{MSE_0}{MSE} \tag{2.3}$$

A value of K below one indicates that the strength of the signal in the data is less than expected given Brownian evolution, while a value near zero indicates very weak evidence of phylogenetic signal in the data. Conversely, a value of K above one indicates stronger signal than expected given Brownian evolution.

Additional methods seek to quantify the fit of a phylogenetic tree to the data in terms of parsimony, i.e., how many evolutionary changes are necessary to account for the observed character states for a given tree. A more parsimonious tree will require fewer proposed changes (and possibly the absence of parallel innovation or re-innovation of a feature) and will be generally considered to provide a better fit to the data. Popular measures of parsimony include the CONSISTENCY INDEX (CI; Kluge & Farris 1969) and RETENTION INDEX (RI; Farris 1989), both of which compute the parsimony score of a tree relative to the most parsimonious (and least parsimonious in the case of RI) possible phylogeny given the data. These parsimony-based measures are employed in the current study in the exploration of the effect of tree topology on reconstruction results (Chapter 6), with extended discussion of their calculation provided in §6.2.2.

2.3.3 Algorithmic approaches to ASR: MCMC and Bayesian inference

Pagel et al. (2004) outline a continuous-time Markov model for efficient reconstruction of the ancestral state of a feature at any number of internal nodes in a phylogenetic tree based on estimations of the rates of transitions between possible states along the branches of the phylogeny. This section provides an overview of this approach to ASR and its software implementation, BayesTraits. Taking the straightforward example of a binary trait (see Table 2.2) with two states i and j, the model takes as free parameters the rates of transition between these states, q_{ij} and q_{ji}, representing the rate of gain and loss of the feature, respectively. The authors (2004: 675) explain that for a phylogeny representing significant time-depth (or genetic divergence; Pagel (1994)), the model must be able to accommodate the possibility of multiple state changes along a given branch. The model representation of the four logically possible rate parameters is given as a matrix Q, note that the parameters on the diagonal of the matrix are given as the negative of the other rate in the row:[3]

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[3] For models with a larger number of states, i.e. for multistate or continuous characters, Pagel et al. (2004: 675) give the rate parameters on the diagonal of Q as minus the sum of the rest of the rate parameters in the row.

(5)

$$Q = \begin{array}{cc} & \begin{array}{cc} 0 & 1 \end{array} \\ \begin{array}{c} 0 \\ 1 \end{array} & \begin{bmatrix} -q_{ij} & q_{ij} \\ q_{ji} & -q_{ji} \end{bmatrix} \end{array}$$

The probabilities of the rate parameters that make up Q over an interval t are given as the exponentiation of Q times the interval t (Pagel et al. 2004: 675):

(6)

$$P(t) = e^{-Qt} = \begin{bmatrix} P_{ii}(t) & P_{ij}(t) \\ P_{ji}(t) & P_{jj}(t) \end{bmatrix}$$

We can interpret the individual terms that make up the matrix in (2.9) as representing the probability of beginning and ending a branch of length t in the states specified in a given cell. $P_{ji}(t)$ is the probability of beginning a branch of length t in state j and ending in state i. For $P_{ii}(t)$ and $P_{jj}(t)$, this means beginning and ending in the same state. Note that this does not preclude the possibility of multiple state to state transitions over the given interval, it only describes the start and end state.

The goal of reconstructing the state of a feature at various historic points along the phylogeny thus becomes one of computing the relevant rate parameters (Pagel 1999a), as we already have the phylogeny itself and the observed feature states for the taxa at the tips. Pagel (1999b) describes a method for estimation of optimal values for the rate parameters using a maximum likelihood algorithm, while Pagel et al. (2004: 675-676) use Bayes' theorem to additionally estimate the posterior probability distribution of rate parameters. Given a phylogenetic tree T, a set of rate parameters Q, observed feature state data D, we can compute the joint posterior probability of Q given D as:

$$p(Q \mid D, T) = \frac{p(D|Q)p(Q)}{\int_Q p(D|Q)p(Q)dQ} \tag{2.4}$$

In equation (2.4), $p(D|Q)$ is the probability of the data given the rate parameters $p(Q)$ is the prior probability of the rate parameters. The term in the denominator integrates $p(Q)$ over all possible values of Q. Pagel et al. (2004: 676) explain that the probability of a given set of transition rate parameters in Q is equal to their proportion of the total probability, as summed over all possible sets of rate parameters. Moreover, while this integral is in practice intractable to compute directly for the constantly varying values of the rate parameters, a practical solution for estimation of the integral is comes from repeated sampling from the Markov model, for example via MCMC (see §2.1) sampling. Sampled values from a sufficiently mixed Markov chain estimate the posterior distribution of the rate parameters in Q.

An implementation of the Pagel et al. (2004) algorithm for ASR is included in Mark Pagel and Andrew Meade's BayesTraits software package, allowing researchers to efficiently compute the continuous-time Markov model described here. This implementation allows for a number of optimizations for initialization of the rate parameter values as well as how tree topologies are sampled. Initialization of the prior distributions of the rate parameters is a vital component of model set up. Improper rate priors disadvantage the model, constraining it to suboptimal areas of the search space. Meade & Pagel (2019: 15) suggest the use of a simpler maximum likelihood model to estimate appropriate rate priors. Another possibility (Meade & Pagel 2019: 16) is to integrate over possible rate priors themselves via the use of HYPERPRIORS (Pagel et al. 2004), which consist of a (usually uniform) distribution with a user-defined range from which the prior distribution is drawn, thus reducing some of the influence exerted over the MCMC algorithm by the researcher.

Also of importance is the consideration of the model of evolution assumed by the researcher as it relates to transition rates. The model as described so far estimates all of the various rates of transitions between states in Q, as they are taken to be (possibly) different from one another. Another possibility is that two or more transition rates in Q do not differ from one another significantly, which can be modeled by restricting any number of states to always take the same value as an arbitrary member of the set of transition rates in question, which is itself estimated by the model. The fit of the original unrestricted model to the data can be compared with that of any number of related models with restrictions on individual rate parameters via comparison of their marginal likelihoods, i.e. the integral of the likelihood of the model over all values of the rate parameters and the given phylogeny (Meade & Pagel 2019: 14).[4] BayesTraits implements a Stepping-stone sampler (Xie et al. 2011) for efficient estimation of the marginal likelihood. Marginal likelihood comparison via the Bayes Factor metric quantifies evidence in favor of one model over another. See §4.2.3 for an extended discussion of the Stepping-stone sampler and Bayes Factor computation.

Comparison of marginal likelihoods is also useful for testing whether two traits or features vary independently or whether their evolution is correlated. Trait independence in the context of the Pagel et al. (2004) model can be understood as the independence of the state to state transition rates of one trait from the feature state of another trait. If the rate parameters of a given trait depend on the state of another trait, then correlated evolution between the traits is assumed. §4.5 employs this technique in order to determine whether membership features of Pama-Nyungan verb conjugation classes are likely to have evolved separately or in parallel. Chapter 5 further explores the possibility of correlated evolution between conjugation class membership features and the number of distinct verb conjugations a language contains.

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[4] Note that for ASR involving multiple phylogenies, the marginal likelihood also integrates over possible tree topologies

Chapter 3

Morphological typology

The current exploration of the development of verb conjugation classes in Pama-Nyungan employs grammatical data collected for 111 Pama-Nyungan languages. Choice of languages for inclusion in the sample was guided by a desire for sufficient heterogeneity in terms of genetic and geographical distribution. Information about conjugation classes and their membership was drawn from a variety of available sources, including many reference grammars and sketches, a series of typological profiles compiled by Harold Koch and Pascal Jacq, and the extensive Pama-Nyungan lexical database CHIRILA[1]. Languages were coded for grammatical characters including presence/absence of conjugation classes, number of conjugation classes, and whether patterns in conjugation class membership reflect divisions along the lines of verb valence and/or phonological properties of the verb stem. This chapter provides a brief excursus into the nature of the verb conjugation class data, with attention to macro-level distribution of grammatical characters across the family and coding decisions, as well as more focused discussion of many of the subgroups of the Pama-Nyungan family.

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[1] http://chirila.yale.edu/

3.1 The language sample

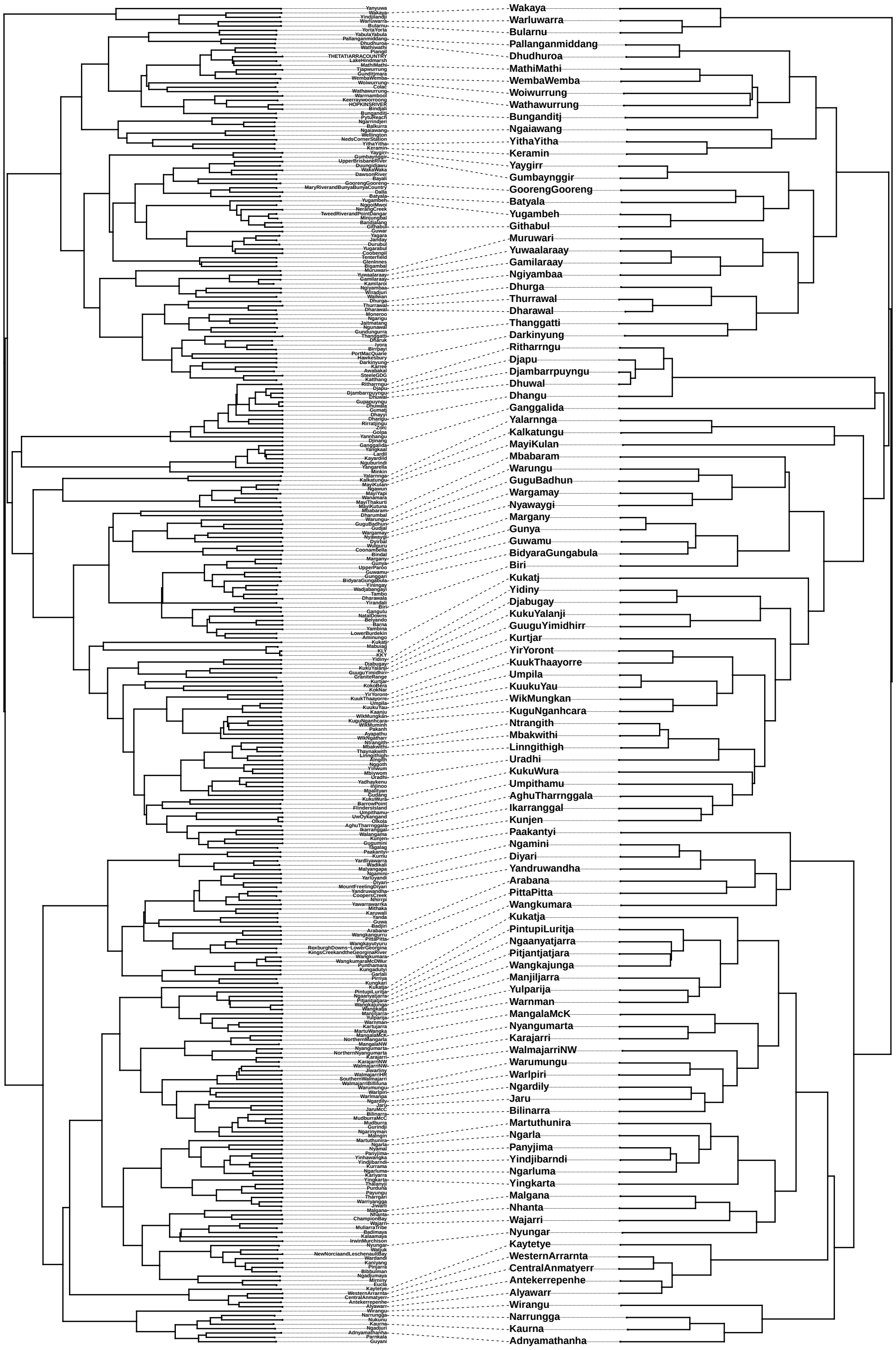

Figure 3.1: 306 language Pama-Nyungan tree inference consensus tree (Left; Bowern & Atkinson 2012; Bouckaert, Bowern & Atkinson 2018); Pruned 111 language sample (Right)

Figure 3.1 shows a side-by-side comparison of the consensus tree resulting from earlier tree inference research (Bowern & Atkinson 2012; Bouckaert, Bowern & Atkinson 2018) and a pruned version of the same tree consisting only of languages that make up the dataset for the current study.[2] Decisions about inclusion and omission of specific languages from the current sample were made based on a variety of factors, especially the existence of accessible and reliable documentation and description for a given language. Attention was also given to accounting for the wide geographical spread of the Pama-Nyungan language family and to include as many of the major subgroups as possible. It should be noted that many of the finer points of the internal structure of Pama-Nyungan remain an open question. While lower-level immediate subgroupings are generally (though not entirely) agreed upon by Australianists, the higher-level connections between subgroups remain a focal point of ongoing research. For the purposes of this study, I will necessarily take the individual subgroup membership of a given language to be consistent with the findings of the aforementioned tree inference projects, as the set of language trees that came out of that research represent the phylogeny upon which the evolution of verb conjugation classes will be evaluated here. The geographical distribution of the 111 language sample that makes up the current study and the 306 Pama-Nyungan languages from Bouckaert, Bowern & Atkinson (2018) is shown in Figure 3.2:

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[2] For a full list of languages included in the sample and their sources, see Appendix.

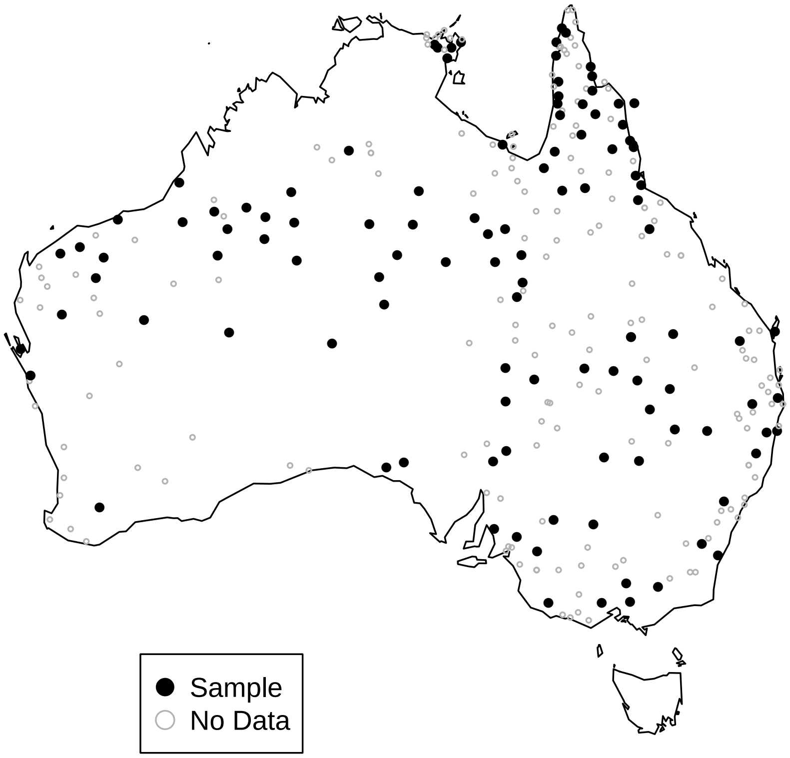

Figure 3.2: Geographical distribution of the language sample

3.2 Typology of individual language subgroups

In Chapter 1 (§1.2), I introduced a few generalizations about the typology of verb conjugation classes in Pama-Nyungan as it relates to wider issues in the theory surrounding inflection classes in morphology. Pama-Nyungan language subgroups and individual languages may vary with respect to the number of verb conjugation classes they contain and/or how conjugation class membership is realized in a lexeme's inflectional paradigm, among other factors. This section provides a more comprehensive overview of the verb conjugation class data.[3] Attempts have been made to present similar morphosyntactic content and conjugation class names for each the surveyed languages, in the interest of allowing the comparison of forms across subgroups and individual languages. In some cases, typically due to incomplete or unclear data, this was not possible. In other cases, descriptive conventions that place a focus on, e.g., aspectual distinctions at the cost of a lack of information about tense, obscure direct comparison. Here available forms which show the general patterns of inflection of the relevant language are included. In the interest of providing a clear and informative presentation of the varied verb conjugation data throughout the Pama-Nyungan family, I have included lists of representative verb stems from different conjugation classes where such information was made available in the literature. Moreover, three languages included in the current study (Bunganditj, Woiwurrung, and Pallanganmiddang) lack sufficient descriptive data to make broad claims about their verb conjugation class inventories and will not be discussed here further beyond noting that they all occur in roughly the same part of the tree.[4]

3.2.1 Subgroups without conjugation classes

A number of subgroups of the Pama-Nyungan family show little to no evidence of verb conjugation classes in the modern languages. While there may be some allomorphic variation present in specific areas of the paradigm, it generally not systematic enough to warrant analysis as reflecting separate conjugations. A case in point is the

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[3] The aim of this discussion is to detail the breadth of the Pama-Nyungan verb conjugation class data, as well as provide insight into decisions about coding and language sample curation. As such, although an effort has been made to present similarities and differences between related languages in an organized way, I will not analyze or assert any claims about cognacy between verb stems, inflectional material, or conjugation classes beyond what has been included in descriptions of the individual languages or language subgroups.

[4] In the ancestral state reconstruction analysis, these languages were coded as uninformative for all three characters. See Appendix.

Thura-Yura subgroup, including Wirangu, Kaurna, Adnyamanthanha, and Narungga (Simpson & Hercus 2004). Verbs in these languages inflect with a single set of affixes, with Simpson & Hercus (2004: 203) noting that the only deviation from the expected verbal suffixes is seen in a handful of irregular verbs that do not allow analysis of a larger pattern. Schebeck (1974) describes the presence of valence-changing suffixes in Adnyamanthanha, including a transitivizer *-ŋku* and a detrasitivizer *-(r)i*, but gives no indication beyond this that verbs in the language can be divided into any categories based on patterns of inflection.

The Karnic languages Diyari, Ngamini, Arabana, Pitta Pitta, Yandruwandha, and Wangkumara similarly lack conjugation classes across the subgroup. For Pitta Pitta, Blake (1979a: 201-202) gives a single set of inflectional endings, including *-ya* present, *-ka* past, a zero-marked (∅) future, and *-na* imperative. Yandruwandha (Breen ms) has a single set of suffixes as well, with no conjugation classes. Hercus (1994: 157-9) outlines allomorphy patterns for the present tense marker in Arabana which appear to involve morphophonological alternation (*-rda* for stems with nasal clusters and *-rnda* for other stems). She ultimately concludes (1994: 131) that there is not sufficient evidence to define verbs as belonging to different conjugations in the language.

The Arandic languages Kaytetye, Arrernte, Alyawarr, Antekerrepenh, and Anmatyerre categorically lack conjugation classes as well. As with Thura-Yura and Karnic, the Arandic languages make use of a single set of inflectional endings for all verbs. Wilkins' (1989) analysis of Arrernte gives a single set of inflectional endings and cites (1989: 6) a number of major sound changes in the history of Arandic that has had the consequence of eliminating or otherwise obscuring older conjugation markers (see also Wurm 1972). Yallop (1977: 58) gives an overview of inflectional endings in Alyawarr, Arrernte, and Anmatyerre, again providing no evidence of conjugation classes.

Verbs in the Kulinic languages Wathawurrung, Wemba Wemba, and Mathi-Mathi take a single set of inflectional endings and do not have different verb conjugation classes. Blake et al. (1998: 109), based on description by Mathews (1902), give invariant past tense *-ik*, future tense *-iny*, and a zero-marked present for Wathawurrung. Mathi-Mathi (Blake et al. 2011: 98) has a similar set of tense suffixes and no ability to divide verbs into classes based on patterns of inflection.

Additional subgroups without verb conjugation classes included in the survey are the Lower Murray languages (Ngaiawang, Yitha Yitha, Keramin), Bandjalangic (Githabul, Yugambeh), Yuin-Kuric (Dhurga, Thurrawal, Dharawal, Thanggatti, Darkinyung), Thaypan (Aghu Tharrnggala, Ikarranggal), and Gippsland (Dhudhuroa) languages.

3.2.2 Wati

The Wati languages provide a nice example of a subgroup with a clearly defined profile in terms of its verb conjugation classes. Languages from this subgroup included in the current sample include Kukatja, Pintupi-Luritja, Wangkajunga, Pitjantjatjara, Ngaanyatjarra, Manjiljarra, Yulparija, and Warnman. Verbs in these languages generally belong to four distinct conjugation classes, including two open classes and two smaller, closed classes. Descriptions of individual Wati languages vary in their naming conventions, but the similarity across the family can be seen in the imperative endings:[5]

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[5] Imperative forms are a typical source of distinctiveness in Pama-Nyungan verbal paradigms. Unlike many of the languages included in the sample, the Wati future forms are regular across conjugation class lines.

Language	N/RR	NG	L	∅
Warnman	-rra	-wa	-la	∅
Yulparija	-rra	-wa	-a	∅
Manjiljarra	-rra	-wa	-a∼-la	∅
Ngaanyatjarra	-rra	-wa	-a∼-la	∅
Pitjantjatjara	-rra	-wa	-a∼-la	∅

Table 3.1: Imperative endings for four verb conjugations in five Wati languages

Verb conjugation class memership in Wati highlights a trend present across the Pama-Nyungan languages with four or more conjugations, namely that patterns in both transitivity and phonological properties of the stem are identifiable for most or all of the conjugation classes. In Wati, the open conjugations generally divide along the lines of transitivity and contain polysyllabic roots, while the smaller classes are of mixed transitivity and typically contain mostly monosyllabic verb roots. A case in point is Yulparija (Burridge 1996), which has two open conjugations ∅ (intransitive and disyllabic stems) and L (transitive and disyllabic) and two closed conjugations NG (transitive and monosyllabic) and N (two transitive members and one intransitive, all monosyllabic).

Representative verbs for each of the Wati conjugations are taken from brief lists provided for Manjiljarra (Marsh 1976) and Yulparija (Burridge 1996):

- The Wati L-conjugation contains disyllabic stems, including *jiki-* ‘drink’, *paja-* ‘bite’, *punka-* ‘fall’, *waja-* ‘tell, say’, *yungka-* ‘hit (with a thrown object)’, *japirr-* ‘ask’, *munta-* ‘take from’, *parnti-* ‘smell’.
- Membership in the ∅-conjugation includes *wangka-* ‘talk’, *nyina-* ‘sit, be, stay’, *ngarri-* ‘lie down’, *yula-* ‘cry’, *pirta-* ‘run’, *ngara-* ‘stand’, *yilpa-* ‘stay’.

- The monosyllabic N/RR-conjugation contains *ju-* 'put', *ya-* 'go/come', *ma-* 'get'.
- The monosyllabic NG-conjugation has *pu-* 'hit', *ka-/kati-* 'take', *warni-* 'throw', *warla-* 'break', *para-* 'play'.

3.2.3 Ngumpin-Yapa

Languages in the Ngumpin-Yapa subgroup show a great deal of similarity in their verb conjugation class system, though there is somewhat more variation than was observed in the Wati languages. Languages have between four and six distinct conjugations, with the future/purposive inflection showing maximally distinct realizations across the classes. As was outlined for Walmajarri and Warlpiri in Chapter 1, there are some differences with respect to which conjugation classes a language may have, as well as the membership of specific verbs. Recall that for Walmajarri and Warlpiri, Dixon (2002: 217-218) gives a future suffix *-ku*, which is preceded by a marker of conjugation class membership, except in the case of the zero-marked $\emptyset$ conjugation, in which there is no interruption between the stem and *-ku*. Bilinarra (Nordlinger 1990: 84-85) also has five conjugation classes, with inflectional patterns that closely resemble Walmajarri. Jaru (Tsunoda 1981: 77) has six classes, which show a great deal of overlap with the paradigmatic structure of the other Ngumpin-Yapa languages. Finally, Ngardily (Cataldi 2011: 2-4) has four conjugations.[6] Table 3.2 gives the future (purposive in the case of Jaru) forms of verbs belonging to the relevant conjugation classes:

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[6] Cataldi (2011: 2) suggests an earlier, alternate analysis of five conjugation classes, but concludes that that these should be reduced to four by distributing the members of the small fifth class into existing classes as irregular members. This is presumably due to similarities in the inflectional patterns of the members of the putative fifth class, but no further discussion of this analysis is provided beyond citing verbs as irregular in tables and examples. As the coding for the current study collapses four or more conjugation classes into a single feature state, this distinction was not investigated further.

Language	N	NG	L	RR	∅	Y/∅
	‘go’	‘give’	‘eat’	‘bite, chop’	‘cook’	
Walmajarri	*ya**n**ku*	*yu**ŋ**ku*	*ŋa**l**ku*	*patja**rr**ku*	*kampawu*	
	‘go’	‘take’	‘eat’	‘hit’	‘cook’	
Bilinarra	*ya**n**ku*	*ka**ŋ**ku*	*ŋa**l**u*	*pa**rr**u*	*kampawu*	
	‘go’	‘give’	‘eat’	‘bite’	‘burn’	‘fall’
Jaru	*ja**n**gu*	*ju**ŋ**gu*	*ŋa**l**u*	*baja**rr**u*	*gambawu*	*wandiwu*
	‘go’	‘give’	‘eat’		‘excrete’	‘burn’
Warlpiri	*ya**n**ku*	*yu**ŋ**ku*	*ŋa**l**ku*		*natjaku*	*kampa*[**y**]*tju*
	‘go’	‘give’	‘eat’			‘fall’
Ngardily	*ya**n**ku*	*yi**ŋ**ku*	*ŋa**l**ku*			*wantiju*

Table 3.2: Future or purposive forms of Ngumpin-Yapa verbs belonging to different conjugation classes

We see from Table 3.2 that there is a great deal of similarity between the conjugation classes in the sampled Ngumpin-Yapa languages. All five have three or four conjugations in common, though various morphophonological differences exist that change the realization of the conjugation class marker and/or future tense marker in various ways. In Jaru and Bilinarra, the initial consonant of the future marker is not pronounced following /l/ or /rr/, while only Warlpiri retains this consonant intervocalically in what is presented here as the ∅ conjugation. As is the case in many Pama-Nyungan subgroups, certain verbs appear in different classes in different Ngumpin-Yapa languages. A case in point in Table 3.2 is *kampa-* ‘cook, burn’, which appears the zero-marked class in Walmajarri and Bilinarra (and in one of the zero-marked conjugations in Jaru) and the *y*-marked class in Warlpiri.[7] Ngardily has a

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[7] Warlpiri is the only Ngumpin-Yapa language surveyed that shows evidence of a *y*-marked conjugation class.

possible cognate in *kupa-*, which 'cook' takes the *-l* suffix in future *kupalku.* The verb *wandi* ~ *wanti* ~ *wani* 'fall' appears in a zero-marked class in Jaru and Ngardily, while in Bilinarra, the future is *waniŋku*, aligning its form paradigm with that of the NG conjugation. This heterogeneity of class membership for certain verbs is taken by Dixon (1980, 2002) and others to constitute evidence in favor of the reduction in the number of conjugation classes in certain Ngumpin-Yapa via the collapsing of distinctions between individual classes.

Koch (2014, Forthcoming) notes that due to the small size of Ngumpin-Yapa monomorphemic verb inventories, identification of any individual class as 'open' is speculative. Note though that like the Wati languages, we can draw generalizations about conjugation class membership based on both transitivity and phonological properties of verb stems for many of the languages in this subgroup. Specifically, conjugations tend to contain either mostly transitive or mostly intransitive members on the valence dimension, and either monosyllabic or disyllabic stems on the phonological dimension.

Examples of verbs belonging to each of the Ngumpin-Yapa conjugation classes are:

- Walmajarri (Hudson 1978: 43) has transitive N-conjugation stems *lan* 'pierce, spear', *-man*'do' and intransitive *yan* 'go'; NG-conjugation *lung* 'cry', *nyang* 'look, see', *pung* 'hit', *waang* 'follow', and *yung* 'give', most of which are transitive; RR-conjugation *patya* 'bite, chop', *-karra* 'place', *jaja* 'eat or drink without sharing', and *kunja* 'sprinkle'; ∅-conjugation has transitive *tyula* 'tell', *karrpi* 'tie, bind', *kanytyi* 'stamp, tread on, dance', *luwa* 'hit with missile', *mapa* 'spread, rub on', and intransitive *karri* 'stand', *wanti* 'fall'; and L-conjugation *laparny* 'run', *ngany* 'eat', *many* 'speak', and *yukarny* 'lie down'.
- Nordlinger (1990: 84-85) lists the conjugation class affiliation of seventeen Bilinarra verb stems, including N-conjugation *ya-* 'go', *ma-* 'do, get'; NG-conjugation

ka- 'take', *jayi-* 'give', *nya-* 'see', *pu* 'pierce', *wa/wani-* 'fall'; RR-conjugation *yuwa-* 'put', *pa-* 'hit'; ∅-conjugation *kampa-* 'cook', *yinpa-* 'sing', *karrwa-* 'have', *paya-* 'bite, drink', and *jiya-* 'burn'; and L-conjugation *ma-* 'say' and *nga-* 'eat'.

- Tsunoda (1981: 81-82) also lists the membership of a number of Jaru verbs, broken down by transitivity. The N-conjugation has several transitive *dun-* 'scold', *man-* 'get', and *lan-* 'spear', and a single intransitive *jan-* 'go, come'. The NG-conjugation is split roughly equally between transitive *buŋ-* 'hit', *gaŋ-* 'carry', *naŋ-* 'see', *juŋ-* 'give', *wawaŋ-* 'wipe' and intransitive *buŋ-* 'burn', *luŋ-* 'cry', *bulaŋ-* 'call out'. The listed RR-conjugation stems include transitive *bajan-* 'bite', *gajan-* 'kick', *jaan-* 'put', *gundan-* 'wet' and intransitive *jaan-* 'be' and *wajan-* 'become'. The ∅-conjugation is entirely transitive, with stems *dambun-* 'kiss', *garun-* 'hold', *maran-* 'tell', *wawan-* 'search for', and *lawan-* 'shoot', among others, plus the transitivity-neutral *luwan-*, which is glossed as the 'avoidance-language verb'. The listed L-conjugation membership is transitive *ŋan-* 'eat' and intransitive *man-* 'do, talk'. Finally, the Y-conjugation is intransitive, with members *wandin-* 'fall', and *banydin-* 'smell'.

3.2.4 Marrngu

Mangala (McKelson 1974), Nyangumarta (Sharp 2004a), and Karajarri (Sharp 2004b) comprise the Marrngu subgroup. McKelson (1974: 30-33) provides evidence of three distinct inflectional patterns in Mangala corresponding to three conjugation classes, but does not elaborate the size of individual classes or their membership beyond a handful of example forms. Looking at the included future tense forms *manguna* 'take.FUT', *buŋguna* 'hit.FUT', and *wanduna* 'stop.FUT', we can plausibly identify a future tense marker *-gu*[8], which is preceded by either *-n*, *-ŋ*, or ∅, giving rise to

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[8] This would require the /g/ to be lost in the zero-marked class, which is not unreasonable considering parallels in, e.g., Ngumpin-Yapa.

conjugation classes that are common both within Marrngu and Pama-Nyungan more generally, particularly in Ngumpin-Yapa (§3.2.3).

There is a great deal of overlap in the inflectional paradigms of Nyangumarta and Karajarri verbs. Both languages have four clearly definable conjugation classes, though Sharp (2004a: 162) notes that phonological alternation of nasal consonants in certain Nyangumarta nonfuture forms led O'Grady (1964) to propose a fifth class. Table 3.3 presents the imperative and future tense suffixes in both languages:[9]

Content	Language	NY	L	N	NG
Future	Nyangumarta	*-ulV*	*-lV*	*-nkulV*	*-ngkulV*
	Karajarri	*-ku*	*-lku*	*-nku*	*-ngku*
Imperative	Nyangumarta	*-a/i*	*-lV*	*-rra*	*-wa*
	Karajarri	*-ya*	*-la*	*-rra*	*-wa*

Table 3.3: Future and imperative endings for four Marrngu verb conjugations

Both Nyangumarta and Karajarri have two larger, open classes (NY and L in Table 3.3) and two smaller, closed classes (Classes N and NG). The open classes in both languages consist of mostly disyllabic stems and membership shows correlation with transitivity; The NY conjugation is mostly intransitive, while L is mostly transitive. Membership in Classes N and NG is again correlated with transitivity, with most of the members of either class being monosyllabic stems.

The makeup of the Mangala conjugation classes is not readily apparent from McKelson's data, but Nyangumarta and Karajarri have the following exemplars:

- The open NY-conjugation contains tens of disyllabic stems, most of which are

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[9] A *V* denotes an vowel that participates in morphophonological processes based on properties of the stem. Sharp (2004a: 165) notes that the future suffix is morphologically complex in Nyangumarta, consisting of the potential marker plus *lV*. She additionally gives two allomorphs of the future suffix for Nyangumarta, the alternate not given in the table adds *-iny* in place of the final *V*.

intransitive, including *jari* 'flow', *jupa* 'abate', *kampa* 'cook', *karnti* 'climb', *milpa* 'come', *purrpa* 'blow', and *karli* 'dig', as well as transitive *nguka* 'abduct', *nyirni* 'scoop', *ruwa* 'hit with something', *yura* 'hit with missile', semitransitive *panja* 'ignore', and ditransitive *karri* 'want'. This conjugation also contains derived inchoative and stative constructions, which take a single argument.

- The L-conjugation contains causatives, compound affective constructions, and over one hundred mostly transitive, disyllabic monomorphemic stems including *jaka* 'make fire', *jala* 'tell', *jani* 'cover with ash', *kalku* 'take care of', *mingka* 'separate', *murni* 'collect', *wirla* 'hit', *yirri* 'see', plus a small number of intransitives, including *piju* 'swell', *nganyja* 'breathe', *wala* 'return', *wupi* 'crouch'.[10]

- The NG-conjugation is closed-class and features monosyllabic stems *ka-* 'carry, take', *pu-* 'hit', *nya-* 'see', and *yi-/yu-* 'give', which are polyvalent, plus a number of compounds derived from these stems. A single disyllabic stem *para-* 'run' is also listed in the NG class.

- The N-conjugation has intransitive *ya-* 'go' and transitive *ma-* 'get', plus compounds derived from these stems. Sharp (2004b) mentions a third monomorphemic member of the N-conjugation, but does not list it.

3.2.5 Kartu

Wajarri (Marmion 2012), Nhanta (Blevins 2001), Malgana (Gargett 2011), and Yingkarta (Dench 1998) represent the Kartu language subgroup, all of which are described as having two conjugation classes, though Blevins (2001: 93-95) posits a small third class for Nhanta, which patterns with both of the major classes in different parts

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[10] Sharp (2004a: 163) notes that a number of ambitransitive verbs appear in either the NY or L conjugation, depending on their meaning. Examples include *jupa* 'diminish (NY-conjugation); extinguish (L-conjugation)' and *jurti* 'leak (NY); pour (L)'.

of the paradigm. As is the case in most languages with two conjugation classes, Kartu shows correlation between class membership and transitivity, although this is a tendency more than an absolute. To illustrate, counts of transitive and intransitive members of each class are given in Table 3.4 for Wajarri and Yingkarta:[11]

Class 1	LANGUAGE	Transitive	Intransitive
	Wajarri	40	252
	Yingkarta	31	7
Class 2	LANGUAGE	Transitive	Intransitive
	Wajarri	149	34
	Yingkarta	43	5

Table 3.4: Counts of conjugation class membership by verb valence in Wajarri and Yingkarta

Gargett (2011: 34-35) notes that incomplete data makes providing a meaningful count of conjugation class membership in Malgana implausible. Blevins (2001: 90) does not give raw numbers on membership and generalizes conjugation class membership in Nhanta as unaccusative vs. unergative, rather than intransitive vs. transitive.

The Kartu languages show more variation than the other subgroups discussed so far with respect to the form of inflectional suffixes across languages. In Wajarri (Marmion 2012: 96), the mostly transitive conjugation adds /(r)n/ or /(r)l/ to the tense or mood suffix in nearly all cells of the paradigm that is not present in the mostly intransitive class. In Yingkarta (Dench 1988: 41), the same transitive conjugation adds an /l/ before the tense or mood suffix. Moreover, Yingkarta inflectional suffix forms are quite different in their realizations from the rest of the subgroup. In

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[11] On the relatively large inventory of verbs catalogued for Wajarri, Marmion (2012: 91) notes that the coining of new verbs through various derivational processes is quite productive in the language, cautioning that raw counts are potentially unrepresentative of spontaneous language usage, but that the proportion of transitive and intransitive members in each of the conjugation classes is representative.

Nhanta (Blevins 2001: 91), the conjugation consisting of transitive and unergative verbs inflects for a wider range of tense and aspect distinctions than its intransitive and unaccusative counterpart, while the latter interrupts the stem and tense suffix with /nh/ in many cells of the paradigm. Gargett (2011: 38) gives a smaller set of inflectional endings for the two Malgana conjugations, which show differences in the present and future inflections, but do not vary in a way that indicates a putative conjugation class marker as compared for example with the aforementioned /nh/ in Nhanta. These differences are illustrated by the future tense endings for the four language, as summarized in Table 3.5:[12]

LANGUAGE	Y	L
Wajarri	*-ya*	-(*r*)*la*
Yingkarta	*-wu/-ku*	*-lku*
Nhanta	–	*-ndha*
Malgana	*-manha*	*-nmanha*

Table 3.5: Future tense inflectional endings in four Kartu languages

Descriptions of the Kartu verb conjugation classes and their respective membership are as follows (based on discussion in Dench 1988 and Blevins 2001):

- In Yingkarta, the Y-conjugation has disyllabic, intransitive stems *ngathi-* 'cry', *pungka-* 'blow (of wind)', *wangka-* 'speak, say, talk', *thurni-* 'laugh', *warni-* 'fall', *wapa-* 'come', *ngurnta-* 'lie down, sleep', *karnka-* 'cry out', plus a few transitive stems, including *kalku-* 'wait for', *patharri-* 'hit', and *kurlkarini-* 'hear, listen to'. The L-conjugation in Yingkarta contains primarily disyllabic, transitive stems, including *jarti-* 'eat', *ngaka-* 'catch, hold', *ngapa-* 'cover', *nhuli-* 'chase', *pirri-*

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[12] The Wajarri present tense suffixes (Marmion 2012: 96) appear to be the same as the Malgana future suffixes. Class 1 in Nhanta does not distinguish present and future tense with separate suffixes (Blevins 2001: 90); the nonpast/present suffix series is Class 1 *-nda*∼*-ndha*, Class 2 *-ndha*.

‘cut’, plus intransitive members like *yukarri-* ‘stand’ and *yinti-* ‘flow’.

- In Nhanta, membership is somewhat different from in the other Kartu languages. Here, Blevins’ Y-conjugation consists of transitive and unergative intransitive stems, while the NH/L-conjugation is entirely unaccusative intransitive. Only two NH/L-conjugation members are listed, namely *calyaba-* ‘be happy’ and *pitu-* ‘want, be eager to’. Y-class stems include transitive *aja-* ‘bite’, *arliba-* ‘lend’, *wumba-* ‘steal’, *arndi-* ‘smell’, *awu-* ‘light, stoke’ plus intransitive *wada-* ‘sing’.
- Nhanta contains a smaller, third conjugation, with mixed membership in terms of transitivity. Listed D-conjugation stems are transitive *uudada-* ‘take something away’, semitransitive *wathada-* ‘wonder’, and intransitives *wadada-* ‘hop’ and *wadadicada-* ‘hopping along’.

3.2.6 Ngayarta

Five Ngayarta languages were included in the language sample: Ngarluma (Kohn 2001), Yindjibarndi (Wordick 1982), Panyjima (Dench 1981), Ngarla (Westerlund 2015), and Martuthunira (Dench 1995). Ngayarta provides an interesting example of the loss of conjugation classes in certain languages that are preserved in related languages. To illustrate, we can partition the subgroup into three parts on the basis of their verb conjugation class inventories.

In the first group are Ngarluma and Yindjibarndi, both of which have four conjugation classes. Two of these are considered open classes with larger inventories, while the other two are smaller, closed classes. Membership shows correlation with transitivity; in Ngarluma (Kohn 2001: 30), membership in the mostly intransitive conjugation is 85% intransitive, while the remaining three classes are 90-100% transitive. Wordick (1982: 81) does not give counts or exact proportions, but notes that there is one large, mostly intransitive class, and that the other classes may contain intransitives but are mostly transitive. Yindjibarndi seems to have further delineation among the transitive conjugations based on the final segment of the stem. One transitive class contains only /i/-final stems, while another contains /a/-final stems. The third transitive conjugation has stems ending in /a/ or /u/. By contrast, the intransitive conjugation stems end in any vowel. This phonological basis for describing the mostly transitive conjugations in Ngarluma is not discernable from the available data. Yindjibarndi features a great deal of syncretism in the inflectional suffixes across conjugation classes, while this is less so in Ngarluma.

Lists of stems demonstrating membership by conjugation class are not offered in descriptions of Ngarluma, though Wordrick (1982) provides the following examples for Yindjibarndi:

- ∅-conjugation stems include *kampa* 'burn', *karpa* 'ascend, rise, fly up', *karri* 'be standing, stop, be', *kunti* 'refuse, decline', *manku* 'get, take hold of', *ngarrku* 'eat', *ngayhi* 'cry, and *nha* 'see', among many others.
- L-conjugation stems *paa* 'bite, sting', *pama* 'leave', *pampaa* 'test, try', *panhthu* 'touch, feel', and *kartaa* 'poke, pierce', among others.
- The R-conjugation contains stems *manta* 'enclose, snare', *munta* 'take something away from someone', *ngarra* 'hit with a thrown object', and *nyirra* 'cover, paint'.
- N-conjugation stems include *pani* 'grind', *panyi* 'take a step', *parnrti* 'smell, sniff', *thani* 'chop'.

The second group consists of Panyjima and Ngarla, both of which have two conjugation classes. Here the correlation with transitivity is again observable from the data. Consistent with the general pattern found across Pama-Nyungan in languages with two conjugations, the mostly transitive class includes a segment between the stem and tense, aspect, or mood suffix that is not visible in the mostly intransitive class. In Ngarla (Westerlund 2015: 50), this segment is generally one of /rr/, /rn/, or /n/, while Panyjima (Dench 1981: 98) has /rn/, /n/, or more commonly /l/. Moreover, while Westerlund and Dench both give generalizations about the size of the relative conjugation class inventories, a comprehensive listing is not offered. The verbs included in examples are very much in line with the ∅ and L-conjugation stems listed above for Yindjibarndi.

Rounding out the discussion is Martuthunira (Dench 1995: 139), which exists between the other two sets of Ngayarta languages with three conjugations. As with its relatives, Martuthunia has one mostly intransitive class and one mostly transitive class that interrupts stem and inflectional suffix with /l/, /rn/, or /n/. The third conjugation class is smaller, entirely transitive, and has /rr/ or /rn/ between the stem and suffix in most cells of the inflectional paradigm. Preset tense suffix forms illustrate the patterns of inflection found across the Ngayarta subgroup:

LANGUAGE	∅	L	R	RR/N/M
Ngarluma	*-gu*	*-lgu*	*-gu*	*-rrgu*
Yindjibarndi	∅	*-ku*	*-ku*	*-ku*
Martuthunira	*-nguru*	*-rnuru*	*-rnuru*	
Panyjima	*-ku*	*-lku*		
Ngarla	*-yan*	*-rri*		

Table 3.6: Present tense inflectional suffixes for five Ngayarta verb conjugation classes

Dench (1995) lists some members of the ∅ and R-conjugations, while noting that a number of ambitransitive stems can appear as either ∅ or L-conjugation, depending on their usage. Listed membership is as follows:

- The mostly intransitive ∅-conjugation has listed stems *nyina* 'sit', *puni* 'go', *kanarri* 'come', all of which are intransitive, plus transitive stems *nhawu* 'see (tr.)', *yungku* 'give'. Also included in this conjugation are derived passives, inchoatives, psychological state verbs, and bodily noises.

- *thani* 'hit' is the only example given of the L-conjugation, though Dench notes that this class contains many transitive stems plus causative derivations.

- A number of ambitransitive stems are identified that belong to either the ∅ or L-conjugation, depending on their usage. These include *kampa* 'cook, burn (L); be burning, cooking (∅)', *thurnta* 'rub, paint (L); rub/paint self (∅); *puntha* 'wash, bathe (L); wash, bathe self (∅); *yinka* 'chisel' (L); 'thrust' (∅), and *tharrwi* 'put into (L); put on (clothes) (∅)'.

- The smaller R-conjugation, which Dench suggests may be in the process of being lost, is described as having four members, including *wantha* 'put, place, leave', *warntitha* 'throw', *patha* 'blow (of wind), hit with thrown implement', and *kanytya* 'keep, hold'.

Dench (1995: 138) additionally gives an overview of the loss of conjugation classes in several Ngayarta languages, noting that Martuthunira represents an incomplete stage of the process of reshuffling members of the smaller conjugation classes into larger ones, this process having reached completion in Panyjima and Ngarla. Leveling of the paradigm in the form of syncretism in Yindjibarndi to a far greater degree than the other Ngayarta languages may reveal an intermediate step in the evolutionary process, with loss of distinctiveness between conjugations plausibly leading to loss of minor conjugations entirely.

3.2.7 Paman

The Paman languages show a great range of diversity with respect to their verb conjugation class typology. These languages are generally further subdivided based on geographical and typological considerations, a sketch of the verb conjugation class systems in these smaller subgroups follows.

Northern Cape York

The Paman languages of the northern Cape York peninsula of northeastern Australia are represented in the current study by Umpila, Kuuku-Ya'u, Ntrangith, Uradhi, the Wik languages Wik-Mungkan and Kugu Nganhcara, Linngithigh, and Mbakwithi. The source for Ntrangith is Hey (1903: 14-17), who gives invariant present, past, and future inflection for a list of verbs. A number of irregular verbs are also identified, but these do not indicate evidence of conjugation classes in the language.

Umpila and Kuuku-Ya'u (Thompson 1988: 32-34) are described as having three verb conjugations; the majority of the first two conjugations are transitive while the third is mostly intransitive. Conjugation class membership is not predictable from the final segment of the stem. There is a good deal of syncretism across various cells of the inflectional paradigms; the nonfuture suffixes are Class 1 *-la/-na*, Class 2 *-nya*, Class 3 *-la*, while the future suffixes are Class 1 and Class 2 *-ka* and Class 3 *-tha/-cha*. Thompson gives exemplar verbs for each of the three conjugations as Class 1 *kayina* 'hang up', Class 2 *kuutyanya* 'look, see', and Class 3 *ilpiina* 'return'. Additional verbs identified for each class are:[13]

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[13] Pascal Jacq (Koch & Jacq n.d.) notes interesting connections between certain verbs listed for Umpila and Kuuku-Ya'u. In some cases, similar verbs with similar meanings, but belonging to different conjugations, differ in the final vowel of their stems. A case in point is Class 1 *thaangkii* 'bathe' vs. Class 2 *thaangkaa* 'wash'. Moreover, a single example indicates a difference in conjugation class (and transitivity) corresponding with a difference in the length of the stem-final vowel; Class 1 *pinti* 'pierce' vs. Class 3 *pintii* 'leak, be open'. While this is an interesting finding, it does not appear to be an absolute pattern found across the verbal lexicon.

- Class 1 *thaangkii* 'bathe', *pi'a* 'keep', *pinti* 'pierce with sharp implement, open', *uuntha* 'swim', and *aa'i* 'dance, play (children)'
- Class 2 *thaangkaa* 'wash' and *waatyii* 'turn around, turn over'
- Class 3 *kalmi* 'come', *niina* 'sit', *kalu* 'carry', and *wuna* 'sleep', *pi'i* 'wait', *waatyaa* 'roll over, cause to turn', *pintii* 'leak, be open (intr.)', *ungkaa* 'cry, sob, weeb', and *ilpii* 'return'.

Uradhi (Crowley 1983: 359-365) has four verb conjugations, with the first being further subdivided into two subclasses based on slight differences in inflectional patterns. As with other Pama-Nyungan languages with four or more conjugations, membership seems to show correlation with both transitivity and phonological properties of the stem. Conjugation 1 is described as being small and closed, consisting of transitive monosyllabic verbs, including *wa* 'burn, cook', *ra*∼*ya* 'throw, and *u* 'give'. The second conjugation is open and mostly contains transitive verbs ending in /a/, though there are some exceptions. Conjugation 3 verbs are also mostly transitive and typically have final /u/. Finally, nearly all of the verbs in the fourth conjugation are intransitive, all of which end in final /a/ or /i/.

Though they are both classified as Wik languages, Wik-Mungkan and Kugu Nganhcara have extensive differences in their verbal inflections. Wik-Mungkan (Kilham et al. 2011: 406-407) verbs take a single set of inflectional suffixes, which are portmanteau in their indexing of subject person and number and tense, aspectual, or mood distinctions. Kugu-Nganhcara (Smith & Johnson 2000) also shows subject indexing on the verb, but subdivides verbs into four conjugation classes.[14] Transitivity and phonology appear to play a role in defining class membership, though the correlation with transitivity is not as pronounced as in other Pama-Nyungan languages; Conju-

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[14] One of these conjugations contains a single transitive verb *kali-* 'carry' (Smith & Johnson 2000: 408), and as such the number of conjugations was coded as three rather than four. This may represent an earlier minor conjugation that has been lost.

gation 1 stems end in non-high vowels and are mostly transitive, Conjugation 2 has high vowel final stems and a mix of transitive and intransitive verbs. The six-member Conjugation 3 is mostly intransitive stems ending in *-na*, with one exception. If we speculate the previous existence of a fourth transitive closed conjugation, we have in the modern language the remnants of a four conjugation class system with two large classes and two small classes. Interestingly, there seems to be extensive leveling of the paradigmatic distinctions in Kugu Nganhcara; Conjugation 1 is only differentiated from the other two conjugations in the unmarked subject suffix in the present tense. Thus the division of verbs into conjugations is supported entirely on properties of the verb stems and argument structure themselves, rather than patterns of inflection as in most Pama-Nyungan languages.

Smith & Johnson (2000: 406) give some details about the membership of each of the Kugu Nganhcara conjugation classes, including the following inventories:

- The first conjugation includes *waa* 'give', *maa* 'pick up, collect, buy', *mungga* 'eat', *pithtya* 'burst (itr.)', *uwa* 'go, come', *eke* 'get up', *wegbe* 'keep, retain', *ente* 'ask for', *endye* 'singe', plus reciprocals like *odh-o* 'give to each other, share'.

- Conjugation 2 has high-vowel-final stems *ngii* 'hear, *thii* 'throw, chuck', *uwi* 'see', *wanki* 'return', *yumpi* 'do, make', *pigu* 'hit', and *nuptu* 'bark'.

- Conjugation 3 has six members; *thawa* 'speak, say', *nhiina* 'sit', *thana* 'stand', *mangalana* '(lightning) flash', and *wuna* 'camp, stay'.

- *kali* 'carry' is described as being the lone member of a potential fourth conjugation class.

Finally, we consider Linngithigh and Mbakwithi, both of which are described as having had four verb conjugations based on patterns of inflectional endings. Mbakwithi (Crowley 1981: 174) inflectional endings were discussed in Table 1.5 (§1.2.2) with reference to distinctiveness and opacity as measures of paradigm complexity and the ability to predict a verb's conjugation class membership from some or all of its form paradigm. Recall that verbs in this language belong to one of four conjugations, which show correlation with transitivity and phonlogical properties of the stem. This latter criterion is especially true in the further division of each conjugation class into two subclasses based on stem phonology. For Linngithigh (Hale 1966: 183) discussion of verb conjugation classes is limited to paradigms of suffixes for the four classes across four tense and mood distinctions and a few example forms. As such, no strong claims about membership can be formulated.

Crowley (1981: 174-176) offers the known membership of each of the four Mbakwithi conjugation classes at the time of description:

- Conjugation 1 stems include *bwa* 'break', *ya* 'give, bring', *yu* 'spear', *tyi* 'see, look at', *pu* 'do, throw', *kwii* 'have, keep, look after', *napu* 'swallow', *tya* 'split', *ga* 'poke', and *ra* 'wash, rub'.
- Examples of Conjugation 2 stems include *ŋa* 'dig', *kanaŋa* 'find', *karagwa* 'crawl', *tyama* 'jump', *winiga* 'scratch', *riyiga* 'smash', *ta* 'stand', and *rumu* 'bend down', plus reflexives.
- Conjugation 3 is smaller than the first two and includes *bwi* 'kill', *di* 'suck', *riŋi* 'punch', *wati* 'dive', and some reciprocals.
- The mainly intransitive Conjugation 4 includes *narama* 'stand', *gwagata* 'swim', *ga* 'peel', and *twa* 'tell'.

Southwestern Paman

Kunjen, Kuuk Thaayorre, and Yir Yoront are spoken in the southwestern part of the Cape York peninsula. Data for Kunjen comes from Sommer (1970: 248), who provides a table of inflectional endings indicating two conjugations, but does not elaborate on class membership. There is considerable syncretism across the two classes, but they do differ in the present, imperative, and past tense forms:

CONTENT	Class 1	Class 2
Present	-*n*	-*y*
Imperative	-*l*	-*y*
Past	-*r*	-*l*

Table 3.7: Present, imperative, and past inflectional suffixes in Kunjen

Kuuk Thaayorre (Gaby 2006: 344-351) also has two conjugation classes, with a strong correlation between membership and verb valence, as is common in Pama-Nyungan two verb conjugation systems. As with Kunjen, there is a good deal of overlap in the form paradigms of the two sets of inflectional endings, though they differ in the nonpast (Class 1 has -*r*, Class 2 is zero-marked) and past perfective (Class 1 -*rr*; Class 2 -*r*).

Attested membership in Kuuk Thaayore demonstrates this correspondence between conjugation class and transitivity. Class 1 has a few intransitives, *munth* 'sink', *pic* 'burst', *piinth* 'grow', and *riic* 'run', plus a larger set of transitives, including *kal* 'carry', *kat* 'hold', *matp* 'smash', *mungk* 'eat', *path* 'bite', *piit* 'keep', *rint* 'cook', *thaath* 'scorch', *thunp* 'throw', *wak* 'follow', and *yump* 'do'. Conversely, Class 2 is mostly intransitive, including *kerp* 'finish', *koop* 'wait', *nhiin* 'sit', *than* 'stand', *thongk* 'arrive', *wun* 'lie', *yuuc* 'ache', and reflexives, plus the transitive verb *kooc* 'bark'. Semitransitive members of Class 2 are *wene* 'want, become' and *yik* 'say', .

Yir Yoront diverges from its neighbors included in this section; Alpher (1973: 226-241) defines five conjugations, though one has a single member and was omitted from consideration in the language coding process. Of the remaining four conjugations, two are mostly transitive and two are mostly intransitive. As is common in the Pama-Nyungan context, the purposive forms are maximally distinctive in their realization (markers of conjugation class membership are highlighted in bold):

	L	R	n̪	l̪
Form	*ma**l**e*	*ta**r**e*	*worŋa**n̪**e*	*lorma**l̪**e*
Gloss	'tread on'	'arise'	'smell'	'accumulate'

Table 3.8: Purposive forms of four Yir Yoront verbs belonging to different conjugation classes

In addition to the exemplar verbs highlighted in Table 3.8, Alpher (1978: 231-240) offers the following additional forms:

- L-Conjugation stems include *moy-* 'swim', *kom-* 'forget, overlook', *mom-* 'grab', *la-* 'swear at, curse', *yam-* 'carry', *kar-* 'hit, see', *mul* 'warm up', *pat-* 'eat, bite', *le-* 'insert', *mir* 'dry up', and *ma-* 'tread on, fall on'.
- R-conjugation stems include *luw-* 'break', *ta-* 'ascend', *koy-* 'dig (yams)', *lay-* 'poke, jab', *pay-* 'growl', *pe-* 'bury', *way-* 'wipe', and *telpa-* 'ascend river bank'.
- *tar-* 'laugh', *tu-* 'pant, sweat', and *wuŋ* 'sing, dance, play' are all n̪-conjugation verbs.
- Additional l̪-conjugation stems include *warm-* 'die', *kolm-* 'bend', and *wolm-* 'get small and dry, shrink'.

Yalanjic

Kuku Yalanji (Patz 2002: 88-92) is described as having two conjugations, which strongly correlate with transitivity (Class ∅ is 92% transitive, while Class L is entirely composed of intransitive verbs). Patz notes that extensive syncretism across the inflectional paradigms of the two conjugation classes is likely to lead to further loss of distinction in the future. In fact, the two classes only differ in the forms of the nonpast and imperative inflectional suffixes:

CONTENT	∅	L
Nonpast	*-l*	*-y*
Past	*-ny*	*-ny*
Imperative	∅	*-y*
Irrealis	*-nyaku*	*-nyaku*

Table 3.9: Inflectional endings for Kuku Yalanji verb conjugation classes

Patz (2002: 88-89) does not provide a comprehensive listing of ∅-conjugation forms. The known membership of the L-conjugation is given as *daka* ‘climb, rise’, *janji* ‘swim, bathe’, *kalji* ‘vomit’, *wala* ‘enter’, *walngka* ‘hang’, *wandi* ‘come out, wake up’, *warrki* ‘turn off at crossroads’, *wurrka* ‘ache’, *kadaba* ‘break’, *jalama* ‘jump’, and *jirayma* ‘crave, long for’.

The verb conjugation class system of Guugu Yimidhirr (Haviland 1979) was discussed in detail throughout Chapter 1. Recall that the language has three conjugation classes, whose membership is correlated with transitivity. This includes two mostly transitive conjugations and a smaller class of mostly intransitive verbs. Haviland (1979: 82-83) lists a handful of verbs belonging to each of the three conjugation classes:

- Most L-conjugation stems and disyllabic, including *balgal* ‘make, wash’, *wagil* ‘cut’, and *barrbil* ‘camp, spend the night’.

- V-conjugation stems include intransitive *baanngaa*∼*baarrngaa* ‘sing out’, *biinii* ‘die’, *bulii* ‘fall down’, *dhadaa* ‘go, walk’, *dudaa* ‘run’, *gadaa* ‘come’, *nganggaa* ‘be confused, be unable, not understand’, *wuurii* ‘play, dance’, *yuulii* ‘stand, be standing’, and transitive *dirrbaa* ‘abduct’, *banydyii* ‘wait for’, and *maandii* ‘take, bring’.

- The R-conjugation verbs highlighted by Haviland include *buunydyirr* ‘gather, heap up', *yidyirr* 'get stuck', and the trisyllabic *yidyawurr* 'sneeze'.

Other Paman

Djabugay (Patz 1991) divides verbs into two conjugation classes. One class is predominantly intransitive (73%), while the other is mostly transitive (80%). Here the distinction between conjugations is well defined, with the presence of /l/ between the stem and inflectional suffixes marking tense, aspect, or mood. A partial paradigm illustrating these differences is given in Table 3.10:

CONTENT	Class 1	Class2
Present	*-ng*	*-l*
Future	*-na*	*-lna*
Past	*-ny*	*-ny*
Irrealis	*-ybarra*	*-lbarra*

Table 3.10: Inflectional endings for Djabugay verb conjugation classes

Yidiny (Dixon 1977: 206) has three conjugation classes, two of which correspond to the Djabugay conjugations, and a third consisting of a small set of 13 transitive verbs and two intransitive verbs. Thus membership is correlated with verb valence to a large degree. The two transitive classes have /l/ and /r/ between the stem and inflectional suffix, much like the pattern seen in Table 3.10 for Djabugay. Dixon (1977: 208) provides the membership of this third, mostly transitive conjugation, including transitive stems *bada* 'leave', *balŋa* 'hit with a stick', *banda* 'follow', *bundu* '(doctor) wipes(s) off pain', *buybu* 'blow, spit at', *dadu* 'put blanket down', *danda* 'rub', *nayŋu* 'throw', *gayba* 'make body feel good', *gaymba* 'follow, sneak up on', *nyirda* 'put sitting down', *walŋu* 'peep in/around', *yaga* 'hunt away', and *yumba*, plus intransitives *bayga* 'feel sore, have pain' and *dunyda* 'wade across stream'.

Breen (1988) notes that Kukatj verbs can be divided into two major conjugation classes, with further subdivision among the classes possible in the identification of subclasses using phonological properties of the stem. Class membership is described as being correlated strongly with transitivity; Conjugation 1 is 90% transitive, while Conjugation 2 is entirely intransitive. The paradigms of several verbs are given to illustrate the differences in the inflectional patterns of major classes and their subclasses. Representative verbs for the two major classes are given in Table 3.11:

CONTENT	Class 1	Class 2
Gloss	‘bite’	‘speak’
Stem	*kiyel-*	*yirngk-*
Imperative	*kiyelk*	*yirngkey*
Past	*kiyen*	*yirngkaan*
Present	*kiyenj*	*yirngkaanj*
Purposive	*kiyenhenk*	*yirngkenhenk*

Table 3.11: Partial form paradigms of two Kukatj verbs belonging to different conjugation classes

We see from Table 3.11 that while the two classes are syncretic in the purposive inflection, they are otherwise distinct from one another. Moreover, identification of a putative conjugation class ‘marker’ (i.e., a segment intervening between stem and suffix) is not straightforward for Kukatj, as compared with for example Djabugay or Yidiny.

Additional Class 1 stems outlined by Breen include *thurpel-* ‘make’, *kjar-* ‘carry’, *wir-* ‘rub’, *pal-* ‘get up’, *pliil-* ‘hit’, *klwil-* ‘tie’, *minewir-* ‘shake’, *nhaa-* ‘see’, *yuw-* ‘give’, and *ngalkeleman-* ‘lift’. In addition to *yirngk-* ‘speak’, Class 2 stems include *kiin-* ‘go’, *kt-* ‘fall’, and *yin-*∼*naa-* ‘sit’.

3.2.8 Maric

The Maric languages included in the language sample show somewhat more variation in their verb conjugation class systems as compared with other subgroups. Guwamu and Bidyara (Breen 1973) lack conjugation classes entirely, a single set of suffixes are provided. The same is true for Biri, with Terrill (1998: 34) noting that this lack of conjugation classes in the language is unusual for languages of the Maric subgroup, the general geographic area, and Australian languages more generally.

Warungu (Tsunoda 2011) is described as containing three conjugation classes, which are differentiated in the nonfuture and apprehensional forms:

CONTENT	L	Y	∅
Gloss	'stab'	'sit'	'run'
Nonfuture	*babal*	*nyinay*	*wadali*
Apprehensional	*babalga*	*nyinangga*	*wadalingga*

Table 3.12: Nonfuture and apprehensional forms for three Warungu verbs belonging to different conjugation classes

In the forms in Table 3.12, we see evidence of conjugation class being overtly marked in the nonfuture (L conjugation takes *l*, Y conjugation *y*, ∅ is zero-marked). Tsunoda (2011) documents a correlation between conjugation class membership and valence, with one large class for transitive verb roots (Class L) and another for intransitives (Class R). The third class is a smaller, closed class, consisting of a single transitive root and a few intransitives. Tsunoda further notes that at the time of description, the conjugational class of a large number of verb roots in the language was unknown.

Different still to the other Maric languages is Gugu Badhun (Sutton 1973), which shows evidence of two major classes. The verb conjugation class system in Gugu Badhun is similar to that of Warungu, though the former lacks the zero-marked class of the latter. Of the two classes that remain, membership seems similarly divided according to transitivty – one class contains mostly intransitive verbs, though it does include some transitive roots as well, while the other class consists of a number of transitive verbs and a single intransitive, *baya-* 'sing'.

The closely related Margany and Gunya (Breen 1981a: 314-324) have two conjugation classes each, which are distinctive only in the purposive suffix, which is *-ngu* for the L class and *-lu* for class two in both languages. Membership is said to correspond directly with transitivity. Breen (1981a: 324) further notes that younger Gunya speakers at the time of documentation used *-lgu* as the purposive form for all verbs.

3.2.9 Warluwaric

Breen's descriptions of the Warluwaric languages Warluwarra (1971), Wakaya (1974), and Bularnu (n.d.) were introduced in Chapter 1 (§1.2.3) with respect to the theoretical question of whether a closed-class morphological system can be said to be driven by, rather than simply correlated with, other aspects of the language, in this case the phonology. Recall that Warluwaric languages are typologically distinct from the rest of the languages in the sample, and the Pama-Nyungan languages more generally, in that there is little to no observable correlation between conjugation class membership and valence. Instead, the descriptive profile of conjugation classes in these languages includes information about phonological properties of the stem. Each of the languages has four conjugation classes, with stem-final segments indicating membership in a given class, with noted exceptions.

Breen's (2004: 227-236) summary of the typology and development of Warluwaric conjugation classes offers insight into the inventory of stems in each conjugation. While the description of Bularnu is notably lacking in terms of lists of verbs, Breen offers exemplars of the four conjugation classes: TH-conjugation *yanga* 'see', J-conjugation *garri-* 'stand', 0-conjugation *matha* 'hit', and RR-conjugation *yiwarra* 'sit'. Warluwarra has additional TH-conjugation stems *madja* 'eat (vegetable food)', *djirra* 'be sick', *warra* 'grind', *gurra* 'like', and *gunugurra* 'be sick of'; J-conjugation stems *garri-* 'stand', *larri-* 'hear', and *barri-* 'sneak up'; 0-conjugation *nati-* 'do what', *latji* 'dance', *barlardi-* 'show', and *birrtji-* 'swallow'; and RR-conjugation stems *bitjarra* 'make (a fire)', *nakarra* 'cut', *wurrgharra* 'run', *numarra* 'break', *wurrgharrarra* 'chase', and *yatjuwarra* 'smell (itr.)'. Wakaya lacks the RR-conjugation of its relatives, and instead has an NTH-conjugation, whose inventory includes *ma* 'hit', *lirla* 'call out', *miny* 'hold', *wulema* 'bury', and *nheng* 'get'. Wakaya also has TH-conjugation *kek* 'cry', *ngelb* 'enter', and *ngiib* 'make'; J-conjugation *marr* 'talk', *kirr* 'stand', *berarr* 'sneak up', and *benbarr* 'hide'; and 0-conjugation *benk* 'go', *ngund* 'give', *kujerr* 'laugh', *thuk* 'throw', and *bujuk* 'run'.

Breen (2004: 239) argues that the verb conjugation classes found in Warluwaric do not continue the classes found across the much of the rest of the Pama-Nyungan family. Instead, he hypothesizes that the observed phonology-based classes were innovated in the prehistory of the Warluwaric branch, either replacing the more common valence-based conjugation classes or representing a case of developing a conjugation class system from a previous stage of absence.

3.2.10 Wiradhuric

Ngiyambaa (Donaldson 1980) was discussed in Chapter 1 as well as an example of a language with multiple conjugation classes where membership is based both on transitivity and phonological properties of the stems themselves. This is especially true in the defining of subclasses within the larger conjugation classes. Donaldson (1980: 155-156) additionally provides some examples of verb stems belonging to the various Ngiyambaa conjugation classes, though the description of the L-conjugation is somewhat lacking:

- Y-conjugation stems include monosyllabic *wii-* 'sit', *gaan-* 'bring, take', *ŋu-* 'give', *ŋaa* 'see', and disyllabic *balun-* 'die', *yurun-* 'grow', *gurun-* 'go in', *ŋaarun-*

'drink', *ŋamun-* 'suckle', *baran-* 'rise, fly', *wanan-* 'throw', and *buuwa* 'puff up, swell'.

- The L-conjugation has monosyllabic members *dha-* 'eat', *ma-* 'do, make', and *ga-* 'be', plus disyllabic *baga-* 'dig'.
- The R-conjugation is said to consist of two monosyllabic stems, *dhu-* 'prick, spear' and *dha* 'copulate with'.

The other Wirahduric languages in the sample are Gamilaraay and Yuwalaraay (Williams 1980: 66; Ash, Giacon & Lissarague 2003: 303), which have four verb conjugations each. Of these four classes, two are large open classes and two are small and have closed membership. The two open classes show correlation with verb valence, one is predominantly composed of transitive verbs, while the other is mostly intransitive. The smaller conjugations are somewhat evenly split between transitive and intransitive. Unlike several of the other Pama-Nyungan languages with four or more conjugation classes, there is no mention made of the influence of phonological properties of them stem in the class membership of individual verbs. Conjugation class is marked by patterns of inflection, with a great deal of similarity between the two languages in terms of their verbal inflectional paradigms. Table 3.13 gives future, nonfuture/past, and imperative endings for each of the four classes in both languages as well as comments on their membership:

CONTENT	L	Y	NG	N/R
Future	*-li*	*-y*	*-gi*	*-ri*
Nonfuture/Past	*-y*	*-ni/-nhi*	*-ni/-nhi*	*-ni/-nhi*
Imperative	*-la*	*-ya*	*-nga*	*-na*
Membership	Open	Open	Closed	Closed
Transitivity	Transitive	Intransitive	Mixed	Mixed

Table 3.13: Future, nonfuture, and imperative suffixes in Gamilaraay and Yuwalaraay

Williams (1980: 60-67) provides a few clear examples of verbs belonging to each of the four identifiable conjugation classes in Yuwalaraay:

- L- conjugation stems include *gama* 'break', *bayama-* 'catch', *naanma-* 'drop', *buma-* 'hit, kill', *nima-* 'pinch', *manuma* 'steal', *diima-* 'take out', *wagirma-* 'wash', *waraymа-* 'build', *guuma-* 'collect', *dama-* 'feel, touch', and *mama-* 'stick to'.

- A smaller set of Y-conjugation stems is offered by Williams – *gaawaa-* 'bring, take', *galiya-* 'climb', *baray-* 'fly', *yinaa-* 'go, come', *banaga-* 'run', and *danduwi-* 'sleep, lie down'.

- The NG- conjugation contains *gaa-* 'bring, take', *mawu-* 'dig', *ŋawu-* 'drink', *bundaa-* 'fall', *wana-* 'throw (hard)', *yu-* 'cry', *yulu-* 'dance, play', *balu-* 'die', *gayara-* 'look for', *yuura-* 'move', *daalu-* 'feel sick', *yuu-* 'go into', *ŋayu-* 'tread on', and *ŋamu-* 'suck'.

- The N/R-conjugation has *duu-* 'crawl', *wuu-* 'give', *du-* 'spear, sting', *dila-* 'uncover', and *giguwi-* 'sneeze'.

3.2.11 Dyirbalic

The Dyirbalic languages Nyawaygi (Dixon 1983) and Wargamay (Dixon 1981) are divergent from one another in their verb conjugation class system, perhaps representing another example of loss of conjugation classes in one language that are preserved in another.

Nyawaygi is described (Dixon 1983: 470-473) as having seven distinct conjugation classes, though two of these have two or fewer members. Of the three open classes, one contains only transitive verbs, while the other two only have intransitive verbs as members, with one exception. The smaller closed classes all have four or fewer members, though they do seem to contain either only transitive or only intransitive members, with the exception of intransitive *ya-* 'go' being grouped with transitives *yaa-* 'throw' and *maa-* 'hold (in hand)'. Interestingly the larger classes only contain polysyllabic roots, while all members of the smaller closed classes are monosyllabic. Moreover, intransitive polysyllabic stems show some correlation between the last segment of the stem, with one intransitive class having mostly /a/-final stems, while the majority of stems in the other have final /i/.

A comprehensive listing of stems and their conjugation class affiliation is not provided in Dixon's description of Nyawaygi, though we can discern a few example forms for the three open conjugations. L-conjugation stems include *gunba-* 'cut', *wagiri-* 'spill, pour', and *gidara-* 'put down'. ∅-conjugation stems highlighted by Dixon are *guuba-* 'stand' and *wula-* 'die'. The Y-conjugation contains twelve stems (Dixon 1983: 472), including *bana-* 'return' and *buymbi-* 'paint'.[15] The membership of the closed, monosyllabic conjugations is G-conjugation *nyaa-* 'see', *wu-* 'give', *buu-* 'drink', *?nyuu-* 'smell'; G^y-conjugation *nyii-* 'sit', *yuu-* 'lie down'; N-conjugation *ya-* 'go', *yaa-* 'throw', *maa-* 'hold (in hand)'; and M conjugation *bu-* 'hit'.[16]

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[15] *buymbi-* also appears as an L-conjugation verb and is glossed as 'lick'.

[16] It should be noted that because languages with four or more conjugations were grouped

Dixon (1981: 46) outlines two conjugation classes in Wargamay, which he names ‘intransitive’ and ‘transitive’, telegraphing the relationship between class membership and verb valence. More specifically, Dixon (1981: 47) describes the Wargamay system as consisting of a purely intransitive class, with exemplars *gaga* ‘go, come’, *banma* ‘talk’, and *waadi* ‘laugh’, and a transitive class, including *buudi* ‘take, bring’, *muda* ‘eat’, and *ŋunda* ‘see’. These two sets of verbs take different sets of inflectional endings, though it should be noted that ambitransitive verbs from the transitive conjugation can also occur with intransitive morphology to give an intransitive meaning. A case in point is *ŋunda* ‘see’, which takes transitive morphology in *ŋada maal ŋunda*_**lgani**_ ‘I’m looking at the man’ and intransitive morphology in *ŋayba ŋunda*_**bali**_ ‘I’m having a look’ (continuative suffix indicated in bold in both examples).

Here we find some overlap in the inflectional suffixes between the Wargamay conjugation classes and two of the open classes in Nyawaygi. Table 4.14 gives inflectional suffixes in both languages to illustrate:

Language	Content	L	Y	∅	G	G^y	MA	NA
	Membership	Open	Open	Open	Closed	Closed	Closed	Closed
	Transitivity	Transitive	Intransitive	Intransitive	Transitive	Intransitive	Transitive	Transitive
Nyawaygi	Imperative	∅	*-yga*	*-ga*	*-ga*	*-ga*	*-na*	*-ma*
	Irrealis	*-lma*	*-yma*	*-ma*	*-gima*	*-gima*	*-tyima*	*-tyima*
	Purposive	*-gu*	*-ygu*	*-gu*	*-gagu*	*-nyagu*	*-nyagu*	*-magu*
	Perfect	*-yi*	*-ygi*	*-gi*	*-gi*	*-gi*	*-ni*	*-mayi*
Wargamay	Imperative	*-ya*∼ ∅		*-ga*				
	Irrealis	*-lma*		*-ma*				
	Purposive	*-gu*		*-lagu*				
	Perfect	*-nyu*		*-gi*				

Table 3.14: Inflectional suffix paradigms for Nyawaygi and Wargamay

Thus while the inflectional suffixes of the first and third conjugations in Nyawaygi

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together for coding purposes, the current study remains agnostic about the single-member M-conjugation.

are not identical to those of the two Wargamay conjugations, the amount of overlap is suggestive of their being correlated. Moreover, recalling the notion that paradigm leveling and/or a lack of distinctiveness across conjugation classes may lead to loss of individual conjugations, note the high degree of syncretism between Nyawaygi conjugations 4-6, which only differ in one or two cells of the paradigm.

3.2.12 Mayi

The Mayi languages are represented in the current study by Mayi-Kulan. Breen (1981b: 54-55) notes that Mayi languages have two conjugation classes, which show a clear correlation with transitivity. There is a high degree of syncretism between the inflectional suffixes of these classes. In fact, they differ only in the present tense suffix, which is *-iŋu* (e.g., *kawiŋu* 'fear, be afraid') for the mostly intransitive class and *-lpuŋu* (e.g., *namalpuŋu* 'see, watch') for the mostly transitive class. Otherwise, a single set of inflectional suffixes marks additional tense, aspect, and modality distinctions for both conjugations. Additional stems belonging to the *-iŋu* class are *kur-* 'go', *kaw-* 'be afraid', *wap-* 'go', and *wata-* 'call out, bark', while *pata-* bite and *kuri-* 'carry' represent transitive stems that belong to the *-lpuŋu* class.

3.2.13 Yolngu

The Yolngu languages are characterized by complex patterns of inflection, many of which are analyzed as having a relatively large number of major conjugation classes with multiple subclasses. Representative members of the family included in the current study are Dhangu (MacLellan 1992), Dhuwal (Heath 1980a), Djambarrpuyngu (Wilkinson 1991), Djapu (Morphy 1983), and Ritharrngu (Heath 1980b).

MacLellan (1992: 108-109) defines four conjugation classes for Dhangu, two of which are large, while the other two are small and have closed membership. Various subclasses are defined based on minor differences in the patterns of suffixation. A fifth set of verbs which do not take inflection are described as being loans from Austronesian. MacLellan does not give absolute counts with respect to the transitivity values in the two large classes, instead finding that these contain both transitive and intransitive members. One small class is entirely transitive, while the other is entirely intransitive. No direct description of the phonological properties of the stems in each conjugation class is offered. Table 3.15 presents MacLellan's overview of the Dhangu inflectional suffixes:

CONTENT	Class 1	Class 2	Class 3	Class 4
Neutral	*-n*	*-m(a)*	*-ma*	-∅
Perfective	(*-wa*)*na*	(*-wa*)*na*	*-ŋala*	*-na*
Irrealis	*-u*	*-ŋu*	*-ŋu*	*-yi*
Imperative	*-wa*	*-ŋa*	*-ŋa*	Stem change
Membership	Open	Open	Closed	Closed
Transitivity	Mixed	Mixed	Transitive(?)	Intransitive

Table 3.15: Inflectional suffixes for four Dhangu verb conjugation classes

For the two larger classes, MacLellan does not give a listing of stems, though we can determine from examples that Class 1 has stems *djarryu-* 'stretch', *dhuniya-* 'go down', *garru-* 'talk', *ŋayatha-* 'experience', and *luputhuma-* 'wash, soak'; Class 2 includes *milku-* 'show', *rakara-* 'tell', and *guwatthara-* 'fight, gather, hunt'; Class 3 has *nhama-* 'see' and *ŋama-* 'hear'; and Class 4 has intransitive stems *nyena-* 'sit', *ŋoya-* 'sleep', *gayŋiya-* 'rest', and *ŋarra* 'go, come'.

In Dhuwal (Heath 1980a: 39-43) and Ritharrngu (Heath 1980b: 60-67), six verb conjugations are apparent from the data, with all but one of these being split into subclasses, as is common in analyses of the Yolngu languages. This could potentially be reduced to four for each language considering the similarities between conjugations 1 and 2 on the one hand and conjugations 3 and 5 on the other, though the distinction is immaterial to the current study, as systems of four or more conjugation classes receive the same feature value in the proposed coding schema. Conjugations 1 and 2 are small favor intransitive verbs, though the second conjugation has a few transitive verbs as well. The other conjugations are mostly or entirely transitive. Inflectional endings are given for Ritharrngu in Table 3.16, note that the class numbers for this language do not necessarily coincide with the classes in MacLellan's description of Dhangu due to the linguists' choice in laying out the data:

CONTENT	Class 1	Class 2	Class 3	Class 4	Class 5	Class 6
Present	-∅	-∅	*-n*	*-rn*	*-n*	*-ma*
Past	*-n(h)a*	*-nha*	*-na*	*-ra*	*-na*	*-nha*
Future	-∅	*-i*	*-rru*	*-lu*	*-rru*	*-wu*∼*-ngu*

Table 3.16: Inflectional suffixes for six Ritharrngu verb conjugation classes

Example verbs for Ritharrngu given by Heath (1980b: 63-67) include the following:

- Class 1 has stems *waani-* 'go', *ngaathi-* 'weep', and *kukarri-* 'go hunting'.
- Class 2 includes *nhiina-* 'sit', *thaarra-* 'stand', *nguurra-* 'lie down, sleep', *rluka-* 'eat, consume', and *kuyupa-* 'die'.
- There are three Class 3 stems identified, namely *ngupa-* 'chase', *patha-* 'burn (tr.)', and *kuutha-* 'roast in a stone oven'.
- Class 4 is another small conjugation, containing *kartha-* 'hold', *nhanapa-* 'build a fire', *kurrupa-* 'give', and *karrpi-* 'coil or wrap around', among a handful of others.
- Class 5 is described as being larger (> 100 stems), though a single exemplar is given, namely *jarany-* 'push'

- The membership of Class 6 is also larger than the first four, but smaller than Class 5. Listed stems include *rlakara-* 'tell', *ngaa-* 'hear', *kunka-* 'protect, defend', *nhaa-* 'see', *kaa-* 'carry', *ngulka-* 'fetch', *kuruka-* 'carry on one's shoulder', *ngurrka-* 'throw', and *pu-* 'kill'.

Wilkinson (1991: 307-322) identifies fifteen distinct patterns of inflection in Djambarrpuyngu, ultimately providing evidence for four major conjugation classes and a number of subclasses within these. Phonological properties of the stem are potentially informative in the delineation of subclasses, while the major classes show a correlation with transitivity. As with Dhangu and Dhuwal, Djambarrpuyngu has one class that is mostly intransitive, while the rest have mostly transitive members. Inflectional suffixes appear to cover a range of tense and mood combinations with a single exponent; Wilkinson's (1991: 361) '1st inflection' covers realis nonpast and recent past forms, the '2nd inflection' includes irrealis future forms and imperatives, the '3rd inflection' realis past and remote past, and the '4th inflection' irrealis past tense forms. All four conjugations allow for expression of perfective and imperfective aspect as well. Inflectional endings for the four conjugation classes identified by Wilkinson are given in Table 3.17:

CONTENT	Class 1	Class 2	Class 3	Class 4
1st Inflection	-∅ ~ *-rr*	*-n*	*-m(a)*	*-ma*
2nd Inflection	-∅ ~ *-rr*	*-rr*, *-l*, *-k(u)*, *-rr*	*-ng(u)*, *-l*	*-ngu*, *-ku*
3rd Inflection	*-n(a)*	*-r(r)*	*-ngal*	*-mar*, *-kul*
4th Inflection	*-nya(ra)*	*-na(ra)*	*-nha(ra)*	*-nha(ra)*

Table 3.17: Inflectional suffixes for four Djambarrpuyngu verb conjugation classes

Note from the forms given in Table 3.17 that the 2nd inflection contains a number of different inflectional endings within many of the conjugations, especially Class 2, leading to the analysis of a number of subclasses within the larger conjugations. On conjugation class membership, Wilkinson (1991: 309-322) offers the following forms:

- In the first conjugation class, representative members include *marrtji-* 'go/come, walk (itr.)', *bani-* 'be (of, in water)', *galkirri-* 'fall', *garri-* 'go in, enter', *gukarri-* 'go out hunting', *ŋakirri-* 'cover', *ŋathi-* 'cry, *wandi-* 'run', *buraki-* 'be hurt, wounded', *giritji-* 'play, dance', *gulŋiyi* 'go throuh, enter, be inside', *luka* 'eat, drink, ingest', plus a number of inchoative constructions.
- The second class is described as being the largest, with over four hundred distinct stems. Some examples given include *gurrupa-* 'give', *batha-* 'cook', *bokma-* 'create', *dharaŋa-* 'understand', *dharrpa-* 'hide', *garrpi-* 'tie, bind', *garrmu-* 'try, test, think', *nhuma-* 'smell, sniff', *nhanapa-* 'make, stoke a fire', *bitja-* 'do/be thus', and a number of complex stems including the verbalizing augment *-thu*∼*-tju*, including *wathu-* 'call out to', *barkthu-* 'crack, split', *dhaŋiyu* 'embrace, hug, carry baby in arms', *dhamanytju-* 'grow, get bigger', and *dhalyu-* 'land (of plane, bird)'.
- Examples of stems belonging to the third conjugation are *dharpu-* 'spear', *nha-* 'see', *lupmara-* 'wash', *dalku-* 'harden', *galkitha-* 'make near', *ga-* 'bear, carry', *bela-* 'dig', *larru-* 'look for', *dhadulu-* 'leak', *gunga-* 'block', *ŋurrka-* 'throw', and *ŋayarrka-* 'ask'.
- Two members of the fourth conjugation are given as *bu-* 'hit, strike' and *ŋa-* 'hear, listen', both of which are transitive.
- Djambarrpuyngu is also described as having a 5th set of non-inflecting verbs consisting of loans from Austronesian.

Djapu (Morphy 1983: 62-65) has four conjugations, each of which has between two and four subclasses, which are defined based on differences in patterns of inflection.

The language has one large, mostly intransitive conjugation and three mostly transitive conjugations (one large and two small and with closed membership). As with the rest of the Yolngu languages, phonological properties of the stem are potentially useful for identifying subclasses. A summary of the Djapu inflectional suffixes broken down by conjugation class, with comments on membership, is given in Table 3.18:

CONTENT	Class 1	Class 2	Class 3	Class 4
Unmarked	-*m*(*a*)	-*n*	-(*r*)*n*	-*rr*, ∅
Potential	-*ng*(*u*)	-*rr*	*l*	-*rr*, ∅
Perfective	-*ng*(*al*)	-*r*, -*nan*	-*r*	-*n*
Past (Non-indicative)	-*nha*	-*na*	-*na*	-*nha*, -*ny*
Transitivity	Transitive	Transitive	Transitive	Intransitive

Table 3.18: Inflectional suffixes for four Djapu verb conjugation classes

Morphy also gives membership information for the four conjugation classes as:

- Class 1 has stems *gunga-* ‘shut, block’, *gurruka-* ‘carry, wear’, *ŋurrka-* ‘throw away’, *weka-* ‘give’, *dhiŋga-* ‘die’, *waŋga-* ‘go, come’, *gaa-* ‘carry, bring, take’, *nhaa-* ‘see, look’, *mo-* ‘forget’, *dharpu-* ‘pierce’, *bela-* ‘dig’, *galmu-* ‘prevent from doing’, *gawulu-* ‘paddle’, *lukura-* ‘fish’, *guka-* ‘chase’, *lakara-* ‘tell, call’, *larru-* ‘seek’, *lawu-* ‘bite’, *marra-* ‘fetch, get’, *mengu-* ‘hunt’, *membu-* ‘forget’, *ŋamatna-* ‘do properly’, *ŋarakala-* ‘find’, *dhadalu-* ‘seep, drip’, and *gorru-* ‘be in/on’.

- Class 2 has transitive and ditransitive stems *dharaŋa-* ‘recognize, understand’, *ŋayatha-* ‘grab’, *ŋoma-* ‘knead’, *nherra-* ‘put down’, *garrpi-* ‘bind, block up’, *gurrupa-* ‘give’, *gatha-* ‘give’, and intransitive *garrtha-* ‘get caught/stuck’.

- Membership in Class 3 is given as intransitive *diltha-* ‘sting, heal’, *litha-* ‘get dry/warm’, *ŋutha-* ‘grow’, semitransitive *galku-* ‘wait’, and transitive *batha-* ‘cook, burn’, *bokma-* ‘create’, *galka-* ‘put into’, *gana-* ‘leave’, *gurrunha-* ‘lay down', *lirrtha-* 'roast in ashes', *manapa-* 'join', *ŋilitja-* 'put into', and *ŋupa-* 'chase, follow'.

- The fourth conjugation class contains mostly intransitives, including *waŋa-* 'talk, say', *nhara-* 'burn', *dharra-* 'be standing', *gora-* 'be ashamed', *nhina-* 'sit', *ŋorra-* 'lie', *walma-* 'exit', *yukurra-* 'sleep', *guyaŋa-* 'think', *garri-* 'enter', *marrtji-* 'go, come', *buaki-* 'be hurt', *ŋathi-* 'cry', *galki-* 'fall over', *wandi-* 'run', plus transitives *buna-* 'arrive', *luka-* 'ingest', *mulka-* 'hold', *manaŋi-* 'steal', and *guyaŋi-* 'think'.

3.2.14 Tangkic

Ganggalida (Keen 1983: 224)[17] is described as having two conjugation classes in the verbal system, one is mostly transitive and the other is mostly intransitive. These classes are identifiable via the shape of certain suffixes in the imperative and desiderative mood forms. Forms of the transitive *kuri-* 'see' and intransitive *wara-* 'walk' are given as exemplars of the two conjugations:

Mood	Content	Class 1	Class 2
Indicative	realis	kuritya	waratya
Imperative	realis	kurika	waratya
	irrealis	kuriki	waratyi
Desiderative	realis	kurita	waratyulu
	irrealis	kurita	warata

Table 3.19: Form paradigms for two Ganggalida verbs belonging to distinct conjugation classes

Thus we see maximally distinct realis imperative forms between the conjugations,

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[17] Keen's description uses the name 'Yukulta' for the language; Harvey (2009: 198) notes that Ganggalida is the appropriate name.

with Class 1 taking *-ka* and Class 2 *-tya*. The irrealis imperative (i.e., hortative) and realis desiderative (expressing intent) suffixes are also distinct, while the realis indicative and irrealis desiderative (expressing desire) suffixes are syncretic across the classes.

It is important to note that the Tangkic languages are not always classified as belonging to Pama-Nyungan. Inclusion of Ganggalida in the current study is motivated by the findings of previous phylogenetic studies of the Australian languages. Bouckaert, Bowern & Atkinson (2018) initially included Tangkic as an outgroup (i.e., outside Pama-Nyungan) in order to test specific assumptions about the higher-level structure of Pama-Nyungan, but ultimately found evidence against it being an outgroup. Consideration of Tangkic as belonging to the Pama-Nyungan family additionally has consequences for the higher-level structure of the tree. Ultimately, Ganggalida was included in this survey based on the Bouckaert, Bowern & Atkinson findings, but continued research is needed in order to confirm or deny Tangkic's membership in Pama-Nyungan with more certainty.

3.2.15 Waka-Kabic

Gooreng Gooreng (Brasch 1975: 45-50) has two conjugation classes, whose membership aligns with transitivity in much the same way as other Pama-Nyungan languages with two verb classes. Specifically, one class contains almost exclusively transitive verbs, while the other has mostly intransitives. Brasch gives a breakdown of conjugation class membership for a small set of verbs in terms of final segment of the stems and how many syllables they contain. This does not allow a straightforward analysis of phonology influencing conjugation class membership, though it is notable that the mostly transitive conjugation only contains vowel-final stems, while the mostly intransitive conjugation has a small set of consonant-final stems. Inflectional suffixes for the two conjugations are given in Table 3.20:

Content	G	L
Present	*-gim*	*-lim*
Past	*-min*	*-nmin*
Imperative	*-ga*	*-la*
Purposive	*-gu*	*-lu*

Table 3.20: Inflectional suffixes for Gooreng Gooreng verb conjugation classes

Brasch (1975: 46-47) describes the conjugation class membership of a small set of stems, including G-conjugation *nya-* 'see', *yan-* 'go', *bum-* 'hit', *wege-*∼*bege-* 'hunt/fight', *balba-* 'stand', *nyina-* 'sit', and L-conjugation *yaa-* 'speak', *waba-* 'come', *gawa-* 'cut', *bagi-* 'kill', and *yaŋga-* 'make'.

Batyala (Bell 2003: 92-93) has three verb conjugation classes, two of which can be further divided into subclasses based on minor inflectional differences. In general, secondary subclasses each contain a single member, which acts as a semi-irregular member of the larger class. Correlation between conjugation class membership and transitivity is unconvincing in Batyala; the first and third conjugations are equally split between transitive and intransitive members, while the second conjugation is mostly transitive. In terms of phonological properties of the stem, disyllabic stems are spread across the three conjugation classes, while the first conjugation has the only monosyllabic and trisyllabic stems. Stem-final segment is also far from informative; the one attested /u/-final stem is in the first conjugation, while stems ending in both /a/ and /i/ are found in both the first and second conjugation. The third conjugation is made up of a small number of /a/-final stems. Ultimately, Batyala was coded as uninformative for correlation between either transitivity or phonology and conjugation class membership. Table 3.21 summarizes the inflectional suffixes for each major conjugation class:[18]

CONTENT	Class 1	Class 2	Class 3
Present	*-m*	*-n*	*-m*
Past	*-mi*	*-mi*	*-mi*
Imperative	∅	*V:*	*-y*
Purposive	*-ngu*	*-ngu*	*-ngu*

Table 3.21: Inflectional suffixes for Batyala verb conjugation classes

Matching any of the Batyala conjugation classes to those of Gooreng Gooreng is not straightforward, as the suffixes realizing a given morphosyntactic property are often phonologically distinct from either Gooreng Gooreng conjugation and/or syncretic across all three Batyala conjugations.

Bell (2003: 94-96) provides the following examples of verbs from each of the three Batyala conjugation classes:

- Conjugation 1 has intransitive stems *balu* 'die', *bayari* 'bring', *budara* 'blow', *baya*∼*baga* 'come', *wudi* 'be afraid', *wuli* 'swim', *yunma* 'sleep, lie down', and transitive stems *bayi* 'hit, kill, bite', *binda* 'send, let go', *daba* 'sing', *gaya* 'bite', *marba* 'cook', *wanda* 'climb', and *yaŋa* 'make'.

- Conjugation 2 has transitive stems *bawa* 'spear, beat with a spear', *bunjba* 'hit with an instrument', *dama* 'catch, take hold', *gamŋa* 'give, fetch', *nanmi* 'ask, question', *margi* 'burn, light a fire', plus intransitive *bumi* 'fall'.

- The third conjugation has three transitive stems *numba* 'show', *wagaara* 'hunt', *wuna* 'leave', and three intransitive stems *baba* 'stand', *nina* 'sit, stay, live', and *bara* 'be mad'.

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[18] *V:* indicates lengthening of the stem-final vowel, rather than suffixation.

3.2.16 Gumbaynggiric

Eades (1979: 297) finds that Gumbaynggir verbs take a single set of inflectional suffixes, indicating a lack of verb conjugation classes in the language. This contrasts with Yaygirr (Crowley 1979: 377), which has two conjugations. Crowley notes that comprehensive membership in these two classes was unknown at the time of description, and that one conjugation has a nasal or /y/ between the stem and inflectional suffix in some cells of the paradigm, while the other class does not have any overt marker (i.e., zero-marking).

3.3 Grammatical characters and coding

Ancestral state reconstruction, like other linguistic phylogenetic endeavors, involves inferring unknown properties of an older stage of the linguistic system being investigated based on known properties of the modern languages. To this end, each of the 111 surveyed Pama-Nyungan languages was coded for a number of grammatical features. In practice, this involves isolating a specific grammatical feature and devising a compact, abstract schema for representing both the typological profile of each individual language and the patterns or generalizations that exist across the sample. Characters in linguistic phylogenetics can vary along (at least) two major dimensions or categories – discrete vs. continuous and binary vs. multistate. The current study makes use of discrete characters of both the binary and multistate varieties.

First, Each language in the sample was coded based on whether it has two or more distinct conjugation classes or a single set of non-alternating inflectional suffixes. It is widely assumed that conjugation classes were a feature of the ancestor(s) of the modern Pama-Nyungan languages at some point in the past and that these were subsequently lost either partially or entirely in the case of modern languages that lack conjugations. This character allows us to explore these predictions and also to determine at what stage of development verb classes were likely to have been lost. This character is discrete and binary, representing the presence (1) or absence (0) of verb conjugation classes in a given language.

Next, languages were coded for number of distinct verb classes. This is a discrete, multistate character, with integer values representing the number of conjugation classes in a given language based on its description. Languages without conjugation classes were coded as 0, while languages with four or more conjugation classes were coded as 4. Note that while some grammars distinguish certain verb classes with one or two members, the current study does not count classes that contain a single stem or two stems when the given inflectional endings do not provide clear evidence of shared patterns of exponence. Identification of these small sets of verbs as distinct classes is generally based on comparative data and reconstructions, as they likely represent the remnants of older classes that have all but been lost. In practice, this decision affected a minimal set of languages, and is unlikely to influence model results. Kugu-Nganhcara (Smith & Johnson 2010) was coded as having three conjugation classes, excluding a fourth conjugation with a single member, while Guugu Yimidhirr's (Haviland 1979) monosyllabic verbs with nonpast *-maa* and *-naa* were also excluded as forming a conjugation class based on a lack of coherent inflectional patterns among the listed forms. As discussed in §1.1.2, Haviland (1979: 85) found that these irregular forms were being included in existing conjugation classes based on elicitation data, further providing evidence against considering them part of a separate class. Conversely, Muruwari is described (Oates 1988) as lacking conjugation classes, but further inspection allows one to make a strong case for there being four conjugation classes in the language which pattern with those found in closely-related languages. In all other cases, languages were coded in agreement with description and analysis in the literature.

Inclusion of this character is important in examining the nature of the historical development of conjugation classes. Moreover, we can evaluate the assumption that verb classes can only be lost and not gained or innovated. However, it should be noted that the estimation methods will consider the number of conjugation classes from the maximally stratified language in the data as an upper bound. In other words, it is not possible to infer a transition to a state with more conjugation classes than are present in any of the languages under consideration. This contradicts a faithful interpretation of Dixon's reconstructions, which predict a maximal set of conjugation classes in the proto-language based on the principle that observation of an existing distinction reflects its original presence. In Chapter 4, I further evaluate the possibility of reconstructing a larger set of conjugation classes for the root node, including a randomization model that assigns probability weight to larger conjugation class inventories.

Languages were also coded based on the patterns that exist in the membership of different conjugation classes. We see from descriptions that for a large number of Pama-Nyungan languages, verb classes consist of mostly intransitive or transitive roots, although it is rare to find a conjugation that contains only intransitive or transitive members. In other languages, membership appears to be divided along phonological properties of the stems themselves. In some, the final segment of the stem is an indicator of conjugation class membership, while the more common situation is to separate disyllabic from mono- and trisyllabic stems in the formation of conjugation classes. In several languages that contain three or more conjugation classes, we observe a combination of these two strategies, whereby both transitivity and phonology play a role in determining class membership. This often consists of two conjugations for disyllabic stems, one transitive and one intransitive, with one or more additional conjugations for stems with one or three syllables. In systems with four or more conjugations, these additional classes continue the transitivity distinction as well.

It should also be noted that a lack of reliable data or description for a small subset of the language sample leads to an inability to make a cogent claim about some or all of the verb conjugation class typology of a given language. These languages are coded '-', indicating that they are uninformative for the relevant character. The full set of grammatical characters and their permissible values are summarized in Table 3.22:[19]

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[19] A full list of the sampled languages, character coding, and sources is given in the Appendix.

No.	Character	Type	Permissible Values
C1	Conjugation classes	Discrete, Binary	0 (Absence) 1 (Presence) – (Unclear, No data)
C2	Number of classes	Discrete, Multistate	0 (Single set of affixes) 2 (Two conjugation classes) 3 (Three conjugation classes) 4 (Four+ conjugation classes) – (Unclear, No data)
C3a	Valence-based membership	Discrete, Binary	0 (absence) 1 (Presence) – (Unclear, No data)
C3b	Phonology-based membership	Discrete, Binary	0 (absence) 1 (Presence) – (Unclear, No data)

Table 3.22: Grammatical characters for Pama-Nyungan verb conjugation classes

Figure 3.3 provides a visualization of the distribution of languages with respect to Character 1 in terms of their geographical location:

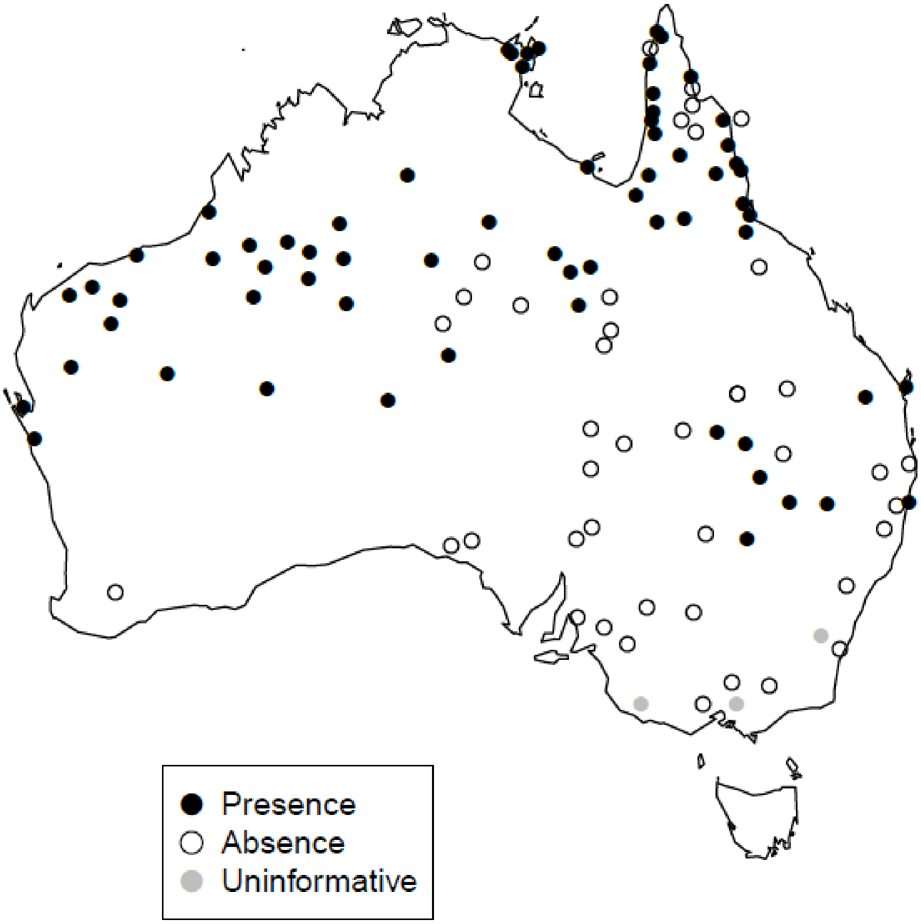

Figure 3.3: Geographical distribution of Character 1 (presence and absence of conjugation classes)

Figure 3.4 indicates the phylogenetic distribution of the character:

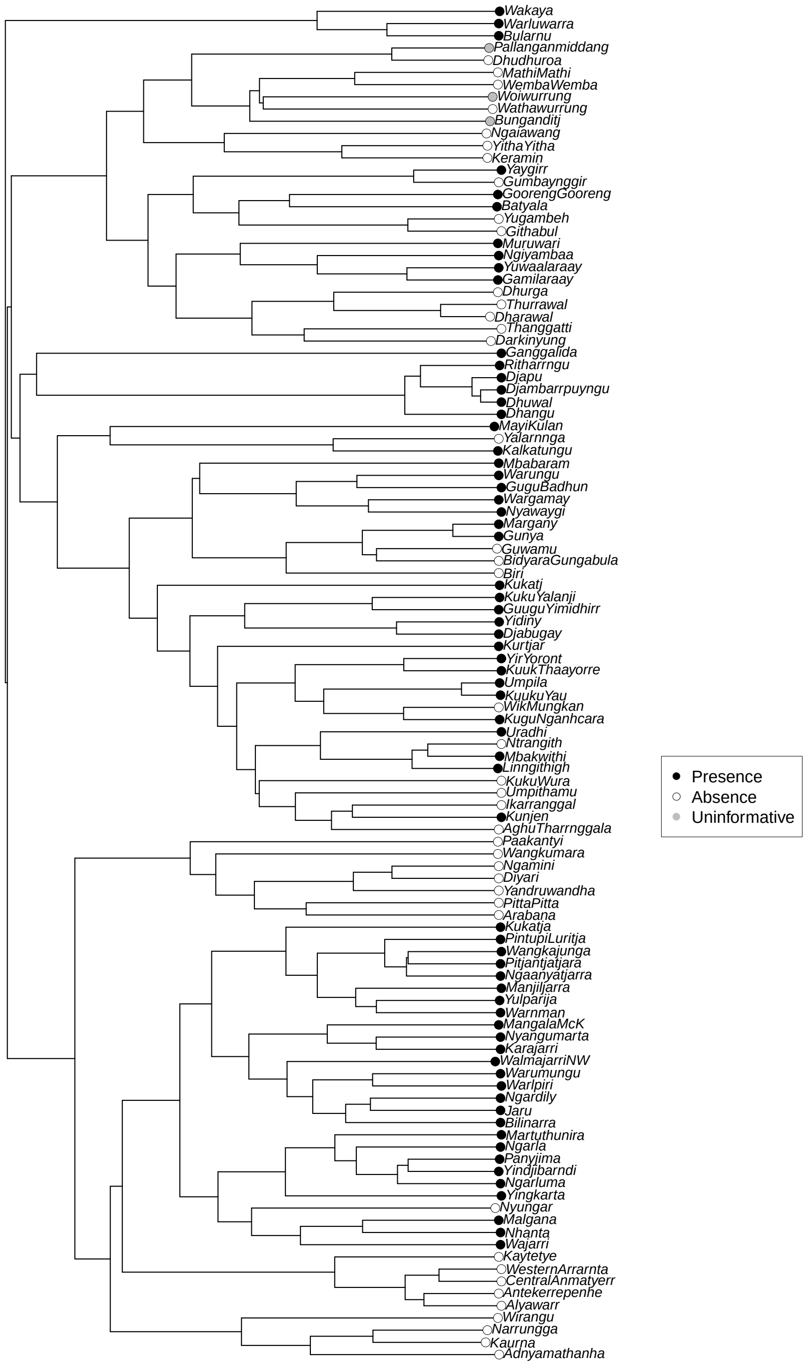

Figure 3.4: Phylogenetic distribution of Character 1 (presence and absence of conjugation classes)

Figure 3.5 projects the phylogenetic distribution of Character 1 onto the map:

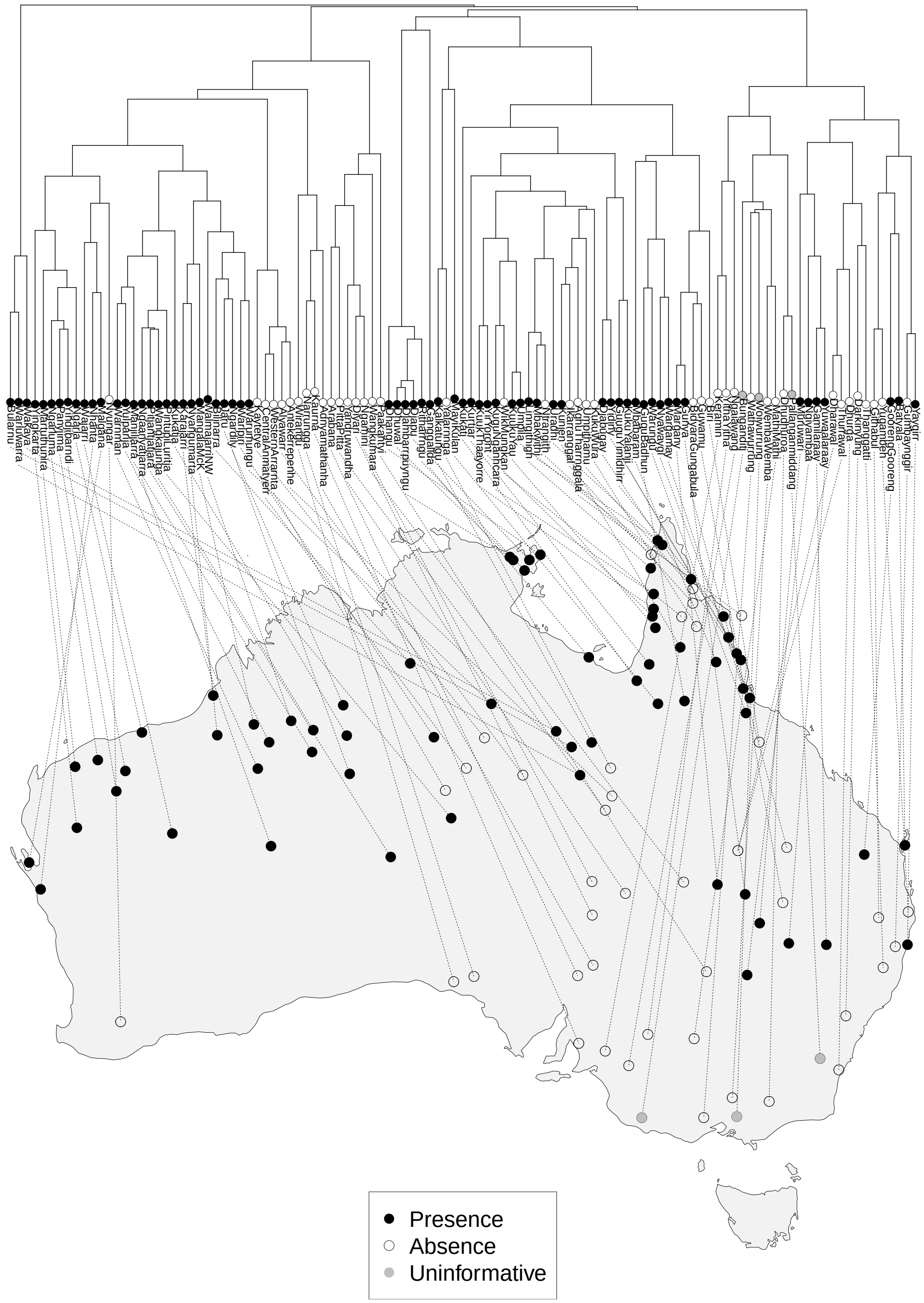

Figure 3.5: Combined geographical and phylogenetic distribution of Character 1 (presence and absence of conjugation classes)

From Figures 3.3 and 3.5, note the existence of a geographical pattern of distribution wherein the presence of verb conjugations is a defining feature of the languages of the eastern, central, and northern portions of the Pama-Nyungan language area, with an additonal pocket in the southeastern part of the continent. Languages lacking verb conjugations are mostly found in the southeastern quadrant of the continent, although they additionally stretch north into central Australia as well. Moreover, note that (Figures 3.4 and 3.5) there is relative homogeneity among the various subgroups that make up the larger phylogeny with respect to Character 1. Presence of conjugation classes is a defining feature for example of the Wati, Yolngu, and Ngayarta subgroups. Conversely, the Thura-Yura, Karnic, Arandic, and Yuin Kuri, among others, all lack verb conjugations entirely.

Next, consider Figures 3.6 and 3.7, which plot the geographical and phylogenetic distribution of Character 2 (number of conjugation classes), respectively:

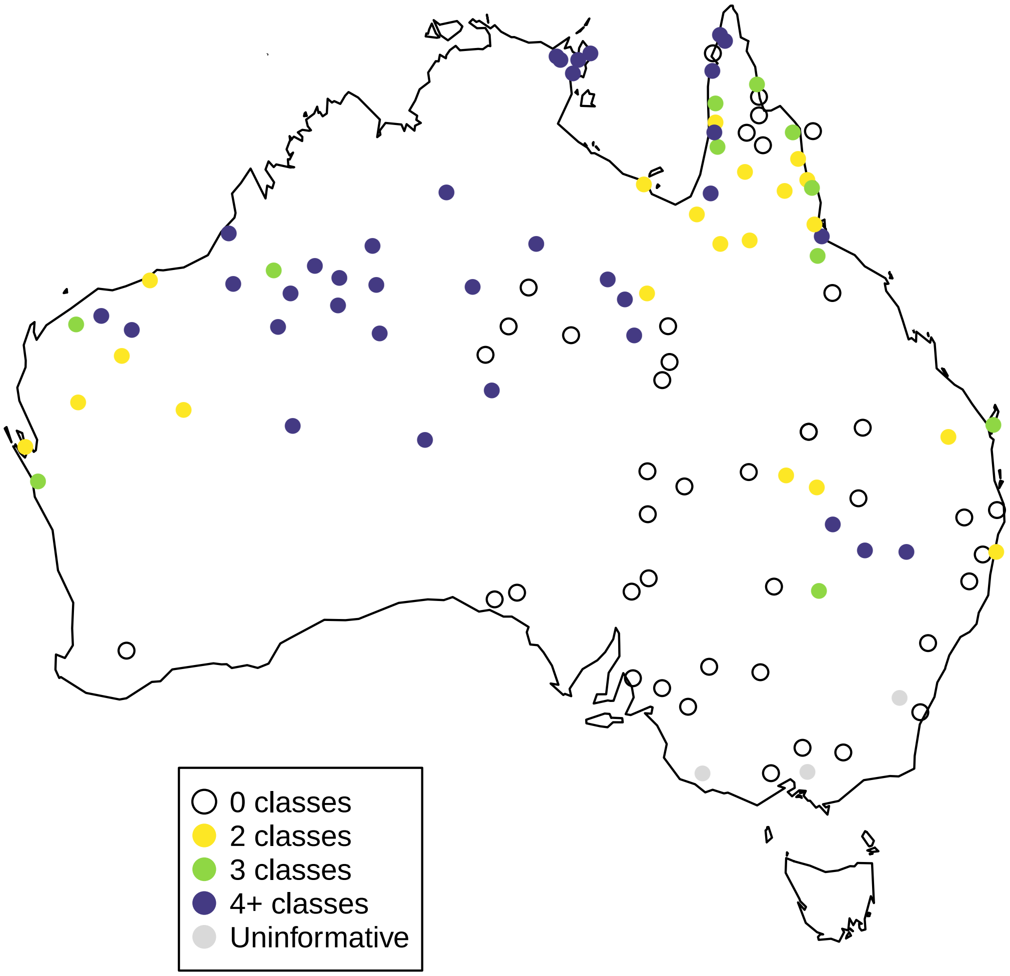

Figure 3.6: Geographical distribution of Character 2 (number of verb conjugation classes)

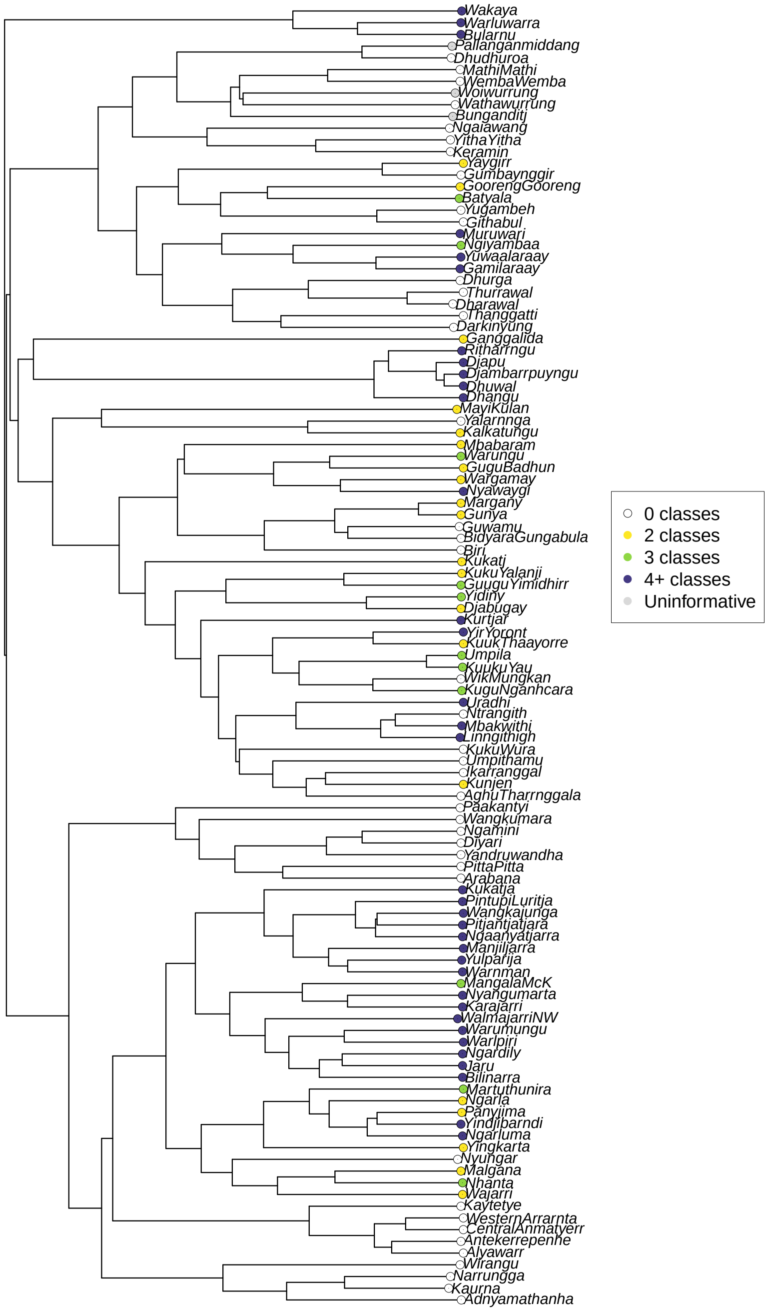

Figure 3.7: Phylogenetic distribution of Character 2 (number of verb conjugation classes)

Note (Figure 3.6) that while we see more diversification among the Pama-Nyungan languages in terms of how many verb conjugation classes they contain, a number of geographic patterns are observable. Beyond the languages that lack verb conjugations in the southeastern part of the continent, we find a large concentration of languages with four or more conjugations in central and western Australia, as well as along the northern coastal regions. Languages with two and three conjugations typically found in northeastern Australia, as well as in the extreme western regions. In Figure 3.7, we again see a relatively high degree of similarity between languages that share close genetic affiliation, although many subgroups are notably more heterogeneous with respect to Character 2 as compared with Character 1. The Yolngu, Wati, and Warluwaric languages in the sample feature exuberant verb class systems with four or more classes distinguished. Members of the Pama and Maric macro-groups show a good deal of variation with respect to number of verb conjugations.

Figures 3.8 and 3.9 show the geographic and phylogenetic distribution for Character 3, which describes observable patterns in conjugation class membership:[20]

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[20] Characters 3a and 3b (See Table 3.1) are combined for the purposes of the map and tree shown in Figures 3.8 and 3.9.

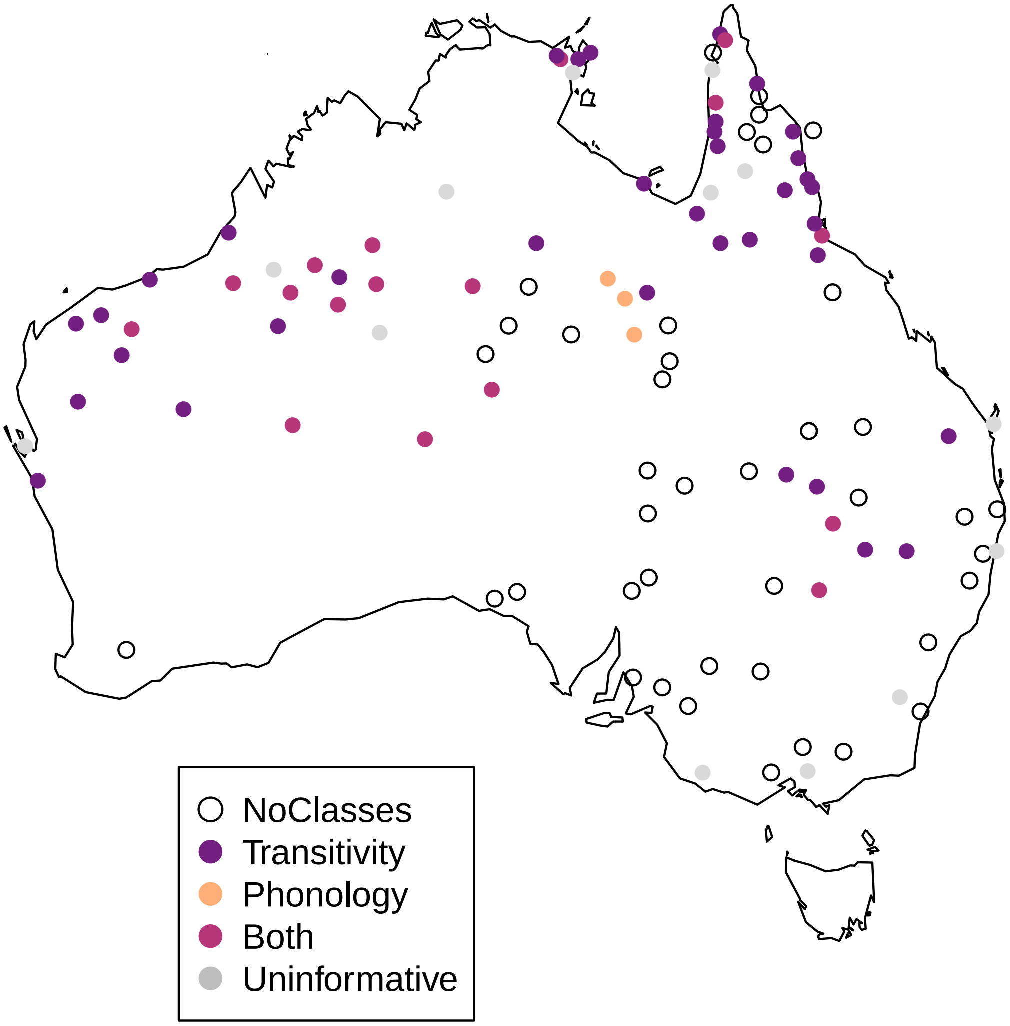

Figure 3.8: **Geographical distribution of Character 3 (conjugation class membership type)**

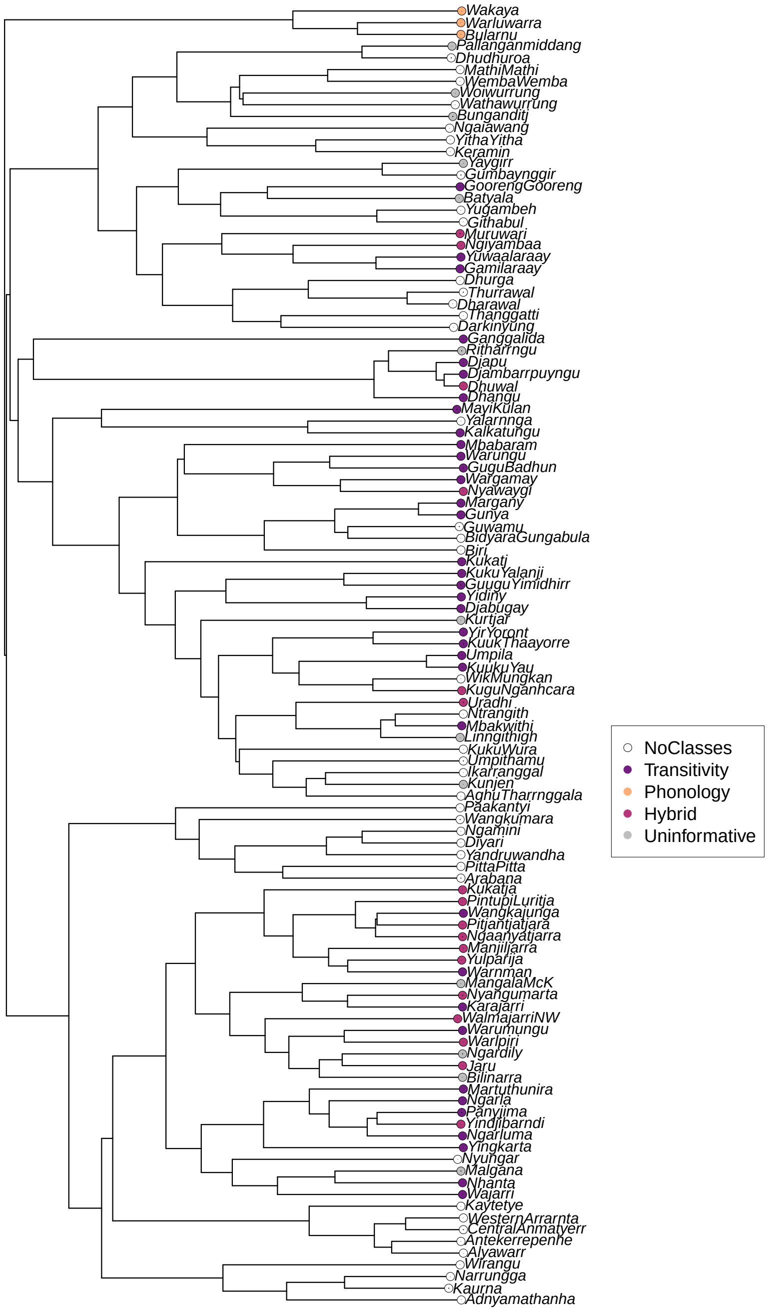

Figure 3.9: Phylogenetic distribution of Character 3 (conjugation class membership type)

Conjugation class systems where membership appears to be determined by verb valence are found across the perimeter of Australia, with pockets in the western, southeastern, and northern coastal regions. Languages of this type often minimally show evidence of two conjugation classes, allowing separation of transitive and intransitive stems into separate classes. A small number of languages in the central region show evidence of phonology-based class membership. In these languages, classes often consist of more or less equal numbers of transitive and intransitive verbs, instead grouping verbs based on phonological properties of the stem such as the final segment or number of syllables it contains. A large concentration of languages in central and eastern Australia determine class membership using both verb valence and phonological properties of the stem. In these systems, usually consisting of four or more conjugation classes, verbs are generally distributed into classes based on transitivity and the number of syllables in the stem. Thus a language of this type may contain a single class for intransitives and two transitive classes, one for disyllabic stems and the other for mono- and trisyllabic stems. In Figure 3.9, note that the Warluwaric languages employ a phonological basis for determining conjugation class memberhsip. Many Pama and Maric languages divide stems into classes based on verb valence, though there are some exceptions to this. Hybrid systems are found across the Wati subgroup.

Additional patterns emerge when observing the relationship between the number of conjugation classes a language contains and the way class membership is determined. Hybrid and phonology-based systems usually contain four or more conjugations, though there are exceptions. There is more variation in the number of conjugations in transitivity-based systems, although the number tends to be lower, often two. One possible interpretation of this is that maintenance of the transitivity distinction comes at the cost of preserving the phonological basis for sustaining a larger number of conjugation classes. This is in line with the aforementioned observation by Haviland (1979) that Guugu Yimidhirr speakers were actively recategorizing verbs from smaller conjugations into the larger ones on the basis of verb valence.

This chapter has provided a typological survey of the verb conjugation class systems of the sampled Pama-Nyungan languages, including a discussion of the influence of verb conjugation class membership on the patterns of inflection for various language subgroups, as well as coding decisions and the geographical and phylogenetic distribution of the coded verb conjugation class features. This data forms the observed profile of the modern Pama-Nyungan verb conjugation class apparatus, which is subsequently used as input to ancestral state reconstruction models. We next turn to the results of stochastic reconstruction of the verb conjugation class system in the evolutionary history of Pama-Nyungan.

Chapter 4

Ancestral state reconstruction

This chapter details results of ancestral state reconstruction for the aforementioned grammatical characters under investigation, namely the presence and/or absence of conjugation classes in the prehistory of Pama-Nyungan, the number of distinct conjugation classes, and what factors (i.e., valence, phonology) determined conjugation class membership.

4.1 Phylogenetic signal

Calculation of of the phylogenetic signal in the data with respect to a phylogeny is a necessary preliminary step in sound ancestral state reconstruction analyses. We want to be sure that the distribution of observed character states sufficiently resembles the result of an evolutionary mechanism, rather than randomness or areal diffusion due to intensive language contact. §2.3.2 provided a detailed overview of the methods of calculating phylogenetic signal employed here. This section outlines the evidence for phylogenetic signal for each of the morphological characters under consideration. The pruned consensus tree (Figure 3.1) is taken as the reference phylogeny upon which phylogenetic signal is evaluated for each of the following tests.[1] For each character, uninformative languages were necessarily omitted from the relevant test.

Recall that for binary data, Fritz & Purvis' (2010) D statistic evaluates of the strength of phylogenetic signal for binary traits by comparing the distribution of character states to two null hypotheses; 1) Brownian motion and 2) randomly distributed character states. D statistic values are interpreted along a continuum; values at or near 0 resemble Brownian motion, while values near 1 are correlated with random distribution. Moreover, negative values of D indicate a highly clumped or conserved trait, while overdispersed (i.e., well above chance variation) traits lead to D values above 1.

Figure 4.1 visualizes the observed sum of changes compared with the density of the sum of changes for the two null hypotheses used in the D statistic calculation for evidence of phylogenetic signal in the Character 1 data, while Table 4.1 summarizes the results of the D statistic computation for this character:

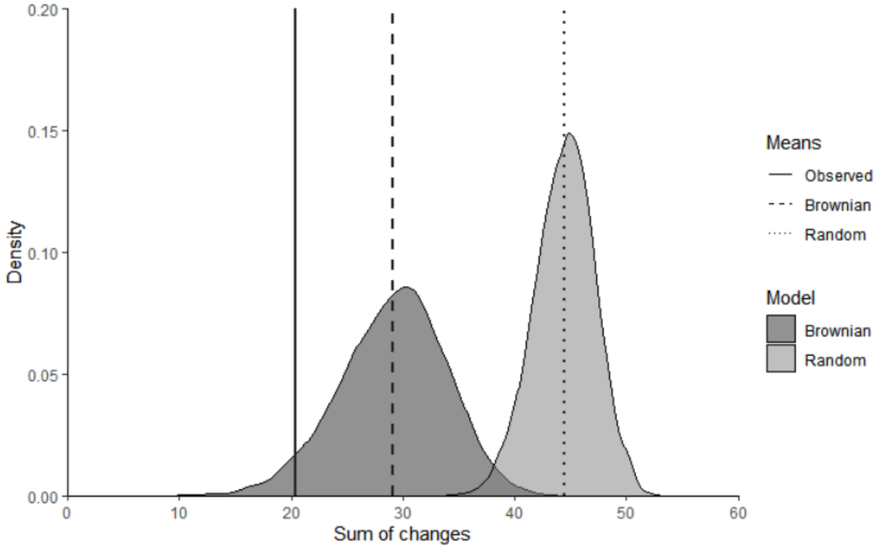

Figure 4.1: Density plot for sum of changes for observed, Brownian, and random distributions of presence/absence data

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[1] Phylogenetic signal changes as the tree topology chases. In Chapter 6, we look at the strength of phylogenetic signal for morphological characters assuming alternate tree topologies as a possible diagnostic for resolving uncertainty in the most representative tree structure.

Δ_{Obs}	Mean $\Delta_{Brownian}$	Mean Δ_{random}	D statistic	P(0)	P(1)
20.41	29.11	44.44	**-0.56**	0.96	0.0

Table 4.1: *D* statistic test results for presence/absence of verb conjugation classes

Figure 4.1 plots the relevant sum of changes values used in the D statistic calculation for the observed (solid line) presence/absence feature alongside the distribution of results for 10,000 simulations each of the Brownian motion (dashed line indicates mean) and random (dotted line indicates mean) models. Note that the sum of changes for the observed data is within the Brownian simulation distribution, but well below the mean, and well outside the random simulation distribution. P(0) is the probability that the observed data evolved on the given phylogeny due to a process resembling Brownian motion, with a value near 1 indicating a strong likelihood for this hypothesis. D value for the observed data (Table 4.1) is $D = -0.56$; recall that a value below zero indicates a trait that is more conserved than would be expected under Brownian evolution and strong evidence of phylogenetic signal.

The third morphological character included in the present study concerns the general observable pattern with which verb roots are divided among conjugation classes. Phylogenetic signal for this character is calculated by binarizing the subcomponents as presence (1) or absence (0) of valence-based or phonology-based conjugation class membership for each language in the sample. Each of these subcomponents is tested for phylogenetic signal using the D statistic method. Figures 4.2-4.3 and Tables 4.2-4.3 summarize the results:

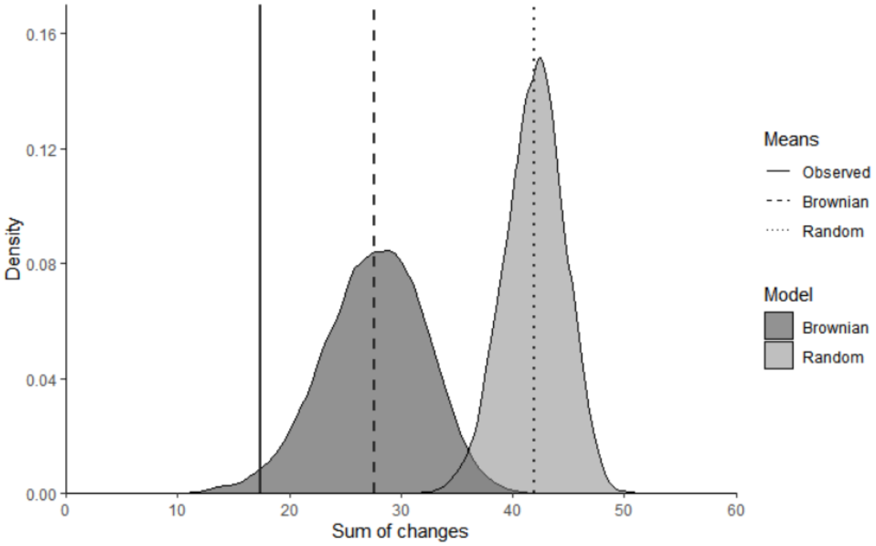

Figure 4.2: Density plot for sum of changes for observed, Brownian, and random distributions of valence-based class membership data

$\Delta_{Observed}$	Mean $\Delta_{Brownian}$	Mean Δ_{random}	D statistic	P(0)	P(1)
17.4	27.6	41.94	**-0.71**	0.98	0.0

Table 4.2: *D* statistic test results for valence-based class membership

With respect to the presence or absence of valence-based conjugation class membership, we again find strong evidence of phylogenetic signal in the data. This is evidenced by a value of $D = -0.71$ (Table 4.2). Recall that the second null hypothesis P(1) is that the observed data is equivalent to randomly assigning character states, a P(1) of 0 provides further evidence of the strong phylogenetic signal in the data.

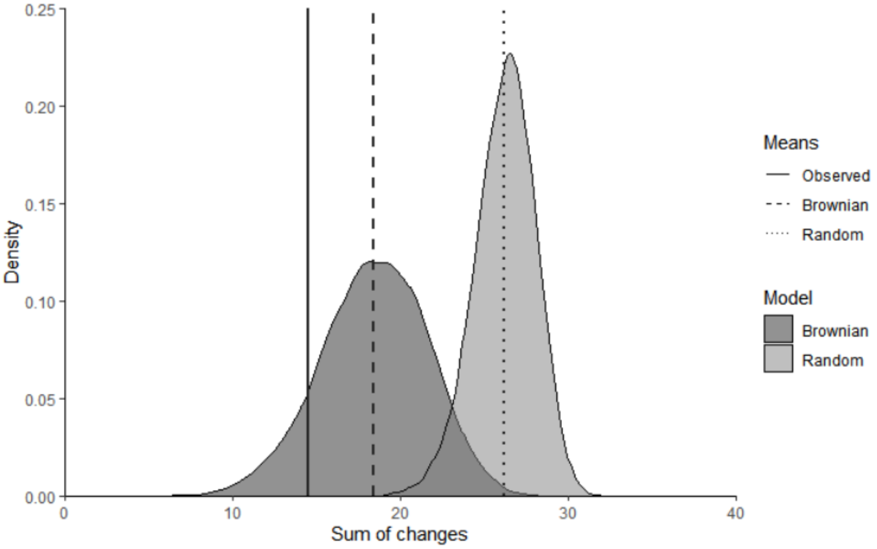

Figure 4.3: Density plot for sum of changes for observed, Brownian, and random distributions of phonology-based class membership data

$\Delta_{Observed}$	Mean $\Delta_{Brownian}$	Mean Δ_{random}	D statistic	P(0)	P(1)
14.5	18.43	26.22	**-0.5**	0.89	0.0

Table 4.3: *D* statistic test results for phonology-based class membership

Results of the D statistic test for the presence or absence of phonology-based conjugation class membership is seen in Figure 4.3 and Table 4.3. Note that while the signal is somewhat less strong than that seen in the previous two traits (see Figures 4.1 and 4.2 and Tables 4.1 and 4.2), a value of $D = -0.5$ does indicate strong evidence of phylogenetic signal.

For the multistate Character 2 (number of conjugation classes), Blomberg, Garland & Ives (2003) randomization test and accompanying metric K provide a useful measure of phylogenetic signal. Recall from §2.3.2 that like Fritz & Purvis' D testing method, the K randomization test involves comparing the fit of the phylogeny to the observed data with the fit to randomly permuted data. A significant difference between the fit to the observed and random data is taken to be evidence of phylogenetic signal. The metric K quantifies the strength of the signal in the observed data as being proportional to the signal in the expected data assuming a Brownian model. A value of K near 0 indicates weak or no signal, while a value above 1 indicates the trait is more conserved than expected under the Brownian model and that the phylogenetic signal in the data is strong. Computation of Blomberg's randomization test and K statistic was performed using the `picante` package in R (Kembel et al. 2010). Results are given in Table 4.4:

K	Variance$_{Obs}$	Mean Variance$_{rdm}$	P-value	Z-score
1.07	0.00054	0.0017	0.0001	-6.157

Table 4.4: K test of phylogenetic signal in number of conjugation classes data

For the number of conjugation classes data (Table 4.4), the K value for phylogenetic signal is $K = 1.07$ indicating strong evidence of phylogenetic signal. Moreover, the observed variance was significantly higher than that of the mean variance over 10,000 iterations of the random simulation model, which randomly distributes character states at the tips of the tree ($p = 0.0001, Z = -6.157$). We can visualize the distribution of K statistic values for the randomization test relative to the observed K:

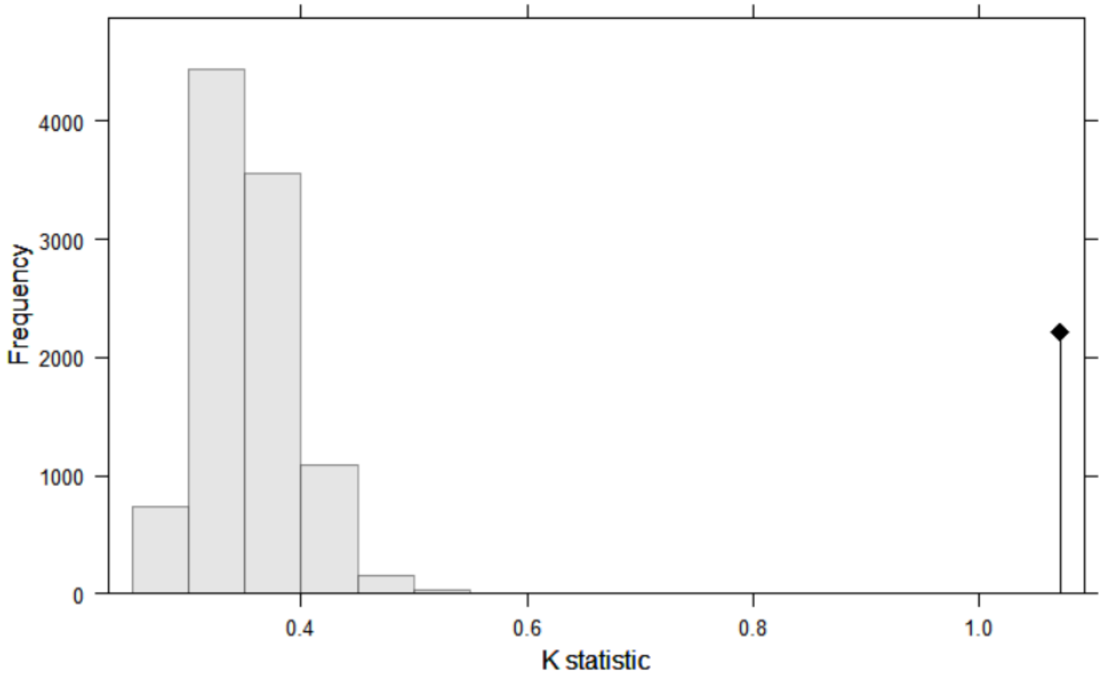

Figure 4.4: Density plot of K for observed data and randomization test

Having demonstrated appreciable evidence of phylogenetic signal across each of the morphological traits under consideration, the rest of this chapter presents the results of ancestral character estimation modeling, with attention to reconstruction at the root node of the Pama-Nyungan phylogeny.

4.2 Ancestral state reconstruction: Model setup and comparison

We can think of ancestral state reconstruction as finding the most probable value for some property for some most recent common ancestor(s) in the tree. Given the observed states of the modern languages and their genetic affiliation, and assuming some nonzero rate of language change, we want to infer backwards along the tree. Returning to the grammatical characters outlined in Chapter 3, 111 Pama-Nyungan languages were coded for presence/absence of conjugation classes. The coded data was then used as input to Pagel & Meade's (2004) ancestral state reconstruction algorithm using the BayesTraits (version 3.0.1) software package. As noted in Chapter 2, this method estimates the rates of transition between character states based on the character data and genetic relationships in the tree in order to determine the probability of each possible state value at a given unknown node in the tree. This method can then be used to reconstruct the value of the root node, which represents the common ancestor of all languages under consideration, as well as any intermediate nodes in the phylogeny. Moreover, Pagel & Meade's method allows tree topology to be a parameter of the model in the form of the use of a set of trees, rather than a single tree. Given a set of trees, a single tree is sampled at each iteration of the model. To this end, models discussed in this chapter were evaluated over a set of 4058 possible Pama-Nyungan phylogenies generated via previous tree inference modeling using lexical cognate data (Bowern & Atkinson 2012; Bouckaert, Bowern & Atkinson 2018), each of which was pruned to include only languages included in the current sample.

4.2.1 Model setup

Reconstructions make use of the multistate Markov chain Monte Carlo model for discrete character traits in BayesTraits, with model runs consisting of 55,000,000 iterations (with 5,000,000 iterations discarded as burn in to allow the chain to begin mixing before observing it) to ensure ample mixing of the Markov chain. While discussion in Meade & Pagel (2019) indicates that 5,000,000 is a relatively large number of burn in iterations, the highly conserved nature of the data combined with relatively low time cost for performing model runs due to a small number of taxa (languages) allows us to err on the side of caution with the burn in phase of the simulation.

Because the Pagel & Meade (2004) method is based on inference of state transition parameters, it is important to set appropriate prior distributions on those transition rates, in order to efficiently constrain the model to searching within useful partitions of the parameter space. BayesTraits allows an optimization method for determining suitable prior values for rate parameters. This involves the use of a hyperprior, which is itself a distribution from which values are selected to inform the prior distributions for the rate parameters of the model. Ultimately, results were consistent across a wide range of values for rate priors for the presence/absence trait. For each of the morphological characters under consideration, comparison of multiple models is provided, with each model representing a distinct hypothesis about the nature of the evolution of a given character. The set of models under consideration for each character includes a baseline model in which no restrictions are placed on the state to state transition rate parameters, as well as various models with specific rate restrictions. Results presented are mean values over five independent model runs. Specific models will be discussed in the relevant section for each character.

4.2.2 Convergence diagnostics

Before turning to the results of the ancestral state reconstruction itself, note that there are several metrics for observing the validity of MCMC model runs in order to determine if the Markov chain shows sufficient variation between observations to be said to have fully sampled from the posterior distribution. If the observed parameter values do not show variation, then there is a high degree of correlation between samples, which generally results from poor phylogenetic signal and/or poor parameter initialization. In other words, we want to see that the chosen parameter settings and length of the Markov chain (i.e., number of iterations, burn in, frequency and quantity of samples) allow the hypothesis space to be fully explored, rather than settling on the locally maximal outcome based on samples drawn from a narrow and/or poorly chosen slice of possible values. One particularly clear way to visualize mixing of the Markov chain is by plotting the observed estimated parameter values at each sample via trace plot. Traces of the two transition rates from the unrestricted model of the presence/absence character illustrate the utility of these visualizations:

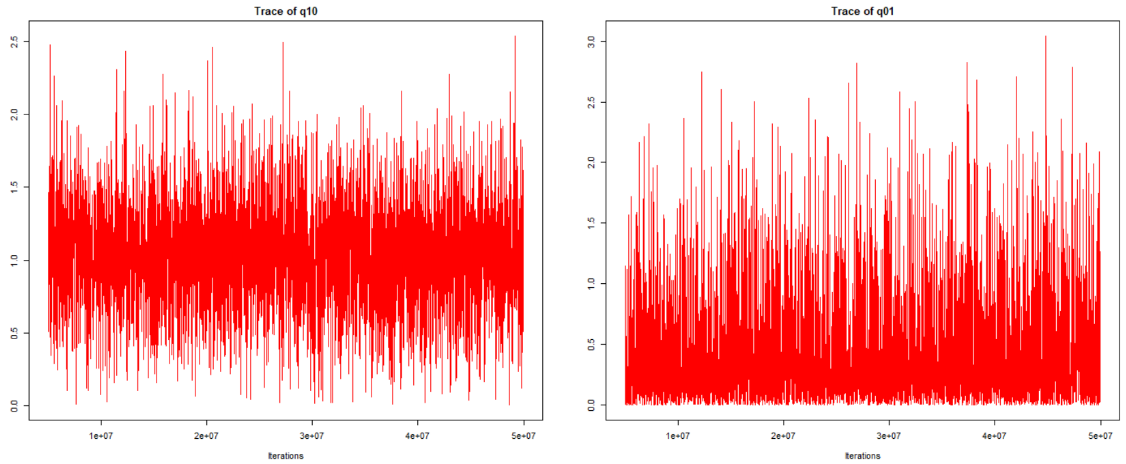

Figure 4.5: Trace plots as a diagnostic of model validity

Trace plots provide a useful visualization of the variance found in the output of a model run. The trace of q10 (Figure 4.5, left plot), representing loss of conjugation classes, demonstrates good mixing of the model chain. Note the variance on both sides of the dense mean. The trace of q01 (Figure 4.5, rightplot) shows variance above the mean value across the sample, while the variance below is truncated as it nears zero (negative transition rate values are impermissible in the model).

A sufficiently mixed chain will show a ‘spiky’ shape in the trace plot, centered around a dense mean value. For each of the parameters in Figure 4.5, we do in fact see an appreciable degree of variability between samples, indicating low correlation between samples and a well-mixed chain. Note that the trace of q01 (Figure 4.5, right-hand plot) shows truncation below the dense band around the mean as the rate value approaches zero. This is often found in instances where the optimal transition rate value is very small, as negative rate values are not possible. Sampling from a tighter range of values may prevent this truncation in some instances. Each of the models under consideration in the larger study were manually validated for sufficient mixing of the Markov chain via visual inspection of traces and the monitoring of acceptance rates, i.e., the proportion of proposed samples that was accepted during each sampling window.

4.2.3 Visualizing models and estimated rates

One useful way to visualize the relative importance of estimated transition rates is through the use of a directed arrow plot, which maps arrows to state to state transitions. Each of the corners of the plot represent a discrete reconstruction state for both traits of the model, arrows between the states are labeled with the transition rate parameters they indicate.[2]

Relative weighting of the transition rates is indicated by modulating the style and thickness of the individual transition arrows; arrow thickness indicates the prominence of the transition rate, with a thicker arrow indicating a larger estimated rate. Dashed lines may be used to visually minimize very small rates, which are unlikely to have exerted much influence over a given model. Figure 4.6 illustrates the utility of these plots for interpreting a model assuming, where q_{ij} and w_{ij} are the transition parameter and estimated rate for transitions between states i and j, respectively:

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[2] This approach to visualizing models and rate weights is inspired by a similar implementation in the R package *phytools* (Revell 2012).

(a) Two rate model, similar rates **(b)** Two rate model, one large rate

(c) Two rate model, one small rate **(d)** One rate model

Figure 4.6: Anatomy of a directed arrow plot – Directed arrow plots visualize model structure and/or the relative size of estimated transition rates resulting from an ancestral state reconstruction model. Arrows between states indicate direction of permissible transitions. Arrow thickness indicates estimated rate size.

Figure 4.6a depicts an simple model with two states and two permissible transitions with identical line weight, indicating the estimated transition rates were the same or similar to one another. This contrasts with Figure 4.6b, in which w_{ij} is estimated to be higher than w_{ji}, which is represented by the thicker arrow. This result would indicate the transition from i to j being much more common in the model than a transition in the opposite direction. In Figure 4.6c, w_{ij} is estimated to be very small, and likely does not exert much influence over the reconstruction. Finally, Figure 4.6d illustrates a model with a single permissible transition between two states; transitions in the other direction are disallowed (i.e., the rate for this transition is restricted to always be zero).

4.2.4 Model comparison with Bayes Factor

Following common practice for interpreting ancestral state resonstruction results for closed class linguistic systems (e.g., Haynie & Bowern 2016 on color systems; Phillips

& Bowern Forthcoming on ergativity), we can compare the output of Bayesian reconstruction models to discern their relative fit to the data. Model comparison is possible in BayesTraits using a 'Stepping-stone' sampler (Xie et al. 2011), which estimates the log marginal likelihood of a given model, and the Bayes Factor metric (Jeffreys 1935), which serves as evidence for favoring one model over another. In Bayesian phylogenetic modeling, the marginal likelihood quantifies the fit of the model to the data. More specifically, it is the probability of the data given the model, averaged over the permissible parameter search space. In practice, this value is difficult to obtain, as it must be calculated (via integration) over all of the model's parameters. As Oaks et al. (2019: 2) note, avoidance of precise calculation of the marginal likelihood explains much of the dominance of the MCMC algorithm in Bayesian phylogenetics. This is a useful feature of MCMC in making phylogenetic modeling computationally practical, but leaves open the question of comparing different models and thus different hypotheses.

Marginal likelihood estimation

Oaks et al. (2019) provides a useful review of a number of methods that have been proposed for estimating the marginal likelihood, which is summarized here. The first of these methods involves sampling parameter values from either their prior or posterior distributions and calculating the mean likelihood of the samples. Newton and Raftery (1994) employ this approach, specifically sampling from the posterior. Oaks et al. (2019: 7) warn that while these sampling methods theoretically provide valid estimates, divergence between the prior and posterior lead to biased results in practice. Sampling from the prior leads to underestimating the marginal likelihood, as the overall size of the parameter space means that parameter values with high likelihood are unlikely to be included in the sample. Conversely, as has additionally been described in Lartillot & Philippe (2006), Xie et al. (2011), and Fan et al. (2011), sampling from the posterior results in overestimation of the marginal likelihood, as samples will be overly concentrated in the high likelihood areas of the parameter space.

As both types of estimation error are related to a potentially large gap between the prior and posterior distributions, efforts to overcome these biases generally involve sampling from distributions intermediate to the prior and posterior themselves. Oaks et al. (2019: 7-11) categorize these approaches into two general categories. One category uses samples from the posterior in conjunction with a 'reference' distribution that is somewhere between the prior and posterior. Here the choice of algorithm differs with respect to how to optimize the choice of a specific reference distribution. Examples include Generalized harmonic mean (Gelfand & Dey 1994), Inflated-density ratio (Petris & Tardella 2003; Arima & Tardella 2012), and Partition-weighted kernel (Wang et al. 2018). The authors discuss (Oaks et al. 2019: 10-11) various reasons why current implementations of these algorithms have proven unsuitable for use with Bayesian phylogenetic models. The more common approach to estimating the marginal likelihood in phylogenetic models breaks the divergence between the prior and posterior into a number of smaller steps. Sampling from these intermediate steps allows for more accurate estimation of the marginal likelihood. Path sampling/Thermodynamic Integration (Gelman & Meng 1998; Lartillot and Philippe 2006; Friel & Pettitt 2008), Stepping-stone sampling (Xie et al. 2011), and Generalized stepping-stone sampling (Fan et al. 2011) employ this approach. As mentioned at the beginning of this section (§4.2.2), BayesTraits implements the Stepping-stone algorithm, which is described here.

In Stepping-stone sampling (Xie et al. 2011: 152-154), the likelihood is exponentiated using a set of exponent values between 0 and 1 and samples are taken from the resulting 'power-posterior' distributions for each exponent value in the set. Thus, where D is the data, θ is the set of model parameters of phylogenetic model M, and

β is a value between 0 and 1, the power-posterior density distribution q_β is given by equation (4.1):

$$q_\beta = f(D|\theta, M)^\beta f(\theta|M). \tag{4.1}$$

Note that $f(D|\theta, M)$ is the likelihood and $f(\theta|M)$ the prior. Normalizing q_β by a constant c_β results in the normalized power-posterior distribution p_β (equation 4.2):

$$p_\beta = q_\beta / c_\beta. \tag{4.2}$$

The authors note (Xie et al. 2011: 152) that p_β is equivalent to the posterior distribution when $\beta = 1.0$ and the prior distribution when $\beta = 0.0$. Assuming a proper prior (integrates to 1), the ratio $c_{1.0}/c_{0.0}$ is equivalent to the marginal likelihood, and it is this ratio that the Stepping-stone algorithm estimates. Thus, the marginal likelihood is estimated by summing over the likelihoods of vectors of parameter values sampled from the MCMC model chain for some number of values of β. In terms of the distribution of the β values, Xie et al. (2011: 154) argue that because the shape of the power-posterior distribution is typically stable except near $\beta = 0$, most of the values of β should be near 0, rather than evenly spacing them along the interval from 0 to 1 (as suggested in Lartillot & Philippe 2006). In accordance with this notion, a Beta(α, 1.0) distribution is used to determine appropriate values of β. Varying α has the effect of varying the skew of the β values, such that they are evenly spaced when $\alpha = 1.0$ and skewed towards 0 when $\alpha < 1.0$ (i.e. more of the values of β are near 0 as α decreases). The number of distinct β values and how many samples should be drawn for each β may vary based on the model and data. Meade & Pagel (2019: 14-15) propose monitoring of run to run variance in determining if the sampler has been parameterized appropriately. This sentiment is echoed by Oaks et al. (2019: 9), who suggest that estimates from multiple model runs should show minor variation and that overall ranking of models/hypotheses under consideration should remain consistent from run to run. The BayesTraits implementation of the Stepping-stone sampler computes an estimation of the marginal likelihood of a model and returns it on the log scale.

Bayes Factor for model comparison

Once estimates of candidate models' marginal likelihoods are obtained, Bayes Factor (Jeffreys 1935), which is calculated as the ratio between two marginal likelihoods, can be used to determine which model provides the best fit to the data. As demonstrated by Kass & Raftery (1995: 776) and Oaks et al. (2019: 3), among others, we can express the posterior probability of candidate model M_1 (Kass & Raftery use H for 'hypothesis') with respect to N competing models using Bayes Rule as in equation (4.3):

$$p(M_1|D) = \frac{p(D|M_1)p(M_1)}{\sum\limits_{i=1}^{N} p(D|M_i)p(M_i)}, \tag{4.3}$$

thus the posterior probability of M_1 is proportional to the product of the prior and marginal likelihood. If we want to compare two models M_1 and M_2, we have:

$$\frac{p(M_1|D)}{p(M_2|D)} = \frac{p(D|M_1)}{p(D|M_2)} \cdot \frac{p(M_1)}{p(M_2)}, \tag{4.4}$$

where the ratio

$$\frac{p(D|M_1)}{p(D|M_2)} \tag{4.5}$$

is the Bayes Factor, i.e. the ratio of the posterior odds of a model to its prior odds. As Lavine & Schervish (1999) explain, Bayes Factor provides a method of quantifying the evidence in support of M_1 with respect to M_2. Kass & Raftery (1995: 777) and Meade & Pagel (2019: 14) suggest the utility of calculating Bayes Factor on the log scale to avoid representational underflow issues associated with multiplying small probability values, as well as doubling the obtained value, which puts the result on the same scale as the likelihood ratio (LR) test commonly emplyed in maximum likelihood model comparison. Thus where Lh is the estimated log marginal likelihood:

$$\text{log Bayes Factor} = 2(\text{Lh complex model} - \text{Lh simple model}), \tag{4.6}$$

where model complexity is quantified in terms of the number of model parameters which must be estimated. This is taken to represent the evidence for the complex model as compared with the simple model. Other definitions make no mention of model complexity or a strict ordering of the two models under comparison for the Bayes Factor calculation. Given the expression of the Bayes Factor ratio on the log scale, both marginal likelihood estimations under consideration will be negative.[3] Thus reversing the order of model log likelihoods in (6) will change the polarity of the log Bayes Factor value (and the specific model for which the evidence is being evaluated), but should not change the determination of which model provides a better fit to the data.

Interpretation of log Bayes Factor (LogBF) values obtained from equation (4.6) is expressed in terms of strength of evidence against the second model under consideration. Here Meade & Pagel (2019: 14) suggest the following interpretation (values in parentheses represent the scale given in Kass & Raftery (1995: 777) where it differs slightly):

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[3] Maximum probabilty of a model is 1.0 and log(1)=0.

LogBF	Evidence against M_2
< 2	Insignificant or weak evidence
> 2 (2-6)	Positive evidence
5-10 (6-10)	Strong evidence
> 10	Very strong evidence

Table 4.5: Interpreting Bayes Factor

Thus the log Bayes Factor ratio quantifies evidence for candidate model M_1 as compared with alternate candidate model M_2. For specific model comparisons, log Bayes Factor can be interpreted along a continuous scale, with very low values representing a lack of evidence for preferring M_1 over M_2 and large values representing overwhelming evidence in favor of M_1.

4.3 Core reconstruction results I: Presence of verb conjugation classes

This section presents the ancestral state reconstruction results for the first morphological character, the presence or absence of verb conjugation classes at the root node of the Pama-Nyungan phylogeny, representing the common ancestor of the modern languages. In defining different models, we investigate testable hypotheses about the trajectory of evolution of the Pama-Nyungan conjugation class system. For this character, four different models (representing distinct hypotheses about the nature of conjugation class evolution in Pama-Nyungan) are compared. Each of these is discussed in §4.3.1 in relation to the hypothesis it corresponds to, followed by results (§4.3.2) and model comparison and selection diagnostics using log Bayes Factor (§4.3.3).

4.3.1 Four candidate models of Character 1: Presence of conjugation classes

The *Baseline* model takes an agnostic approach to restricting the parameter space for estimate transition rate parameters. In this model, which serves as a baseline for comparison with more restricted modifications, both gain and loss are assumed to be permissible and may have different transition rates. This contrasts with the *Single rate* ($q_{01} = q_{10}$) model, which represents the hypothesis that gain and loss are equally likely to occur at the same rate.

In the *No Gain* model, q_{01} is restricted to 0, thus preventing the model from considering representations of trait evolution where gain of conjugations has taken place. As there are languages with conjugations in the observed data, the reconstruction must necessarily be in favor of presence of conjugation classes at the root node. This hypothesis serves as a consequent of Dixon's (1980, 2002) claims that conjugation classes may be lost but not gained in the context of the Indigenous Australian languages. It should be reiterated that this is a weak version of Dixon's claim, as it is uninformative with respect to the proliferation or reduction of conjugation class inventories beyond the specific instances of losing conjugations altogether and innovating conjugations from a preceding state of absence.

The *No Loss* model serves as the converse of the No Gain model, allowing gain of conjugations but not loss by restricting q_{10} to always be 0. Absence of conjugations for many of the modern Pama-Nyungan languages means that this model must predict absence of conjugations at the root node. Though this hypothesis has not been considered in traditional historical linguistic reconstructions of Pama-Nyungan morphology, it is a possible scenario if the innovation of verb conjugation classes is taken to be a defining character among early splits in Pama-Nyungan.

For each model under consideration, transition rate priors were estimated via the use of a hyperprior (see §4.2), with exponential rate priors seeded from a uniform hyperprior distribution on the interval 0 to 1. Figure 4.7 depicts the permissible state to state transitions for each of the models under consideration:

(a) Baseline **(b)** Single rate

(c) No Gain **(d)** No Loss

Figure 4.7: Permissible transitions for four models of Character 1

4.3.2 Results

Table 4.6 presents the results of the four candidate models of the evolution of Character 1, including posterior log likelihood (Lh), estimated transition rates, and feature reconstruction probabilities for the root node:

MODEL	LH	Q_{01}	Q_{10}	ROOT P(1)	ROOT P(0)
Baseline	−50.74	0.436	1.041	0.827	0.173
Single rate	−51.24	0.901	0.901	0.565	0.435
No Gain	−50.35	0.0	1.182	1.0	0.0
No Loss	−54.18	2.019	0.0	0.0	1.0

Table 4.6: Reconstruction model results for four models of Character 1

From Table 4.6 we see roughly similar mean posterior likelihood values for the Baseline, Single rate, and No Gain models, while the No Loss model provides a somewhat worse fit to the data.

The Baseline model estimates q_{10}, representing loss of conjugations, as being two to three times larger than its counterpart, q_{01}. Restricting the rates of gain and loss to take the same value results in a single mean transition rate that resembles q_{10} from the Baseline model, providing further evidence against q_{01} as an important factor in the relative fit of the model to the data. We again find similarity between the mean estimate of q_{10} for the No Gain model and that of the Baseline and Single rate models. Finally, note that for the No Loss model, that the estimated rate of gain of conjugations is twice as large as the rate of loss in the other models and much higher than the rate of gain in the baseline model. This can be interpreted as a recognition that the observed distribution of feature states in the modern languages necessitates a relatively rapid rate of gain of conjugation classes when the root is stipulated to not have them.

Figure 4.8 illustrates the relative size of transition rates estimated in each of the four models:

(a) Baseline **(b)** Single rate

(c) No Gain **(d)** No Loss

Figure 4.8: Estimated transition rates for four models of Character 1

Taking the transition rate parameters from all four models into account, we can conclude that loss of conjugation classes as a feature is much more prevalent in the reconstruction data that innovating conjugation classes, a finding that will be reinforced throughout the thesis in subsequent discussion.

Looking at the reconstruction probabilities for the root node, we see appreciable variation in the predictions made by each of the four candidate models. The Baseline model reconstructs presence of conjugation classes at the root node with a probability of 83% and absence with a probability of 17%. Presence of conjugation classes is also supported by the Single rate model, though the reconstruction is less certain. The No Gain model has the effect of stipulating presence of conjugation classes at the root node, while the No Loss model stipulates absence. Figure 4.9 plots the distribution of root node reconstruction probabilities for Character 1 for the Baseline and Single rate models:

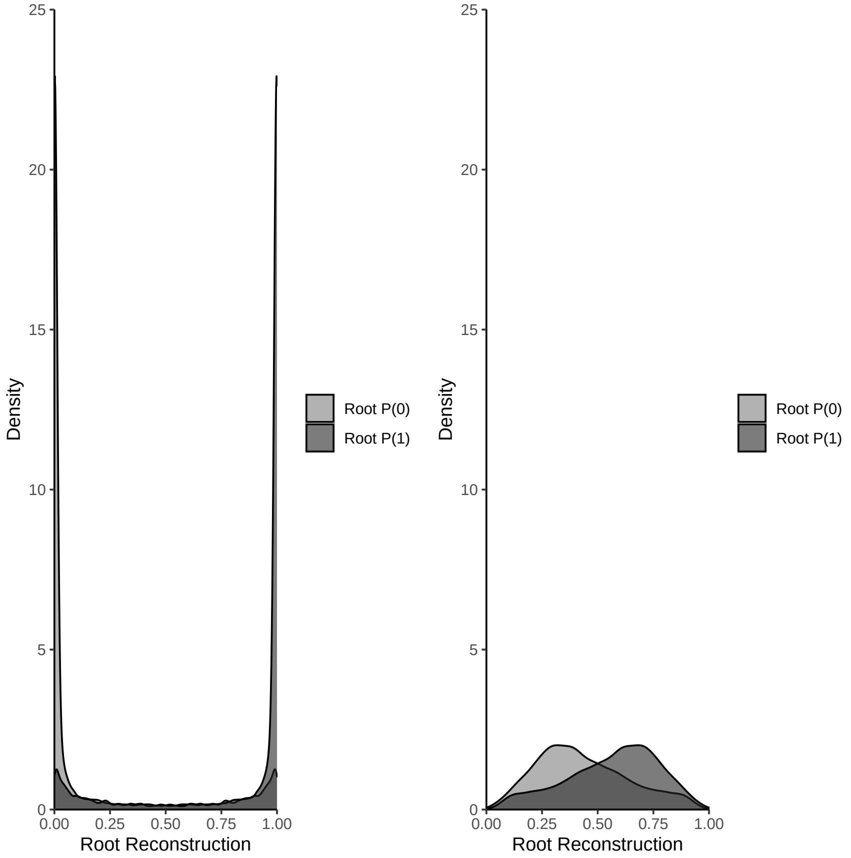

Figure 4.9: Density of reconstruction probabilities for Character 1 – Baseline (left plot) and Single rate (right plot) reconstruction probabilities show differences in model predictions. Not included are the No Gain and No Loss models, each of which allow a single outcome for the root node reconstruction per model.

For the Baseline model, we see large peaks in the reconstruction probability distributions near 1 for presence of conjugations and near 0 for absence. Uncertainty in the model is visible as the smaller minor peaks, indicating the model was occasionally alternating between conclusions. This uncertainty between the two possible reconstructions is evident for the Single rate model, note the mostly overlapping distributions in Figure 4.9.

4.3.3 Model Comparison

We can compare the fit of each of the models of Character 1 using the log Bayes Factor metric and Stepping-stone sampler algorithm outlined in §4.2.2. Here the baseline is compared against each of the alternative hypotheses involving rate restrictions. Initialization of the Stepping-stone sampler for this and subsequent model comparisons use the BayesTraits default values for the beta distribution ($\alpha = 0.4$, $\beta = 1.0$). Moreover, 100 distinct power-posterior distributions were sampled, with each sampled 1000 times. A low degree of variation between estimated marginal likelihood values was observed for each model over multiple model runs, and overall model ranking was consistent from run to run. Log marginal likelihood, log Bayes Factor representing evidence against each model, and reconstruction probabilities for the root node are given in Table 4.11:

MODEL	LH	LOGBF	ROOT P(1)	ROOT P(0)
Baseline	−52.45	–	0.83	0.17
$q_{01} = q_{10}$	−53.06	1.23	0.57	0.43
No Loss	−57.24	9.59	0.0	1.0
No Gain	−52.38	−0.13	1.0	0.0

Table 4.7: Lh, Reconstruction probabilities, and Bayes Factor for four models of Character 1 – LogBF given as compared with Unrestricted model. The LogBF column can be interpreted as the amount of evidence against the model in the specified row.

The data presented in Table 4.11 can be understood as follows. Recalling that a value of LogBF < 2 indicates insignificant evidence against the specified model. Thus we do not find support for favoring the Baseline over the $q_{01} = q_{10}$ (LogBF $= 1.23$) or No Gain (LogBF $= -0.13$) models. Discussion in Meade & Pagel (2019: 22) suggests the somewhat stronger claim that these results indicate preference of the Restricted and No Gain models over the Baseline. Evidence in favor of the Baseline as compared with the No Loss model is strong to very strong (LogBF $= 9.59$) indicating poor fit of the No Loss model to the data. Of additional interest is the observation that the Baseline, Restricted, and No Gain models all reconstruct presence of conjugations at the root node, though the reconstruction probability is weak for the Restricted model. The No Loss model is unique in predicting absence of conjugations at the root node and in its poor fit relative to the other candidates.

4.4 Core reconstruction results II: Number of verb conjugation classes

The second grammatical character for reconstruction is the number of verb conjugation classes in the prehistory of Pama-Nyungan. Recalling the typological overview in Chapter 3, there is an appreciable degree of variation with respect to the number of verb conjugation classes a given language contains. In addition to optimized estimation methods provided by the BayesTraits software package, we can additionally constrain the model via restriction of certain transitions in order to test various hypotheses about the nature of the evolution of this trait. For the number of verb conjugation class feature, languages were coded along four possible feature states – 0 (representing lack of conjugations), 2, 3, and 4 (representing four or more conjugations). The choice of grouping together languages with four or more conjugation classes is somewhat arbitrary, though note that languages with greater than four conjugation classes are mostly concentrated in specific subgroups (e.g., Yolngu), rather than distributed across the family. Reconstruction of four or more conjugations was consistently dispreferred across multiple distinct models (i.e., reconstruction probabilities near zero), leading to the conclusion that elaboration of the trait space to include more permissible values is unlikely to to be of use. Thus we have four possible trait values and a set of twelve possible state to state transitions:

	0	2	3	4
0	–	q02	q03	q04
2	q20	–	q23	q24
3	q30	q32	–	q34
4	q40	q42	q43	–

Table 4.8: State transitions for number of conjugation class model

This leads to a large number of parameters that must be estimated. Note however that we can disallow a number of these state to state transitions, namely those which involve a gain or loss of more than one verb conjugation class in a single generation. For instance, by restricting state transitions that involve multiple gains or losses to always have a rate of zero, this leaves us with half as many rates to estimate. A slow rate of change in the conjugation class system, as evidenced by the highly conserved nature of the trait across the phylogeny, indicates the plausibility of such a constraint on the rate parameters. Six distinct models were considered for this character.[4]

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[4] Subsequent to analyzing the results for these models, an additional two-rate model was investigated which set all instances of gain equal to one rate and all instances in loss equal to the other. Results of this model were categorically worse than the best performing models included in discussion here.

4.4.1 Six candidate models of Character 2: Number of conjugation classes

The *Baseline* model for this character assumes no restrictions on state to state transitions, allowing any number of conjugations to be gain or lost in a single transition and allowing a potentially different rate for each. While estimation of 12 rate parameters in parallel is unlikely to lead to optimal performance for each individual rate, it may allow us to identify parameters that are not improving the fit of the model to the data, and thus candidates for restriction in future models.

Like the Baseline model for the number of conjugation classes character, the *Restricted* model makes no assumptions about what types of gain or loss are permitted. Instead, all rates are restricted to be identical, meaning any possible state to state transition is equally likely to occur at any point in the evolutionary process.

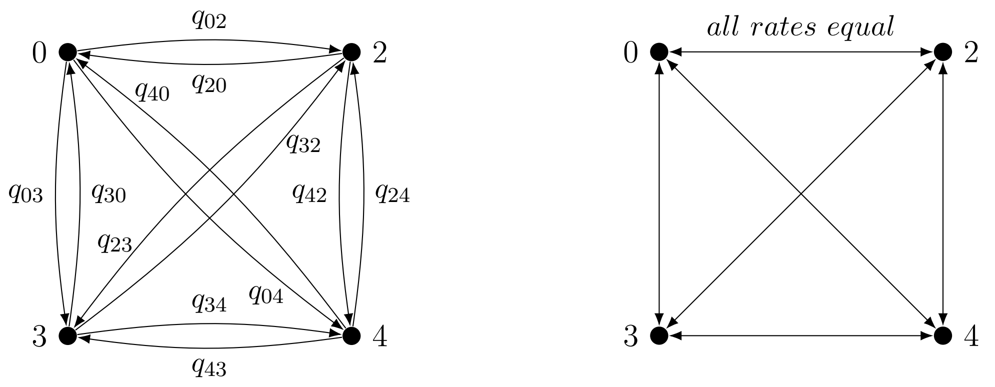
In the *No Gain* model, rates representing an increase in the number of conjugation classes are restricted to always be zero. Note that this conflates innovation of conjugations (q_{01}) with adding to an existing inventory. No restrictions are placed on loss of conjugation classes, thus estimation of 6 transition rate parameters are required (i.e. half that of the Baseline model). The No Gain model can be taken to represent the stronger version of Dixon's hypothesis, in that loss of conjugations is allowed, but adding conjugations does not occur. Due to the evidence for four or more conjugations in the data, these restrictions require reconstruction of the same value at the root node, which is also in line with Dixon's reconstruction of seven conjugations for the ancestral language.

The *No Loss* model restricts transition rates representing reduction of conjugation class inventory to zero, again resulting in six rates that must be estimated. This model requires reconstruction of absence of conjugations at the root node, due to the evidence for such a possibility among the modern languages. In theory, the No Loss models in general conflict with traditional historical reconstruction approaches based on parsimony, as they require multiple independent innovations to account for the data.

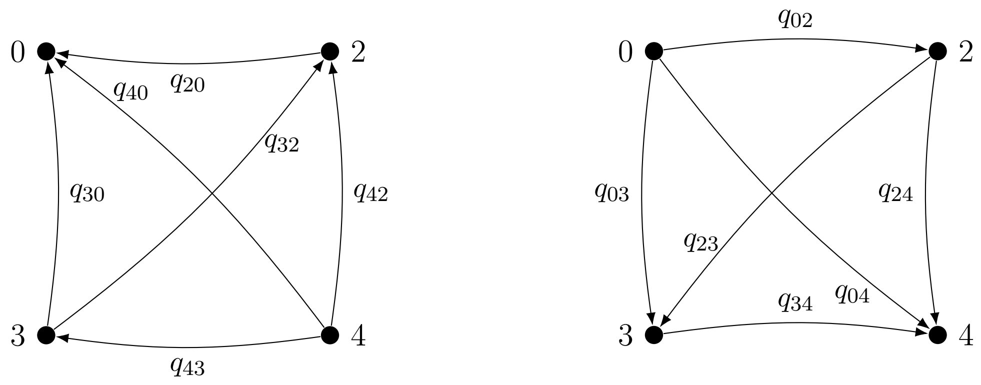
The last two models under consideration for the number of conjugation classes character reduce model complexity by hypothesizing that simultaneous gain or loss of a more than one conjugation class is unlikely to occur. Instead, these models allow at most one conjugation class to be gained or lost at a time by restricting rates representing multiple gain/loss to zero. The *No Jumps* model does exactly this, while leaving open the possibility of innovating conjugation classes from a previous state of absence at any point in the tree. Once again, this results in a reduction of the overall number of rate parameters to be estimated to six (down from 12 in the Baseline model).

The *No Jumps, No Innovation* (NJI) model takes the No Jumps model and removes innovation of conjugation classes as a typological feature (i.e., q_{02}) from the parameter space. This model represents a hypothesis that includes a diluted version of Dixon's claims about the evolution of conjugation classes in Pama-Nyungan, in that it allows gain of conjugations under the specific circumstance that some inventory of conjugation classes exists at the previous evolutionary step. Inclusion of this model is also motivated by the results of, and represents a rate restricted nesting of, the No Jumps model. The No Jumps/Innovation model includes five rate parameters that must be estimated. Note that because q_{02} has been removed from the transition possibilities, reconstruction of absence of conjugations at the root node is not possible, due to the presence of conjugation classes in the data.

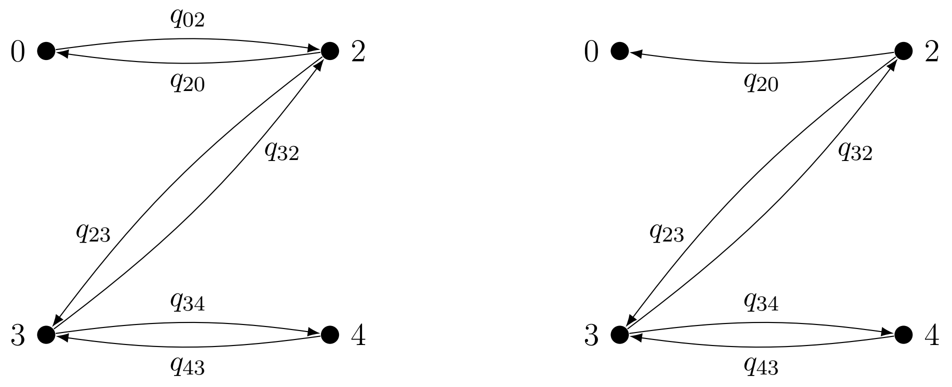
Figure 4.10 illustrates the different rates estimated in each model. Both the Baseline and Single rate models allow the maximal set of twelve state to state transitions, though it should be noted that they are at opposite ends of the spectrum in terms of number of rates to be estimated (twelve and one, respectively):



(a) Baseline **(b)** Restricted



(c) No Gain **(d)** No Loss



(e) No Jumps **(f)** No Jumps/Innovation

Figure 4.10: Permissible transitions for six models of Character 2

4.4.2 Results

Table 4.9 presents the posterior log likelihood and root node reconstruction probabilities for the six candidate models of the number of conjugation classes character. Estimated transition rates are listed in Table 4.10.

MODEL	LH	ROOT P(0)	ROOT P(2)	ROOT P(3)	ROOT P(4)
Baseline	−105.25	0.21	0.37	0.37	0.05
Restricted	−112.25	0.86	0.07	0.02	0.05
No Gain	−107.51	0.0	0.0	0.0	1.0
No Loss	−109.87	1.0	0.0	0.0	0.0
No Jumps	−102.91	0.07	0.49	0.42	0.02
No Jumps/Inv	−102.16	0.0	0.48	0.49	0.03

Table 4.9: Posterior Lh and reconstruction probabilities for six models of Character 2

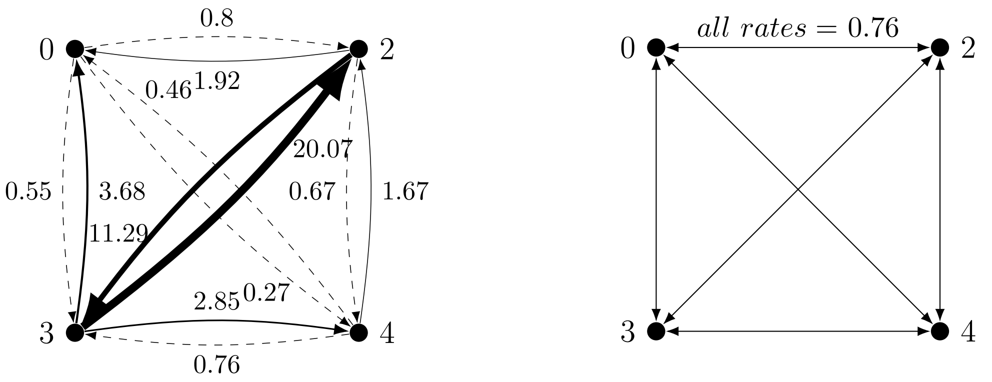
MODEL	Q_{02}	Q_{03}	Q_{04}	Q_{20}	Q_{23}	Q_{24}	Q_{30}	Q_{32}	Q_{34}	Q_{40}	Q_{42}	Q_{43}
Baseline	0.8	0.55	0.27	1.92	11.29	1.67	3.68	20.07	2.85	0.46	0.67	0.76
Restricted	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72
No Gain	0.0	0.0	0.0	6.07	0.0	0.0	1.33	7.44	0.0	0.33	1.18	2.25
No Loss	1.86	0.42	0.28	0.0	3.43	1.23	0.0	0.0	7.77	0.0	0.0	0.0
No Jumps	0.73	0.0	0.0	3.53	12.07	0.0	0.0	21.66	5.42	0.0	0.0	1.05
No Jumps/Inv	0.0	0.0	0.0	3.38	11.97	0.0	0.0	22.53	4.8	0.0	0.0	1.07

Table 4.10: Estimated transition rates for six models of Character 2

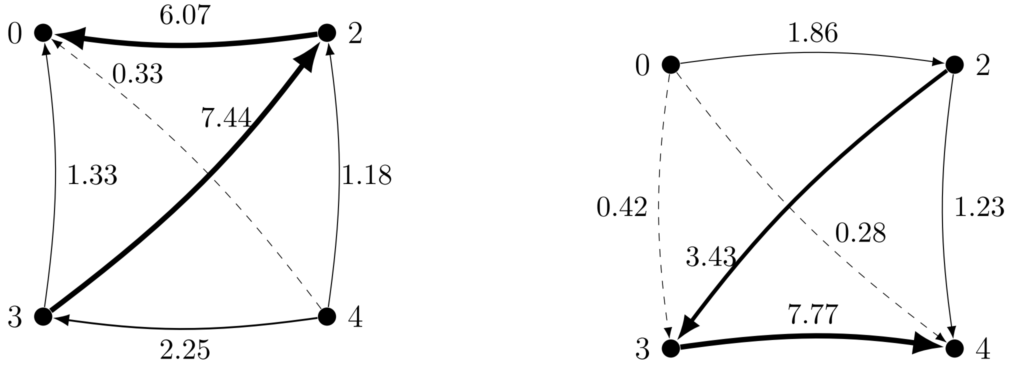
From Table 4.9, we see that there is a wider range of fit to the data of the individual models as compared with Character 1, in terms of posterior likelihood. The Restricted model seems to provide poor fit as compared with the other candidates, while the two No Jumps models fit the data better than the others. Note also that the No Gain model, whose counterpart fared well for Character 1, fails to account for the number of conjugation class data as well as other models, although it does perform better than the Restricted and No Loss models.

Table 4.10 indicates a number of informative generalizations about the relative size of the estimated transition rates, both within and across models. For the baseline model, of particular note are the relatively high estimated values of q_{23} and q_{32} as compared with the rest of the rates, with q_{32} estimated as being twice as large as q_{23}. Many of the estimated rates involving gain or loss of more than one conjugation class in a single transition are very small. In plain terms, we see that most of the gain and loss is predicted by the model to occur between two and three conjugation classes, with moving from a three class to a two class system being more frequent than going from a two class to a three class system. A high estimated rate for q_{23} indicates evidence for proliferation of conjugation class inventory in explaining the data. In other words, these results indicate that gain of conjugations is not only possible, but likely in explaining the data. This effect goes away by design in the Restricted model, though it is interesting that restricting transitions to always be equally likely results in a relatively small estimated rate. For the No Gain model, as with the Baseline model, we see a relatively large estimated rate for q_{32} as compared with many of the additional permissible rates, although the gap is somewhat less pronounced. When gaining conjugations is not allowed, we see that the most frequent transitions involve the movement from a three class to a two class system and the loss of conjugation classes as a feature. In the No Loss model, higher transition rates are estimated for q_{23} and especially q_{34} in order to account for the dispersion of languages with three or more conjugations in the data. Note the smallest nonzero rates are observed for transitions requiring gaining more than one conjugation class in a single step, with the possible exception of q_{24}. Even in the models gain or loss are not allowed, addition or subtraction of multiple conjugations in a single evolutionary step are predicted to be infrequent, while the more frequent transitions involve gaining or losing a single conjugation class at a time. Estimated rates for the No Jumps and NJI models again privilege q_{23} and q_{32}, with moderately sized values for the other rate parameters.

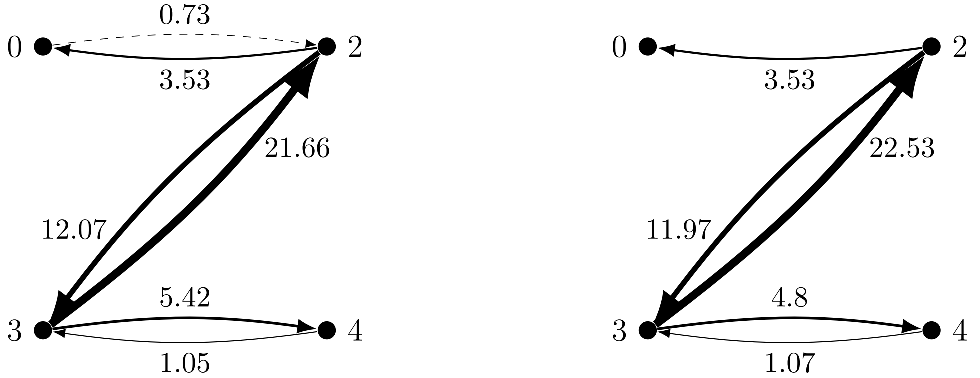
Figure 4.11 visualizes the estimated transition rates for state to state transitions for each of the six candidate models:



(a) Baseline **(b)** Restricted



(c) No Gain **(d)** No Loss



(e) No Jumps **(f)** No Jumps/Innovation

Figure 4.11: Estimated transition rates for six models of Character 2

Reconstruction of the root node is somewhat inconclusive, though there are noteworthy tendencies across the best performing models. For the Baseline model, we see identical probabilities for reconstructing two or three conjugation classes for the root node. There is also a small probability assigned to reconstructing absence of conjugations at the root node, which is somewhat in agreement with the baseline model for the presence/absence character (§4.3.1). Reconstruction of four or more conjugation classes for the root node is assigned a very low probability by the model. The Restricted model estimates a relatively small transition rate for each of the possible state to state transitions, resulting in strong preference for reconstructing absence of conjugation classes at the root node (86%). This outcome is in conflict with the results of the Character 1 modeling, as well as the Baseline for this Character. The No Gain model requires the reconstruction of four or more conjugation classes at the root node, while its counterpart (No Loss) stipulates absence of conjugation classes. The two No Jumps models somewhat resemble the baseline in assigning equal probability space to reconstructing either two or three conjugation classes for the root node. Figure 4.12 plots the distribution of the reconstruction probabilities for the Baseline, Restricted, and No Jumps models:

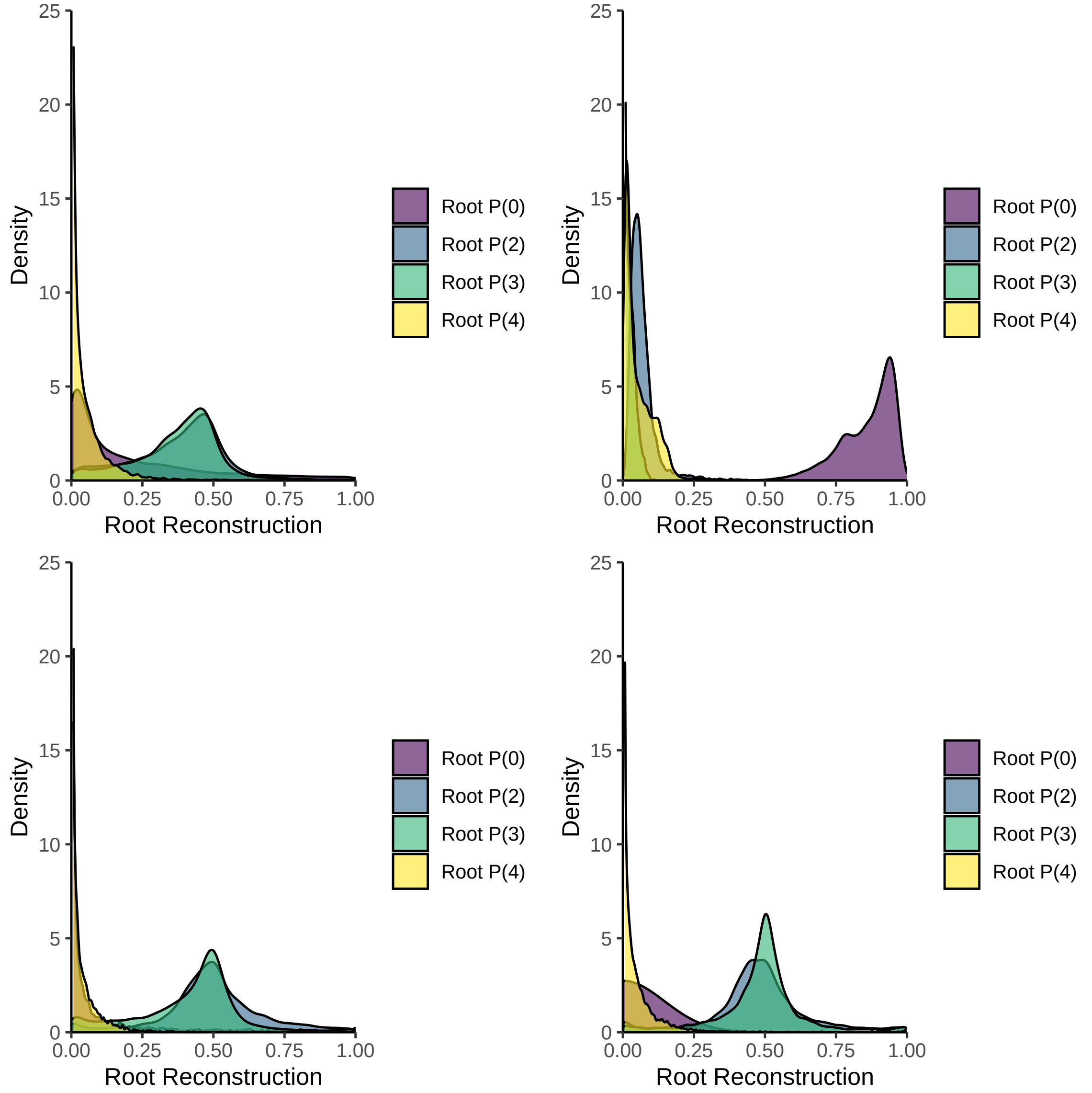


Figure 4.12: Density of reconstruction probabilities for Character 2 – Baseline (top left plot), Restricted (top right plot), No Jumps (bottom left plot), and No Jumps/Innovation (bottom right plot) reconstruction probabilities show differences in model predictions. Not included are the No Gain and No Loss models, each of which allow a single outcome for the root node reconstruction per model.

Note the similarities between the Baseline, No Jumps, and NJI models with respect to the distribution of their root node reconstruction probabilities. In each we see a large probability mass near zero for reconstructing four or more conjugations and for reconstructing absence of conjugations. This is complemented by two mostly overlapping distributions around 50% for reconstructing two and three conjugation classes. The Restricted model (Figure 4.12, top right plot) assigns a high probability to reconstructing a lack of conjugation classes at the root node, while the other possibilities are not well supported by the model.

4.4.3 Model Comparison

Model comparison was performed using the Stepping-stone sampler implementation in BayesTraits, using the same settings as in the presence/absence character, i.e. Beta($\alpha = 0.4$,$\beta = 1.0$), 100 power-posterior distributions sampled 1,000 times each. Run to run consistency was very high in terms of the estimates of model likelihood and the relative ranking of models with respect to one another. Table 4.11 compares each of the models with the Baseline unrestricted model:

MODEL	LH	LOGBF	P(0)	P(2)	P(3)	P(4)
Baseline	−122.4	–	0.2	0.38	0.37	0.05
Restricted	−115.67	−13.45	0.86	0.07	0.02	0.05
No Loss	−120.85	−3.1	1.0	0.0	0.0	0.0
No Gain	−117.88	−9.05	0.0	0.0	0.0	1.0
No Jumps	**−109.99**	**−24.83**	**0.07**	**0.49**	**0.42**	**0.02**
No Jumps/Inv	**−109.638**	**−27.52**	**0**	**0.48**	**0.49**	**0.03**

Table 4.11: Lh, Reconstruction probabilities, and Bayes Factor for six models of Character 2 – LogBF given as compared with unrestricted Baseline model.

Looking at the LogBF values in Table 4.11, we see the poor fit of the Baseline model to the data as compared with the alternatives. The Restricted, No Jumps, and No Jumps/Innovation models are very strongly preferred. This is likely due to overparameterization of the Baseline model, in that there were too many rates to estimate in a single model. Revisions of this model that reduced the number of estimated rate parameters showed a better fit to the data, even if they were themselves unlikely on theoretical grounds (e.g., No Loss). Moreover, note that improved fit of the model to the data does not necessarily increase the certainty of the reconstruction. The two No Jump models, which are strongly favored over the baseline, showed nearly identical probability distributions for two of the four possibilities for the root node. Both the Restricted and No Loss model favor absence of conjugations at the root node (the latter by necessity), while No Gain is unique in reconstructing four or more conjugations (again, by necessity). Table 4.12 recalculates the LogBF ratios, using the No Jumps model as the hypothesis against which the rest of the models are compared:

MODEL	LH	LOGBF	P(0)	P(2)	P(3)	P(4)
No Jumps	−109.99	–	0.07	0.49	0.42	0.02
Baseline	−122.4	24.82	0.2	0.38	0.37	0.05
Restricted	−115.67	11.37	0.86	0.07	0.02	0.05
No Loss	−120.85	21.72	1.0	0.0	0.0	0.0
No Gain	−117.88	15.79	0.0	0.0	0.0	1.0
No Jumps/Inv	**−109.638**	**−2.7**	**0**	**0.48**	**0.49**	**0.03**

Table 4.12: Lh, Reconstruction probabilities, and releveled Bayes Factor for six models of Character 2 – LogBF given as compared with No Jumps model. A BayesFactor value below −2 indicates preference for the indicated model.

Comparing each of the models to the No Jumps model, we find very strong evidence in favor of No Jumps and against the Baseline, Restricted (single rate), and No Gain/Loss models. Note that there is positive evidence in favor of No Jumps/Innovation over No Jumps (LogBF = −2.7), indicating that removal of q_{02} from the parameter space has a strongly positive effect on the fit of the model to the data. Interestingly, we find no evidence in favor of the No Gain model for this character, which has implications for our understanding of the proposed probabilistic reconstructions as they relate to Dixon's hypothesis. Specifically, note that the relevant assumption by Dixon is that conjugation classes cannot be gained over time, leading to the reconstruction of a maximal set of seven conjugations at the root node. For the ancestral state reconstruction models to support this notion, we would want to see some suggestion that the No Gain model and the reconstruction of four or more conjugation classes at the root node are plausible outcomes. Instead, we find neither of these to be the case. In fact, we find strong evidence against reconstructing as many as seven conjugation classes at the root node, based on the results of all of the variable rate models, as well as the single restricted rate model. This point is discussed further in §4.6. First, we employ a Reversible Jump MCMC model to further substantiate the findings of the models presented in this section.

4.4.4 Reversible jump MCMC

In models with a large number of parameters, it is often difficult to efficiently estimate appropriate values for each variable. This was the case seen in the Baseline model for Character 2, where simultaneous estimation of twelve state to state parameters lead to poor fit of the model to the data. As we saw, eliminating certain rates allowed us to 1) reduce model complexity, 2) test specific hypotheses about the evolution of the character, and 3) acheive a better fit to the data.

Reversible jump MCMC (RJMCMC; Green 1995) allows us to determine which of a set of parameters are unlikely to influence model results by integrating over the space of possible models. Thus the RJMCMC takes model dimensionality (i.e., number of free parameters) to vary at each iteration. In addition to setting certain parameters to zero, dimensionality reduction is accomplished by setting groups of parameters to take an equal value, with the number of estimated groups being a free parameter of the model. For a detailed summary of the RJMCMC algorithm and its implementation, see Fan & Sisson (2011). In the context of our model of the number of verb conjugation classes in Pama-Nyungan, the RJMCMC algorithm allows us to delete (viz. restrict to zero) different combinations of transition rate parameters, which may provide insight into whether or not our proposed restrictions to the MCMC models are appropriate. We would like to see evidence that the rates we selected for restriction show a high rate of deletion in the RJMCMC model.

The following discussion details results of RJMCMC modeling of Character 2 in BayesTraits. We can interpret the results of RJMCMC models by looking at various output estimates of the model. These include estimates of how many groups of parameters with the same value best explains the data, how many parameters are deleted, and how often each individual parameter is deleted. Figure 4.13 visualizes the first of these, the estimated number of parameters in the model. We find overwhelming support in favor of a single rate for the non-zero parameters, with less support for two sets of rates.

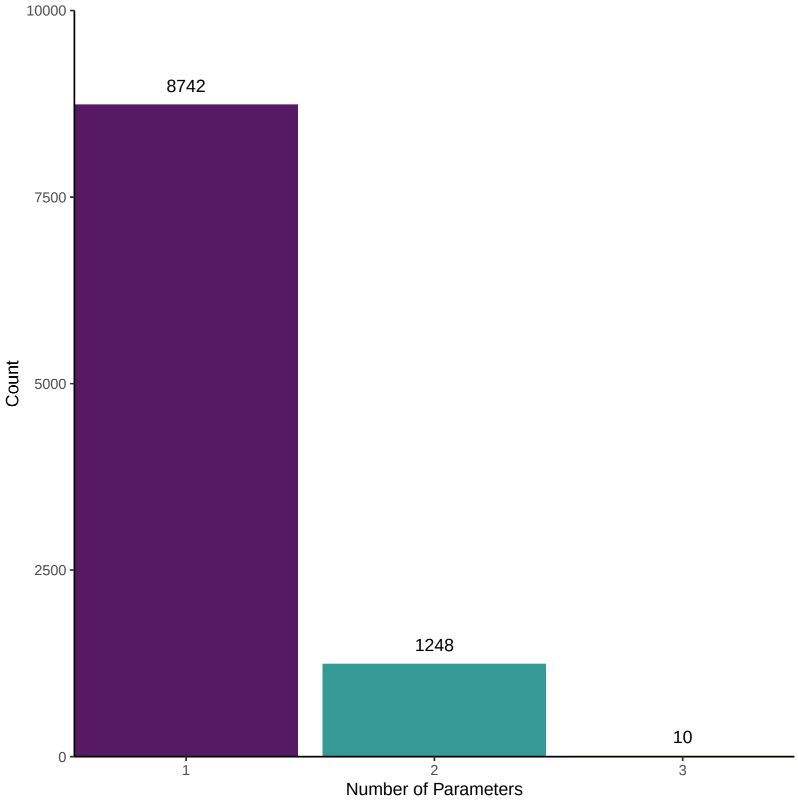


Figure 4.13: Estimated number of parameters in Reversible jump MCMC model of Character 2 – Reversible jump MCMC estimates how many groups of non-zero parameters are appropriate for fitting the data. Groups of parameters are restricted to have the same parameter value. We find evidence in favor of a single rate for non-zero parameters, with less support for two rates.

Figure 4.14 examines the frequency with which the model deleted certain counts of rates. Note that the model favors the deletion of between four and seven rates, with five and six being the most common. Deletion above or below this range is not well supported by the model.

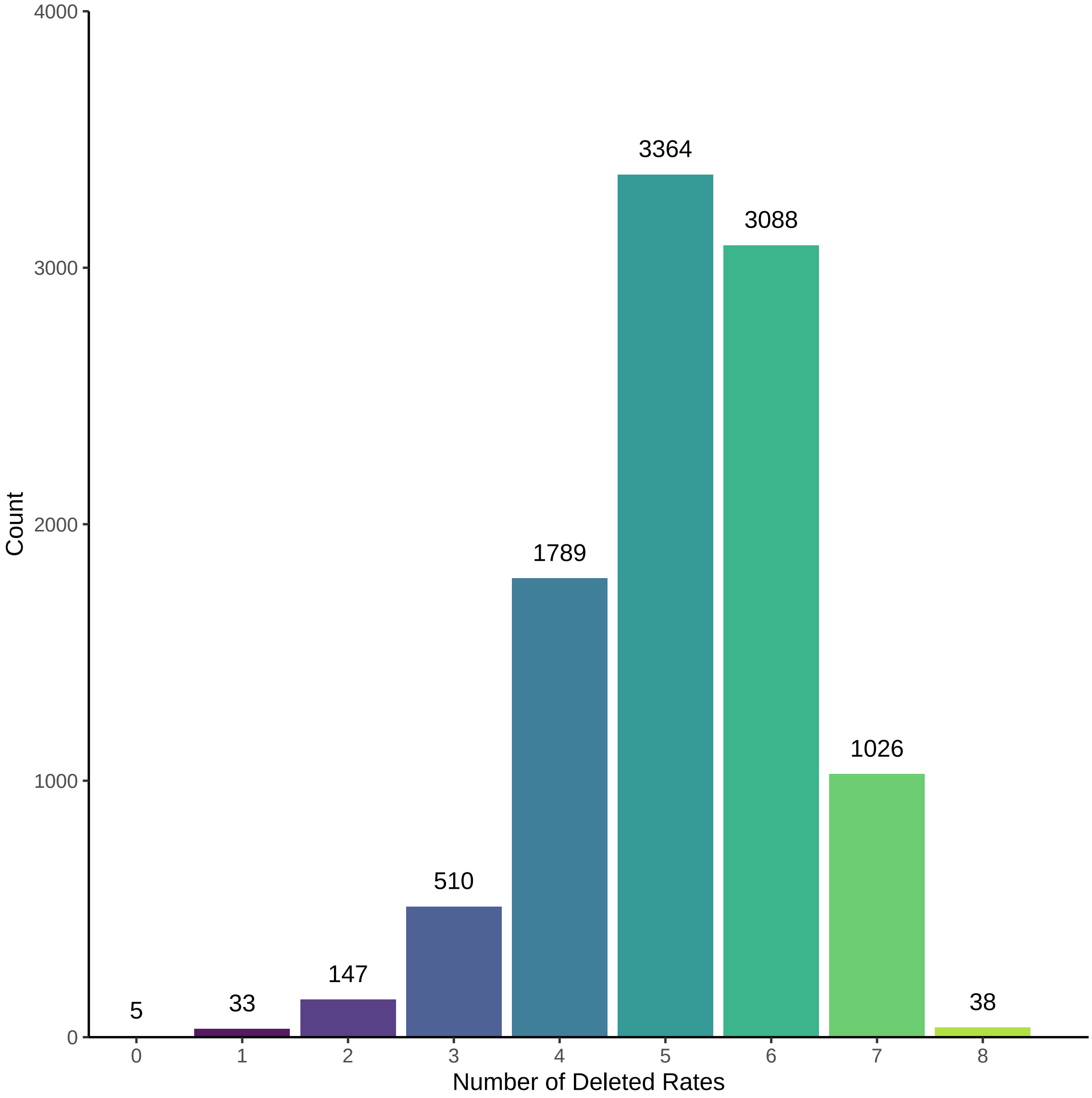


Figure 4.14: Estimated number of deleted rates in Reversible jump MCMC model of Character 2 – Reversible jump MCMC reduces model dimensionality by selecting various rates for deletion at each iteration. Here, we see that the model suggests deletion of five or six rates at a much higher frequency than other amounts. Deletion of less than three or more than seven rates shows little support.

It is also instructive to consider the percentage of samples in which individual rates are deleted. Rates that are infrequently deleted are important in explaining the data, while frequently deleted rates are interpreted as being unhelpful in fitting the model to the data. Figure 14.5 visualizes these rate deletion percentages. Note the high deletion percentage for rates involving gain or loss of more than a single conjugation in one step, as well as innovation of conjugation classes (q_{02}). Exceptions to this include the gain from two to four conjugations and the loss of three conjugations to zero.

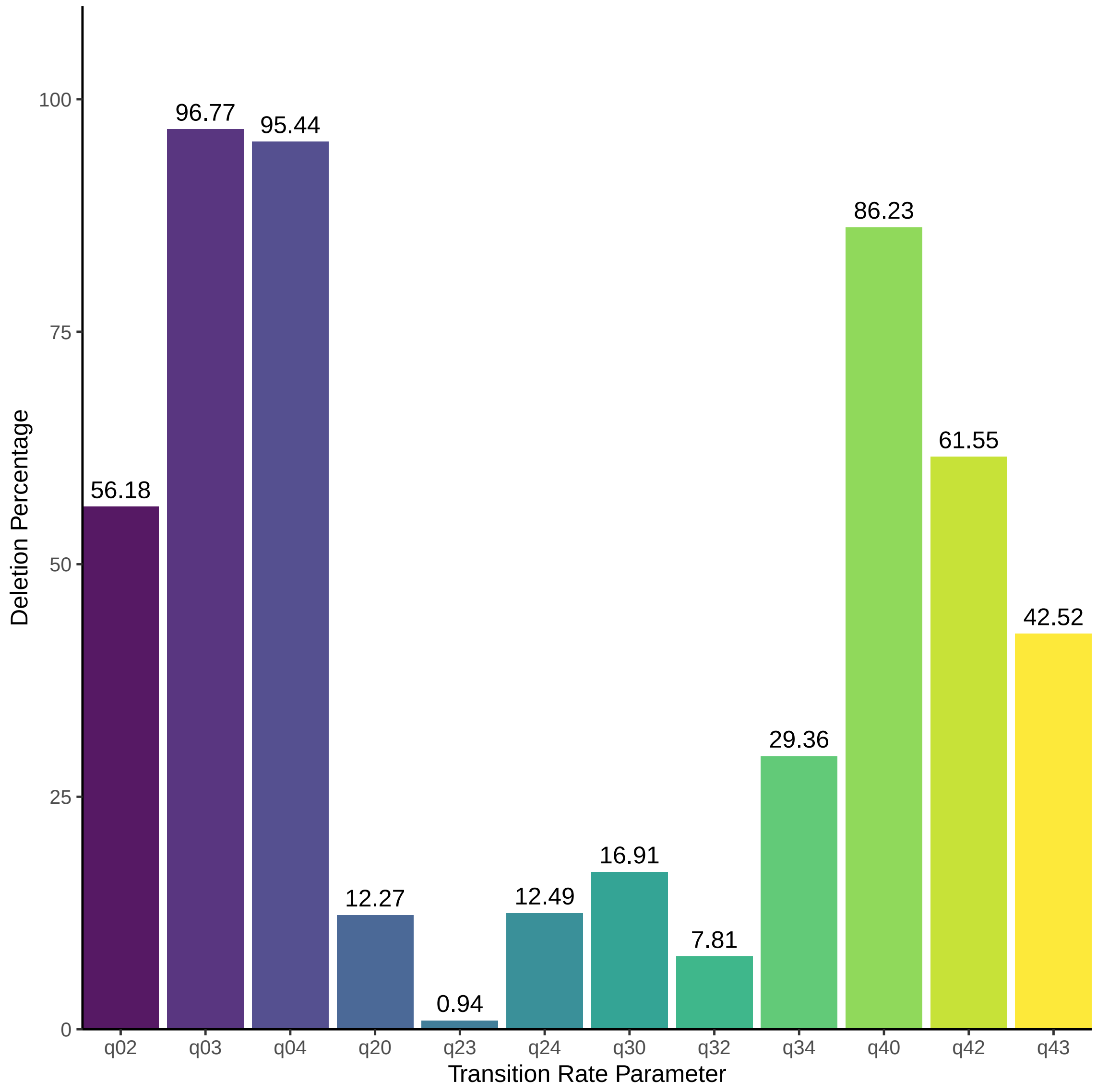


Figure 4.15: Deletion percentage for individual rates in Reversible jump MCMC model of Character 2 – By observing the percentage of samples in which a given rate was deleted, we get a sense of its overall importance to the model in explaining the data. Several rates involving multiple gain/loss events in one step and innovation of conjugation classes are deleted with a high frequency.

There are multiple conclusions we can draw from the results of Reversible jump MCMC modeling that further validate the decisions made in the best performing No Jumps and No Jumps/Innovation MCMC models of Character 2. First, we observe (Figure 4.14) the preference of deletion of between four and six parameters, with five and six being the most common number of rate deletions. Combined with the high deletion percentage for specific rates, we can formulate an interpretation whereby the innovation of any number of conjugation classes from previously not having them is dispreferred by the model, as is the rapid loss of more than one conjugation class in a single evolutionary step. In fact, the five most commonly deleted rates in descending order are those representing transitions from zero to three conjugations, zero to four conjugations, four to zero conjugations, four to two conjugations, and zero to two conjugations, all of which are deleted in over 50% of samples. Transition rates for the gain of three or four conjugations from zero are deleted with a very high frequency. These are all rates which were restricted to zero in the No Jumps/Innovation model. At the other end of the spectrum, transition rates that are rarely deleted are those that represent moving between two and three conjugations. Interestingly, the loss of three conjugation classes in a single step is not a frequently deleted rate. The low deletion percentage for the gain of two conjugations from two to four is perhaps less surprising, two and four+ conjugation systems are the most frequently represented possibilities in the data for languages that have conjugation classes.

These findings additionally have several implications for our understanding of the nature and development of morphological classes. First, while changes in the size of conjugation class inventories occur, they are generally limited to incrementation or reduction of a single class at a time. In other words, gain and loss of conjugations may be taken to be a gradual process that affects specific subsets of the linguistic system before (potentially) spreading to others. In Pama-Nyungan, loss of a two or three class system is more likely than innovation of conjugation classes, while total collapse of a four class system is unlikely. Moreover, a language without morphological classes is unlikely to develop them. Recall that absence of conjugation classes is signaled by a single set of morphological exponents for all verbs (we will leave irregulars and phenomena like suppletion aside). The introduction of distinct conjugation classes involves the coinage of new inflectional material at the level of the form paradigm that does not typically alter the content paradigm. Thus we may conclude that it is this innovation of contentful morphological forms that comes with a prohibitive cost. This claim is reinforced by the lack of influence of the possible innovation of three or more conjugation classes in a single step in the various reconstruction models, in terms of very low transition rates in the standard MCMC approach and near 100% deletion percentage in the reversible-jump model. If creation of one additional (possibly incomplete) set of affixes is difficult, creation of more than one additional set at the same time is next to impossible. Once innovation does occur, gaining additional conjugations is much easier to accomplish. Moreover, an intricate system with a large number of classes shows relative stability in terms of maintaining distinctions.

4.5 Core reconstruction results III: Conjugation class membership features

The third trait under consideration in the current study involves the membership features of conjugation classes. Members of a given conjugation class typically show tendencies in terms of verb valence (i.e. a conjugation class may include mostly transitive or intransitive verbs) or phonological properties of the stem (e.g. number of syllables), or both. Unlike the presence/absence and number of conjugation class characters (§§4.3-4.4), permissible values of this trait are not mutually exclusive, in that several languages in the sample indicate both valence- and phonology-based conjugation classes in tandem. This raises the question of whether the two types of conjugation class evolved independently or in parallel. BayesTraits implements a method of testing for correlation between binary traits which uses log Bayes Factor model comparison between dependent and independent models to quantify evidence in favor of one of the two hypotheses. This section provides an overview of the Independent and Dependent discrete models employed by BayesTraits before discussing their utility for the conjugation class membership character. In Chapter 5, these models will again be employed to determine whether or not there is evidence for correlated evolution between the number of conjugation classes and conjugation class membership features.

The Independent model assumes that there is no correlation between the evolution of two traits. Meade & Pagel (2019: 26) describe this as an independence between the state to state transitions of one trait and the current state of the other. There are four rate parameters for the Independent model, representing the two permissible state to state transitions for the two traits:

PARAMETER	TRAIT	TRANSITION
α_1	1	$0 \rightarrow 1$
β_1	1	$1 \rightarrow 0$
α_2	2	$0 \rightarrow 1$
β_2	2	$1 \rightarrow 0$

Table 4.13: Independent model parameters

The Dependent model assumes that the state to state transitions for the first trait are dependent on the current state of the second trait, and vice versa. There are two permissible state values and two state to state transitions for each trait, thus there are eight transition rate parameters that must be estimated:

PARAMETER	TRANSITION
q_{12}	(0,0) → (0,1)
q_{13}	(0,0) → (1,0)
q_{21}	(0,1) → (0,0)
q_{24}	(0,1) → (1,1)
q_{31}	(1,0) → (0,0)
q_{34}	(1,0) → (1,1)
q_{42}	(1,1) → (0,1)
q_{43}	(1,1) → (1,0)

Table 4.14: Dependent model parameters

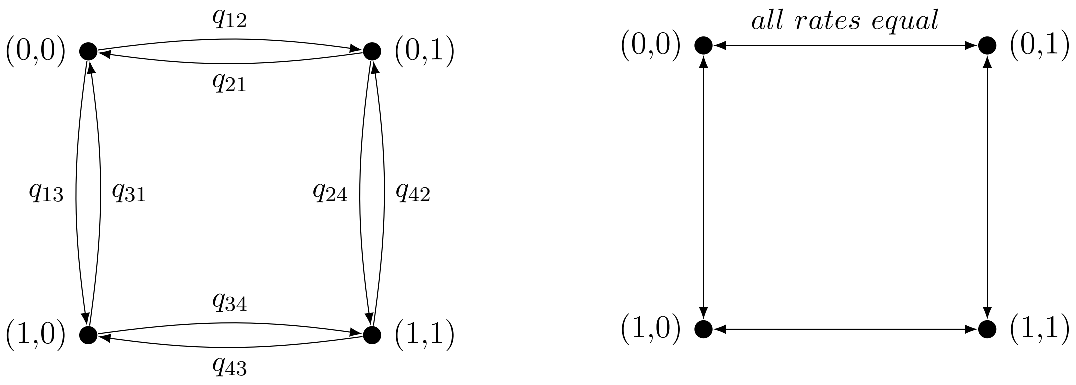
The meanings of the rates in Table 4.14 can be interpreted as, e.g., q_{12} is the rate of transition of the second trait from state 0 to state 1, specifically when the current state of the first trait is 0. Probabilistic reconstruction results of both Independent and Dependent models are expressed as the probabilities of four distinct outcomes – P(0,0) is the probability of reconstructing state 0 for both states, P(0,1) of reconstructing state 0 for the first trait and state 1 for the second trait, P(1,0) of reconstructing state 1 for the first trait and state 0 for the second trait, and P(1,1) of reconstructing state 1 for both states. Meade & Pagel (2019: 28) note that double transitions from (0,0) to (1,1) or (1,1) to (0,0) are restricted to not occur in the model.

4.5.1 Five candidate models of Character 3: Conjugation class membership features

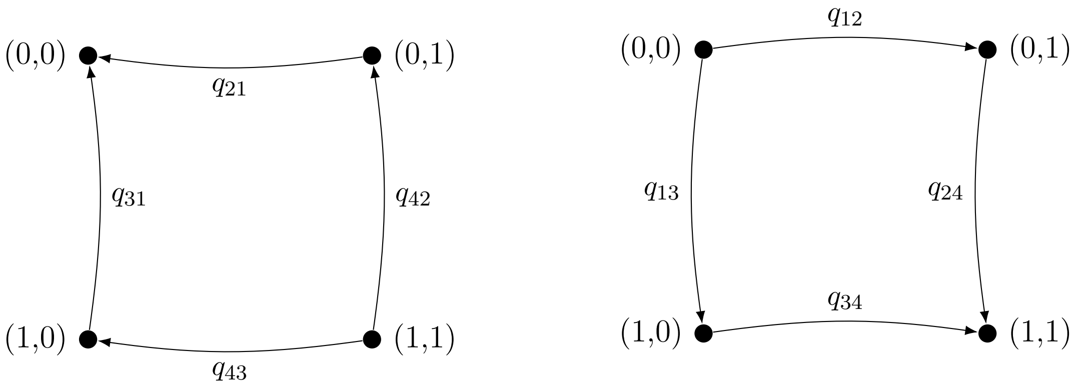
The Independent unrestricted rate model assumes no correlation between the two traits under consideration, and allows each of the four state to state transitions to potentially take a distinct rate. This contrasts with the Dependent unrestricted rate model, which assumes correlation between the evolution of the two traits representing conjugation class membership features, estimating eight transition rate parameters. See the immediately preceding outline (§4.5) and discussion of model results (§4.5.2) for details about the transition rate parameters and what they represent linguistically.

Results of Independent and Dependent models with no further rate restrictions strongly favored the Dependent model over a range of tests. As a result, testing of additional hypotheses was conducted using the Dependent model. Alternate hypotheses under consideration were Restricted (single rate), No Gain, and No Loss, each of which reduces model complexity by eliminating estimation of some number of rates.

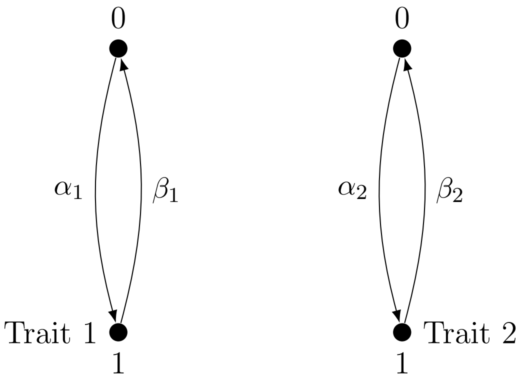
The permissible transitions for the resulting five models of Character 3 are schematized in Figure 4.8:



(a) Dependent, Unrestricted **(b)** Dependent, Restricted



(c) Dependent, No Gain **(d)** Dependent, No Loss



(e) Independent

Figure 4.16: Permissible transitions for five models of Character 3

4.5.2 Results

Posterior log likelihood, root node reconstruction probabilities, and estimated transition rates for the five candidate models of the Character 3 are given in Table 4.15 and Table 4.16.

Model	Lh	P(0,0)	P(0,1)	P(1,0)	P(0,1)
Independent	−82.16	0.5	0.02	0.47	0.01
Dependent	−76.86	0.36	0.02	0.60	0.02
Restricted	−81.3	0.84	0.01	0.15	0.0
No Gain	−82.29	0.0	0.0	0.0	1.0
No Loss	−79.8	1.0	0.0	0.0	0.0

Table 4.15: Posterior Lh and reconstruction probabilities for five models of Character 3

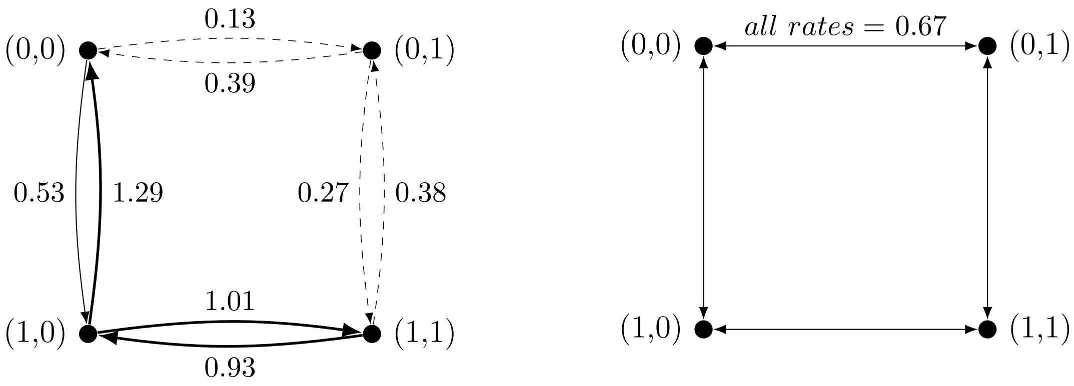
Model	α_1	β_1	α_2	β_2				
Independent	0.6	0.89	0.53	0.82				
Model	q_{12}	q_{13}	q_{21}	q_{24}	q_{31}	q_{34}	q_{42}	q_{43}
Dependent	0.13	0.53	0.39	0.38	1.29	1.01	0.27	0.93
Restricted	0.67	0.67	0.67	0.67	0.67	0.67	0.67	0.67
No Gain	0.0	0.0	0.39	0.0	2.88	0.0	0.19	4.16
No Loss	0.13	1.61	0.0	0.38	0.0	1.67	0.0	0.0

Table 4.16: Estimated transition rates for five models of Character 3

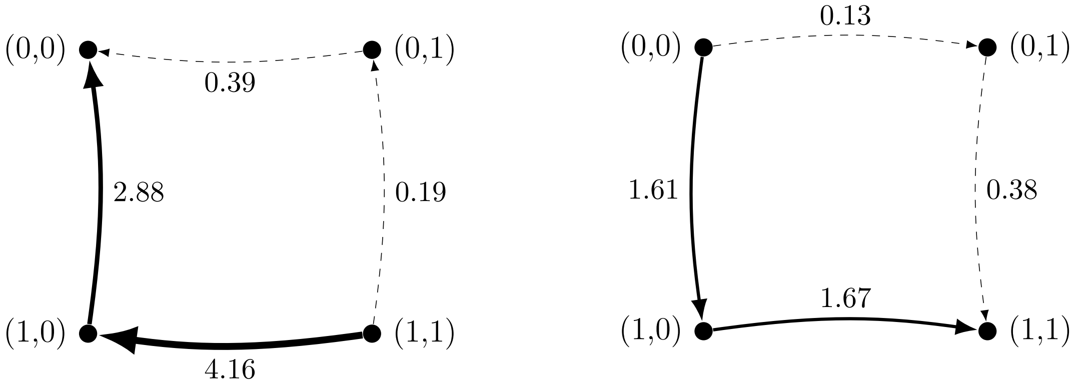
As with previous characters, we see variation in the posterior log likelihoods of the different models under consideration (Table 4.15). The Dependent (unrestricted) model outperforms the other models. The No Loss model does marginally better than the Restricted model, while the No Gain and Independent models provide relatively poor fit to the data.

For the Independent model, we find nearly identical rates for the two rates representing gain of conjugations ($\alpha_{1,2}$) on the one hand, and for the two rates representing loss ($\beta_{1,2}$) on the other. This means that the model estimates that both traits are being gained and lost at the same rate as one another, perhaps previewing the utility of the Dependent model in explaining the data. Moreover, the relative size of the weights indicates that gain is predicted to occur slightly more slowly than loss. Transition rates in the various dependent (correlated evolution) models are relatively low compared with many of the models in previous characters, with many being near zero. In the Dependent model, the transitions with the highest rates are (1,0) → (1,1) and (1,0) → (0,0), which represent the gain of phonology-based membership in the presence of valence-based membership and the loss of valence-based membership in the absence of phonology-based membership, respectively. These are also the highest rates in the additional models that allow them (i.e., (1,0) → (0,0) in No Gain and (1,0) → (1,1) in No Loss). The No Gain model also estimates a high rate for the transition (1,1) → (1,0), which represents the loss of phonology as a determining factor in conjugation class membership in the presence of valence-based membership. In general, the gain and loss of valence and phonology membership features appear to follow a specific pathway across all models. Specifically, transitions between (0,0), (1,0), and (1,1) are predicted to occur much more frequently in either direction than any of the transition pathways involving state (0,1). See §4.6 for further discussion of the implication of this finding.

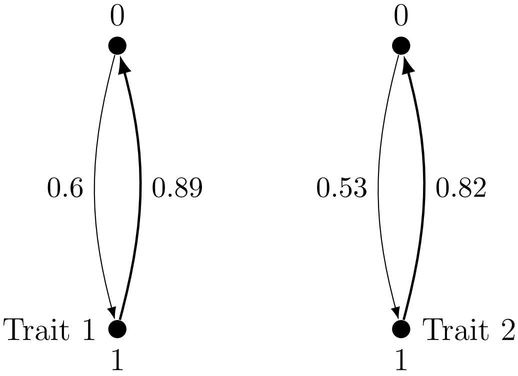
Figure 4.14 visualizes the estimated transition rates for each of the five models under consideration:



(a) Dependent, Unrestricted **(b)** Dependent, Restricted



(c) Dependent, No Gain **(d)** Dependent, No Loss



(e) Independent

Figure 4.17: Estimated transition rates for five models of Character 3

As with Characters 1 and 2, reconstruction probability distributions are somewhat messy, although we do see certain patterns in the results that merit attention. First, note that none of the models under consideration assign a high probability to state (0,1) at the root node. This is perhaps unsurprising, given that there are very few languages in the sample that have conjugation classes that show evidence of phonological features determining class membership without some correlation with valence. Moreover, reconstruction of state (1,1) is unlikely at the root node for all models except for the No Gain model, which requires it. The Independent and Dependent unrestricted models are somewhat in agreement with respect to the uncertainty of reconstructing state (0,0) or state (1,0) for the root node, though (1,0) is slightly favored by the Dependent model. Figure 4.15 plots the distribution of the reconstruction probabilities for the Independent, Dependent, and Restricted models:

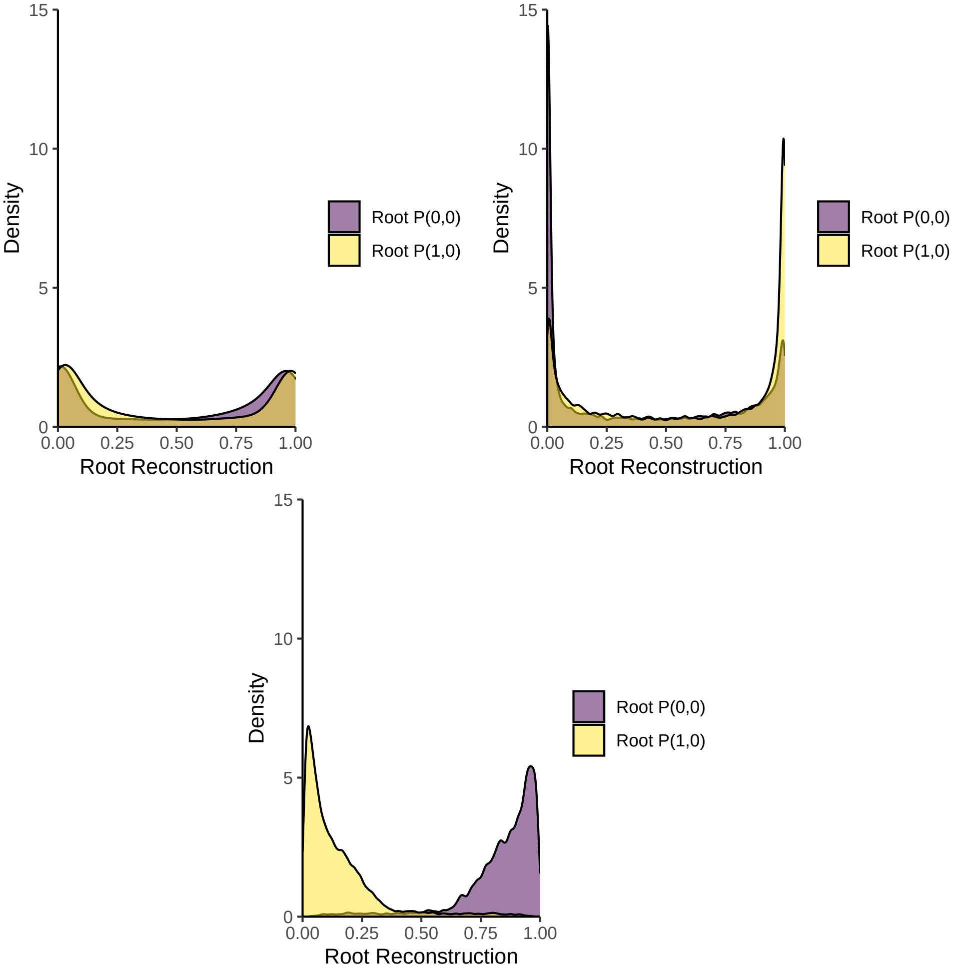


Figure 4.18: Density of reconstruction probabilities for Character 3 – Independent (top left plot), Dependent (top right plot), and Restricted (bottom plot) reconstruction probabilities show similarities in model predictions. Reconstruction probabilities for states (0,1) and (1,1) are omitted, as sharp peaks in density at zero obscure the plot. Not included are the No Gain and No Loss models, each of which allow a single outcome for the root node reconstruction per model.

4.5.3 Model Comparison

Initialization of the Stepping-stone sampler for model comparison via Bayes factor was identical to that of the previous character (Beta($\alpha = 0.4$,$\beta = 1.0$), 100 power-posterior distributions sampled 1,000 times each). Run to run estimates of the marginal likelihood of each model was very low and model ranking was consistent across multiple Bayes factor calculations. Table 4.28 compares each of the models with the Dependent unrestricted model:

MODEL	LH	LOGBF	P(0,0)	P(0,1)	P(1,0)	P(1,1)
Dependent	**−80.72**	–	**0.36**	**0.01**	**0.61**	**0.01**
Independent	−85.14	8.84	0.51	0.01	0.47	0.01
Restricted	−83.51	5.58	0.84	0.01	0.15	0.0
No Gain	−91.77	22.1	0.0	0.0	0.0	1.0
No Loss	−84.84	8.24	1.0	0.0	0.0	0.0

Table 4.17: Lh, Reconstruction probabilities, and BayesFactor for five models of Character 3. LogBF given as compared with Dependent unrestricted model. A BayesFactor value above 2 indicates preference for the Dependent unrestricted model. Note that the Independent model is strongly dispreferred, as are the various restricted dependent models. Evidence in favor of the Dependent unrestricted model is strong to very strong across the board.

LogBF model comparison shows the Dependent unrestricted model as the best fit to the data among the candidate models (LogBF > 5 across the board). As expected, we see that the No Loss and especially the No Gain models provide a very poor fit to the data. The Restricted (single rate) model is also inappropriate in accounting for the data as compared with Dependent unrestricted, confirming that the conflicting reconstruction with respect to the best-fitting models for previous characters is due to poor model fit. Overall, we see that results for reconstruction of this third trait are much less clean than in the previous characters. Possible explanations for this and other facets of the interpretation of the probabilistic reconstructions for each character are discussed in §4.6.

4.6 Interim discussion

This chapter has presented the results of a series of ancestral state reconstruction models representing various hypotheses about the nature of the evolution of verb conjugation classes in the prehistory of Pama-Nyungan. This includes probabilistic reconstruction of three separate traits, representing the typology of the modern

Pama-Nyungan verb conjugation class system. This section offers a summary of model results and the implications for existing reconstructions using the comparative method, especially hypotheses against the gain of individual conjugation classes inherent in Dixon's (1980, 2002) foundational works on the topic.

The first set of models explored the possibility of reconstructing the existence of verb conjugation classes at least as far back as the common ancestor of the modern Pama-Nyungan languages (§4.3). Here we tested four separate hypotheses, with Bayes Factor model comparison demonstrating an inconclusive choice between the three best-fitting models. Based on discussion in Meade & Pagel (2019: 22), a lack of evidence for the Baseline model as compared with the Restricted model, which constrains both gain and loss of conjugation classes as a typological feature to a single transition rate, indicates that the rate representing gain of conjugations is an uninformative factor in explaining the data. This finding is further supported by the good fit of the No Gain model and the very poor fit of the No Loss model. Each of the three best-fitting models reconstruct presence of conjugations at the root node with varying degrees of confidence. It should be noted that the findings of this series of models is in line with what we may refer to as a weak version of Dixon's reconstruction hypothesis that conjugation classes may be lost but are not gained over time. Specifically, we find evidence that conjugation classes may be lost as a typological feature entirely, and once lost, are unlikely to be innovated again. Importantly, this character does not allow us to draw any conclusions about the proliferation of an existing conjugation class inventory, a feature that Dixon's reconstructions predict will not occur.

The second trait reconstruction involved the number of distinct conjugation classes present at the root node (§4.4). Here six different reconstruction models were considered, representing a number of different hypotheses. Languages were coded according to the number of distinct conjugation classes that could be discerned from documentary data. Languages with four or more conjugation classes were grouped together under a single coding value to reduce model complexity, with the expectation that high probability reconstruction of four or more conjugations for the root node would necessitate further separating these into multiple coding values. The best fitting models for this trait, No Jumps and No Jumps/Innovation reconstruct either two or three conjugation classes for the root node, though the choice between the two is inconclusive for both models. Further testing via Reversible jump MCMC modeling indicates a stronger preference for two conjugation classes at the root node and against reconstructing three conjugation classes.

These results allow us to draw a number of interesting conclusions. These well-fitting models allow both proliferation and reduction of existing conjugation class inventories, but eschew gain or loss of more than one conjugation in a single evolutionary step. Moreover, the best fit was obtained via the No Jumps/Innovation model, which reflects our reconstruction results for the previous character as well. Note also that although the 'four or more' grouped coding value was in a sense privileged, in that it conflated a number of genetically and typologically distinct modern languages, a very low probability was assigned to reconstructing this value for the root node for all but one of the considered models. The exception to this was the No Gain model, which more faithfully represents Dixon's reconstruction hypothesis. Recall that Dixon reconstructs seven conjugation classes for the common ancestor of the modern languages, taking evidence of a distinct conjugation in the modern data as evidence of the existence of a correlate in the proto-language. Here our findings differ from Dixon, in that we reconstruct the possibility of gaining conjugation classes. As with the presence/absence character, the probabilistic reconstruction of the number of conjugation classes for the root node of the Pama-Nyungan phylogeny shows support for the less restrictive claim that conjugation classes are unlikely to be innovated after having been lost, but that gain and loss of individual conjugation classes are likely to have occured.

Further validation of this result was provided via Reversible jump MCMC modeling, a generalization of the MCMC algorithm that integrates over the model dimensionality space by both restricting certain rates to be zero and proposing the grouping of sets of remaining rates together under a single parameter value. Here we saw a preference for the deletion of rates involving the innovation of any number of conjugation classes from a state of lacking them altogether, as well as the reduction of conjugation classes once a language has four or more conjugations. These two findings are interesting with respect to existing reconstructions of Pama-Nyungan verb conjugation class evolution. The finding that conjugation classes are unlikely to be innovated in languages that lack them fits with the parsimony-inspired dispreference of predicting parallel evolution of a feature in related languages or the reinvention of a lost system, rather than the existence of that feature at an earlier stage from which both languages descended. However, results of MCMC modeling of Character 2 (both standard and Reversible jump) provide evidence against the stronger claim that Pama-Nyungan languages that have a small number of conjugation classes do not gain new ones. Furthermore, model results indicate that languages with four or more conjugation classes are somewhat unlikely to lose enough classes to go down to an inventory of three or less. This is especially true of the rapid collapse of an intricate system of inflectional patterns. Higher estimated transition rates and lower deletion percentages characterize transitions between two and three conjugation classes, as well as the loss of the conjugation class system from a state of two or three conjugations. Taken together, these results paint a picture in which there are threshholds of stability at four and at zero conjugations, while languages with two or three conjugations may more easily undergo conjugation class inventory incrementation or diminishment.

A third set of reconstruction models focused on verb conjugation class membership features (§4.5). Discussion of generalizations that can be drawn based on verb conjugation class inventories is elementary to description of Indigenous Australian languages, likely due to the influence of Dixon and his focus on the typology of Australian verb conjugation class membership as a whole. Here languages were coded based on the presence or absence of valence- or phonology-based conjugation class membership, or both. As these possibilities are not mutually exclusive, two classes of models were considered. The first of these assumed that valence- and phonology-based conjugation classes evolved irrespective of one another, while the second hypothesized a dependence of the two traits on one another. Bayes Factor model comparison showed strong evidence in favor of the second possibility, indicating correlated evolution between the two traits. Additional nested models were considered, but ultimately the best fit was provided by the Dependent unrelated model. As pointed out in §4.5.6, even for the best fitting model, the probabilistic reconstruction was not conclusive, though the highest probability (61%) was assigned to reconstructing presence of valence-based conjugations and absence of phonology-based conjugations. In fact, many of the considered models assigned near-zero probability to either of the root node states that reflect presence of phonology-based conjugation classes. Improvements to the reconstruction of this character may lie in placing different restrictions on the Dependent model parameters after consideration of alternative hypotheses. It is also important to discuss the nature of documentation of the modern Pama-Nyungan languages with respect to verb conjugation classes, which invariably includes discussion of the evidence for or against the presence of conjugation classes, as well as the number of distinct classes present in a given language. Moreover, generalizations about and/or quantification of individual conjugation class inventories with respect to included verb valence are common, even when no correlation with verb valence can be concluded. Conversely, discussions of positive or negative evidence for phonology as a contributing factor in conjugation class membership are somewhat lacking in the descriptive literature. In addition, complete verb inventories are typically not available. Here the importance of typological descriptions compiled by Harold Koch and Pascal Jacq from various published and unpublished sources (Koch & Jacq n.d.) cannot be overstated.

In sum, the current exploration has provided evidence for the reconstruction of the presence of two verb conjugation classes at the time-depth of the common ancestor of the modern Pama-Nyungan languages, with some additional support for reconstructing a third conjugation class. Moreover, we see evidence against a faithful interpretation of Dixon's reconstruction of a maximal set of seven conjugation classes, though results do suggest that conjugation classes are unlikely to be innovated as a typological feature after having lost them entirely. Once they are gone from a language's verbal typology, they tend to stay absent. Finally, while no strong claim can be offered at this point related to the reconstruction of typological features of the reconstructed conjugation class inventories, we do find some support for valence as a determining factor and against phonology.

The following chapter (Chapter 5) investigates the possibility of correlated evolution between the number of distinct conjugation classes and the recruitment of valence and/or phonology as determining factors for conjugation class membership. Furthermore, note that the reconstruction models described in this section took a set of possible Pama-Nyungan phylogenies obtained via Bayesian tree inference modeling based on lexical cognate data (Bowern & Atkinson 2012; Bouckaert, Bowern & Atkinson 2018). Chapter 6 explores various methods for reducing the number of trees in the sample and the effect a reduced topology space has on reconstruction.

Chapter 5

Correlated evolution of traits

In any comparative phylogenetic reconstruction involving multiple traits, we may want to investigate the possibilty that the evolution of two traits is correlated. As Pagel & Meade (2006) note, correlated evolution may indicate that the two traits in question are both evolving due to some (set of) common evolutionary force or that one trait is influencing the other to change in some way. In Chapter 4, we saw evidence for correlation in the evolution of two character states of a single trait, namely transitivity- and phonology-based conjugation class membership in the prehistory of the Pama-Nyungan languages.

Determining whether or not there is sufficient evidence to claim two traits coevolved involves fitting two ancestral state reconstruction models – 1) an Independent model, which assumes the evolution of the two traits is not correlated, and 2) a Dependent model, which assumes the evolution of the two traits is linked – and quantifying the level of support for the Dependent model using comparison of the models' estimated marginal likelihoods via the Bayes Factor statistic. These Independent and Dependent models (Pagel 1994) are implemented in the BayesTraits software package and require coded data in the form of two binary traits.

This section explores the possibility of correlated evolution between character states of two distinct traits – number of conjugation classes and conjugation class membership features. This is accomplished by breaking both traits into individual binary subcomponents, representing presence or absence of some subcomponent of a larger trait. This method was already applied to the conjugation class membership features trait in Chapter 4. For modeling number of conjugation classes, we have three subcomponents, including the presence or absence of two, three, or four (or more) conjugation classes. This results in six distinct pairings of subcomponents: (2 classes, Transitivity); (2 classes, Phonology); (3 classes, Transitivity); (3 classes, Phonology); (4 classes, Transitivity); (4 classes, Phonology).

5.1 Models of correlated evolution

5.1.1 Meade & Pagel (2016) Independent and Dependent models

A detailed overview of the Independent and Dependent discrete character models (Pagel 2004; Meade & Pagel 2019) was provided in Chapter 4 and is summarized here. The Independent model tracks the evolution of two binary traits on the assumption that the state transitions of one trait do not depend on the current state of the other. In other words, the two traits evolve in parallel, rather than in a correlated fashion. This model estimates four rate parameters, representing the two permissible state to state transitions for the two states. A summary of the estimated parameters was given in Table 4.21 and is repeated here for convenience:

PARAMETER	TRAIT	TRANSITION
α_1	1	$0 \rightarrow 1$
β_1	1	$1 \rightarrow 0$
α_2	2	$0 \rightarrow 1$
β_2	2	$1 \rightarrow 0$

Table 5.1: Independent model parameters

This contrasts with the Dependent model, which assumes the two traits coevolve, i.e., that the state transitions of one trait do depend on the current state of the other trait. This model estimates eight transition rate parameters (two transition rate parameters for each trait, each of which is dependent on the two permissible state values of the opposite trait). In addition to estimated transition rates, the output of the model consists of the probabilities of four possible reconstruction outcomes (0,0) is the reconstruction of state 0 for both traits, (0,1) is the reconstruction of state 0 for the first trait and 1 for the second trait, (1,0) is the reconstruction of 1 for the first trait and 0 for the second trait, and (1,1) is the reconstruction of 1 for both traits. Null transitions, i.e., from (0,0) to (0,0) are restricted to never occur in the model, as are double transitions from (0,0) to (1,1) or (1,1) to (0,0). Table 5.2 outlines the estimated rates in the Dependent model (see also Table 4.22):

PARAMETER	TRANSITION
q_{12}	(0,0) → (0,1)
q_{13}	(0,0) → (1,0)
q_{21}	(0,1) → (0,0)
q_{24}	(0,1) → (1,1)
q_{31}	(1,0) → (0,0)
q_{34}	(1,0) → (1,1)
q_{42}	(1,1) → (0,1)
q_{43}	(1,1) → (1,0)

Table 5.2: Dependent model parameters

Models were run for 50,000,000 iterations (5,000,000 discarded as burn in), sampling every 5,000 iterations, resulting in an output consisting of 10,000 samples for each model. As with previous ancestral state reconstruction models (Chapter 4), priors were selected from a uniform hyperprior. Model marginal likelihood was estimated using the stepping-stone sampling method (Chapter 4; Xie et al. 2011). Each model was run five times, subsequent results, including individual model metrics and model comparison with Bayes Factor use the mean value over these five independent runs. The scale for interpretation of Bayes Factor values, provided in Table 4.6, is given here as Table 5.3 for ease of reference:

LOGBF	Evidence against M_2
< 2	Insignificant or weak evidence
> 2 (2-6)	Positive evidence
5-10 (6-10)	Strong evidence
> 10	Very strong evidence

Table 5.3: Interpreting Bayes Factor

5.1.2 *phytools* `fitPagel` and AIC weight comparison

The R package *phytools* (Revell 2012) provides an alternative test of correlated evolution of binary traits via the `fitPagel` method, which also implements Pagel's (1994; see also Lewis 2001) model of discrete character evolution (see Tables 5.1 & 5.2). The `fitPagel` operation also calculates the Akaike information criterion (AIC; Akaike 1973), a method for comparing the fit of competing models. The AIC metric is informed by the (natural) log likelihood of a model and the complexity of the model in terms of number of parameters. Thus, where L is the maximum likelihood of model M_i and k is the number of parameters of the model:

$$\mathrm{AIC} = -2\ln(L) + 2k \tag{5.1}$$

This means that a low AIC is associated with good fit of the data to the model (i.e., a high log likelihood). The inclusion of the second term of the equation acts as a penalty that privileges simpler models, thus avoiding overparameterization or excessive model complexity.

Wagenmakers & Farrell (2004) note that while direct comparison of raw AIC values is common practice in model selection, it is less informative with respect to the degree of confidence in a given model relative to competitors, especially when differences in AIC are very small. Instead, the authors (2004: 193-194) outline a method for quantifying AIC values along a continuous measure relative to the AIC of the best candidate model (see also Akaike 1978; Burnham & Anderson 2002). This calculation involves finding the difference between the AIC of each model and that of the optimal candidate, i.e., $\Delta(\mathrm{AIC}) = \mathrm{AIC}_i - \min \mathrm{AIC}$ (where AIC_i is the AIC of model M_i). Noting that AIC is an estimate of -2 times the log likelihood of the model (see eq. 5.1; Wagenmakers & Farrell 2004: 194), the relative likelihood L of model M_i is estimated as:

$$L(M_i|\text{data}) \propto exp\left\{-\frac{1}{2}\Delta_i(\text{AIC})\right\} \tag{5.2}$$

Finally, these likelihood estimates are normalized to obtain Akaike weight values for each model. Thus the Akaike weight $w_i(\text{AIC})$ for model M_i is:

$$w_i(\text{AIC}) = \frac{exp\left\{-\frac{1}{2}\Delta_i(\text{AIC})\right\}}{\sum\limits_{k=1}^{K} exp\left\{-\frac{1}{2}\Delta_k(\text{AIC})\right\}} \tag{5.3}$$

Wagenmakers & Farrell (2004: 194) note that an Akaike weight represents the probability that a given model is the optimal model among the candidates, and that the strength of evidence in favor of one model over another can be determined by taking the quotient of the models' Akaike weights. Akaike weight calculation is implemented in *phytools* via the `aic.w` function.

The use of `fitPagel` coevolution modeling and Akaike weight comparison supplements the aforementioned Independent and Discrete model comparison, as this method additionally implements one-sided correlation models (i.e., where Trait 1 depends on Trait 2, but where the converse correlation is not assumed). It should be noted that there are some additional discrepancies between the two methods. Specifically, `fitPagel` requires binary data with no unknown values, which in practice means that a small number of languages must be excluded from the dataset, as feature values for one trait or the other are unable to be determined from the available descriptive literature. Moreover, this approach estimates transition rates along a single phylogeny, rather than sampling from a set of phylogenies as in the Meade & Pagel models. In order to achieve the closest similarity to the Dependent and Independent model setup, `fitPagel` models take the trimmed consensus tree (Chapter 3) as the input phylogeny. While the results of the `fitPagel` modeling are unlikely to be identical to the BayesTraits results due to these differences in model setup and parameters, we might expect to see similar trends more broadly in terms of correlations between subcomponents of the traits under investigation.

5.2 Correlated evolution results I: BayesTraits discrete character models

Independent and Dependent models were run for each of the six combinations of subcomponents of the number of conjugation classes and conjugation class membership features traits in order to determine whether or not there is evidence in favor of the hypothesis that the evolution of these two traits is correlated to some degree. Log Bayes Factor comparison showed strong evidence in favor of correlation between the evolution of number of conjugation classes (all three subcomponents) with the transitivity-based conjugation class membership feature. The phonology-based conjugation class membership feature showed strong evidence of correlation with the four conjugation classes presence/absence subcomponent. There was no evidence in favor of correlation between the evolution of phonology-based conjugation classes and two or three conjugation classes. Marginal likelihood estimates and Log Bayes Factor calculations for each model are summarized in Table 5.4, Figure 5.1 provides a heatmap visualization of the evidence for correlated evolution.

CORRELATION	MODEL	LH	LOGBF
2 classes, transitivity	Independent	−98.74	
2 classes, transitivity	Dependent	−93.937	**9.609**
2 classes, phonology	Independent	−86.238	
2 classes, phonology	Dependent	−85.49	1.5
3 classes, transitivity	Independent	−82.114	
3 classes, transitivity	Dependent	−78.105	**8.017**
3 classes, phonology	Independent	−69.6	
3 classes, phonology	Dependent	−69.807	−0.413
4 classes, transitivity	Independent	−90.86	
4 classes, transitivity	Dependent	−84.947	**11.827**
4 classes, phonology	Independent	−78.318	
4 classes, phonology	Dependent	−74.235	**8.235**

Table 5.4: Estimated marginal likelihood and Log Bayes Factor for correlated evolution models – LogBF provides strength of evidence in favor of Dependent model for each pairing. A BayesFactor value above 2 indicates preference for the Dependent unrestricted model. LogBF values indicating strong evidence in favor of correlated evolution indicated in bold.

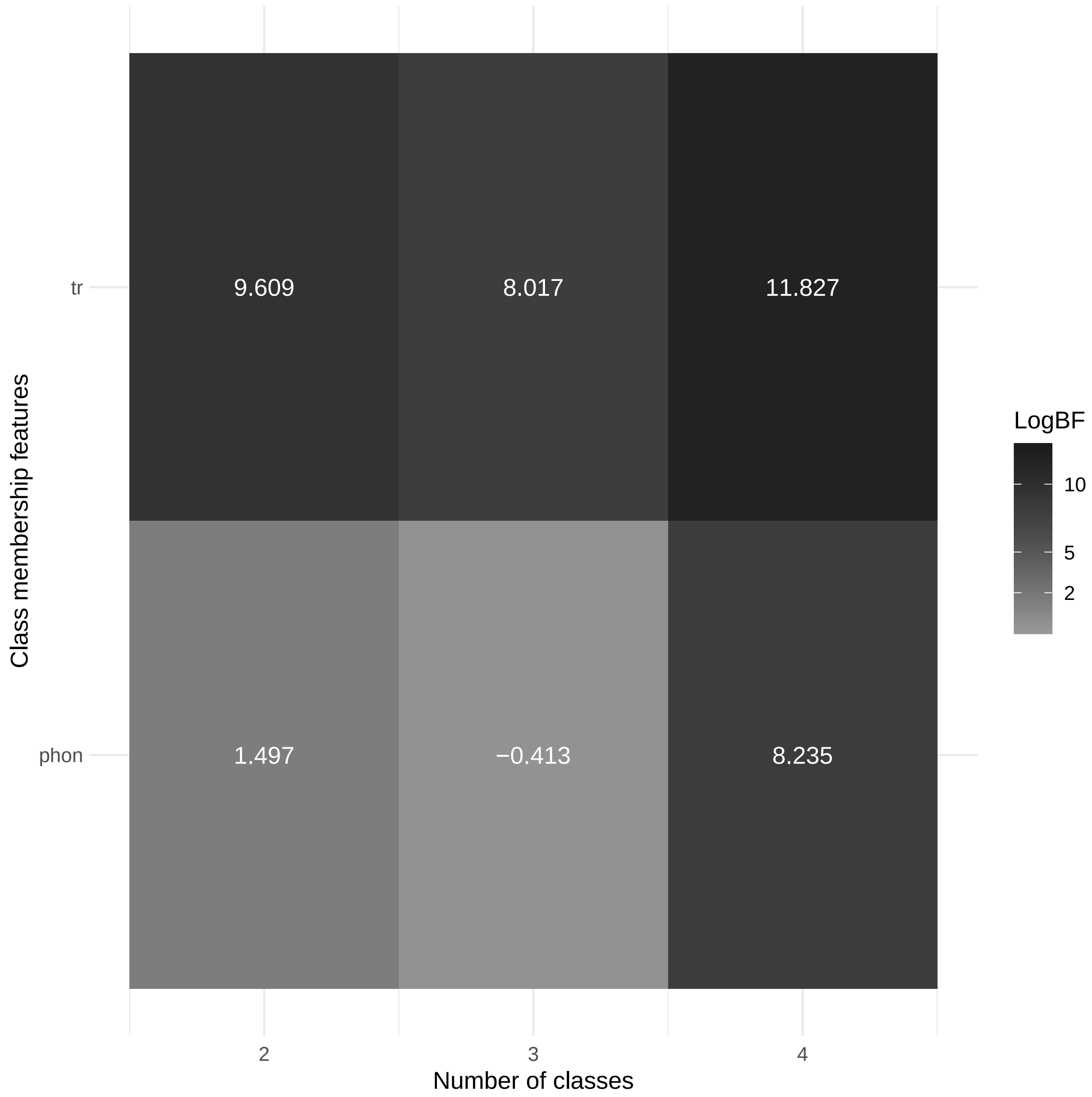


Figure 5.1: Heatmap of LogBF values for six sets of Independent vs. Dependent model comparisons – Visual representation of the evidence in favor of the Dependent (i.e., correlated evolution) model for each of the six possible combinations of class membership features (Y-axis) and number of conjugation classes (X-axis). See Table 5.3 for guidance on interpreting LogBF values. Darker shades indicate more significant evidence in favor of dependent model. Specifically, we see strong evidence in favor of transitivity being correlated with each number of classes subcomponent, while phonology is only correlated with four conjugations.

Thus we see strong evidence in favor of four correlations, namely between transitivity-based membership and each of two (LogBF > 5), three (LogBF > 5), and four (LogBF > 10) conjugation classes and between phonology-based membership and four conjugation classes (LogBF > 5). Leaving aside the interactions between phonology-based membership and two and three conjugation classes, which were not supported by the LogBF comparison, we can investigate the estimated transition rates in order to learn more about which state to state transitions are responsible for the correlated evolution between subcomponents. Table 5.5 summarizes the transition rates for the four dependent models indicating correlated evolution.

MODEL	q_{12}	q_{13}	q_{21}	q_{24}	q_{31}	q_{34}	q_{42}	q_{43}
2 class, transitivity	0.413	0.191	**1.105**	**1.543**	0.906	0.898	**1.259**	0.215
3 class, transitivity	0.733	0.08	0.67	**0.955**	0.502	0.594	**1.009**	0.277
4 class, transitivity	0.391	0.134	**1.307**	**1.351**	0.477	0.427	0.55	0.234
4 class, phonology	0.175	0.643	0.614	0.692	**1.267**	**1.79**	0.203	0.508

Table 5.5: Estimated transition rates for four Dependent models of correlated evolution – Size of estimated transition rate relative to other rates in a given model indicates importance of that transition in the model. Largest rates for each model indicated in bold. See Table 5.2 for an overview of transition rate parameters.

We can also make use of directed arrow plots to visualize the relative size of estimated rates, allowing clear interpretation of the pathways of evolution each model favors. Recall that arrow thickness visualizes relative weight of a given transition rate with respect to other rates in the model. A dashed arrow indicates a very small rate that is unlikely to be providing much influence on the outcome of the model. Figures 5.2-5.5 depict the current model results summarized in Table 5.5:

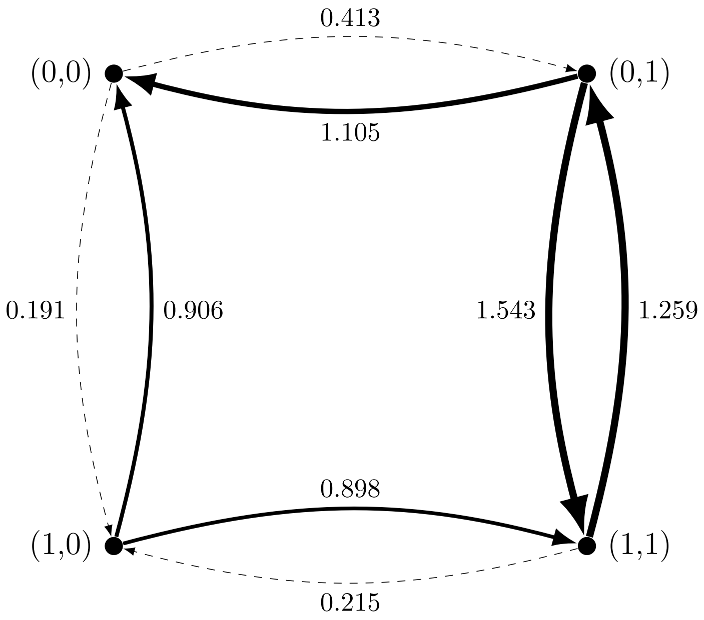


Figure 5.2: Estimated transition rates for Dependent model; 2 conjugation classes and transitivity-based membership

Note the prominence of the transition rates between states (0,1) and (1,0) in both directions, indicating that most of the transitions in the model were related to fluctuations in the 2 conjugation classes feature in the presence of transitivity-based conjugations. A relatively high rate was also estimated for the transitions from (0,1) and (1,0) to (0,0). These rates represent the loss of a given feature in the absence of the other. Reasonable support for the gain of transitivity-based conjugations in the presence of two classes (transition from (1,0) → (1,1)) is also observable. The lowest rates were estimated for transitions to (1,0) from either (0,0) or (1,1), i.e., the model does not support the gain of two conjugation classes in the absence of transitivity-based membership or the loss of transitivity-based membership in the presence of two conjugation classes.

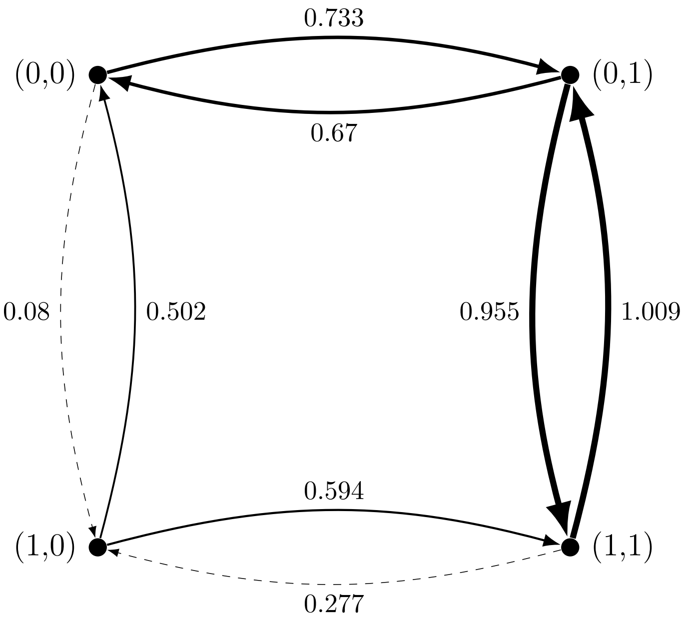


Figure 5.3: Estimated transition rates for Dependent model; 3 conjugation classes and transitivity-based membership

There are many similarities between this model and the previous one. This model privileges transitions involving the gain and loss of three conjugation classes in the presence of transitivity-based membership, a finding in parallel with directed arrow plot (i) in Figure 5.3 for the model correlating the evolution of two conjugation classes and transitivity-based membership and potentially further substantiating the findings of ancestral state reconstruction analysis (Chapter 4) indicating reconstruction of either two or three conjugation classes with equal probability. Moderate support is observable for transitions between (0,0) and (0,1) in both directions, reflecting fluctuation in the gain and loss of transitivity-based membership in the absence of three conjugation classes. Less prominent are the transitions to (0,0) and (1,1) from (1,0). Transitions from (0,0) or (1,1) to (1,0) are not supported.

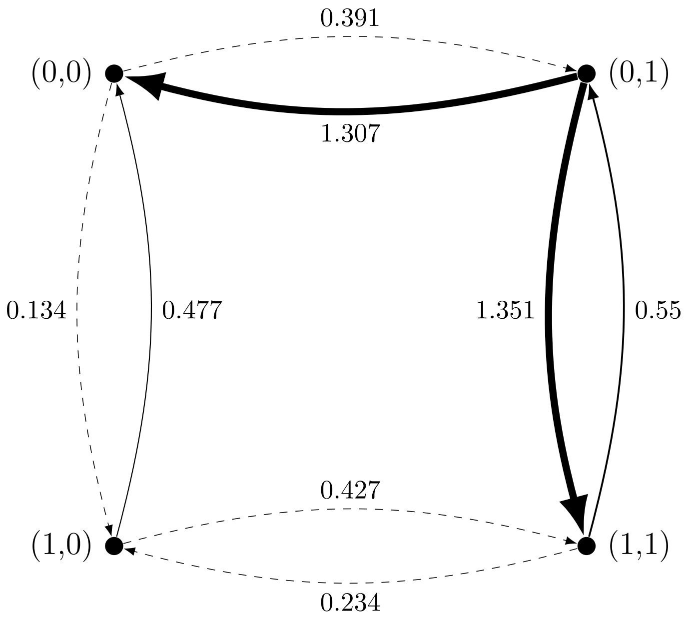


Figure 5.4: Estimated transition rates for Dependent model; 4 conjugation classes and transitivity-based membership

As with the previous two models, a relatively high transition rate is estimated for the transition from (0,1) → (1,1), here indicating the gain of four conjugation classes in the presence of transitivity-based membership. Unlike the previous transitivity-membership models, the transition from (1,1) → (0,1) is not featured. This indicates that the correlation between fluctuations in the number of conjugation classes subcomponent and the presence of transitivity-based conjugations is not bi-directional. Like the two class model and unlike the three class model, the four class model estimates a high transition rate from (0,1) → (0,0), indicating that the loss of transitivity-based membership is associated with the absence of four conjugation classes. The remaining transition rates are unremarkable in terms of their support for other state to state transitions, though note the very low rates for transitions from (0,0) and (1,1) to (1,0), a common thread between the transitivity-based models examined here.

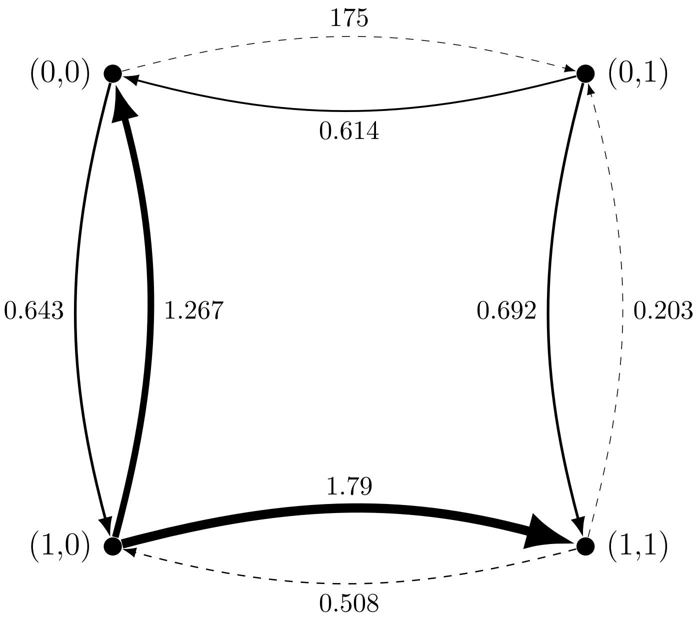


Figure 5.5: Estimated transition rates for Dependent model; 4 conjugation classes and phonology-based membership

The lone model showing support for correlated evolution involving phonology-based conjugation class membership is also distinct from the three aforementioned transitivity-based membership models in terms of the relative size of estimated transition rates. The highest rates are assigned to transitions from (1,0) to (1,1) and (0,0). This can be interpreted as evidence for the scenarios where loss of four conjugation classes is associated with the absence of phonology-based membership and where the gain of phonology-based membership is associated with the presence of four conjugation classes. Moderate support for various other transitions is present in this model, including (0,0) → (1,0) (the gain of four conjugations in the absence of phonology-based membership), (0,1) → (0,0) (the loss of phonology-based membership in the absence of four conjugation classes), and (0,1) → (1,1) (the gain of four conjugation classes in the presence of phonology-based membership). The lowest rates were estimated for transitions from (0,0) → (0,1) (gain of phonology-based membership in the absence of four conjugations) and (1,1) → (0,1) (loss of four conjugations in the presence of phonology-based membership). Each of these findings is consistent with a strong association between exuberant conjugation class inventory sizes (four or more) and phonology-based membership. In other words, languages with four or more conjugation classes tend to gain phonology as a defining factor on class membership.

A few generalizations can be drawn by looking at the relative weighting of transition rates in Table 5.5 and Figures 5.3-5.6, both within and across models. Note that each of the models involving transitivity-based conjugation class membership privilege similar sets of transition rates. More specifically, all three have a relatively high estimated rate for the transition (0,1) → (1,1), which is associated with the transition from state 0 to 1 for the number of conjugation classes subcomponent in the presence of transitivity-based conjugation class membership. Moreover, note that the transition rate for (0,0) → (1,0), which is associated with the transition from state 1 to 0 for number of conjugation classes in the absence of transitivity-based conjugation classes, is the lowest transition rate in all three transitivity feature models. These findings are perhaps unsurprising, in that they likely reflect the strong association between transivitity and conjugation class membership that has been noted in the descriptive literature on Pama-Nyungan languages (Chapter 1) and further substantiated by Bayesian ancestral state reconstruction (Chapter 4), as well as the observation that languages with more verb conjugation classes tend to regularize monosyllabic verbs into their own conjugation class.

Furthermore, note that a different set of transition rates are important for the model of correlation between four conjugation classes and phonology-based membership. For this model the largest rate was that of (1,0) → (1,1) representing the transition from 0 to 1 for the phonology-based membership feature in the presence of four conjugation classes. Also important in this model was the transition (1,0) → (0,0), representing the transition from 1 to 0 for the four conjugation classes feature in the absence of phonology-based conjugation class membership. The relative weighting of transition rates in the model correlating the evolution of four or more conjugation classes and phonology-based membership is highly suggestive of a strong relationship between the two features.

5.3 Correlated evolution results II: `fitPagel` and Akaike weights

As discussed in §5.1.2, the R package *phytools* (Revell 2012) allows for straightforward comparison of multiple different independent and correlated models of discrete trait evolution using weighted AIC values. As noted above, employment of the `fitPagel` method requires minor pruning of the sample to eliminate uncertain datapoints and the reconstruction over a single tree (a consensus tree of the Pama-Nyungan family in this case). Four models of character evolution were fit for each of the six possible combinations of trait subcomponents. The Independent model assumes no correlation in the evolution of the two features, while the Dependent x&y model assumes a bi-directional correlation between the two. These first two models parallel the implementation of Pagel's (1994) discrete character models in BayesTraits. The Dependent x and Dependent y models are novel in the context of the current exploration, testing the hypotheses that one of the features depends on the other, but that the converse correlation does not hold. Specifically, the Dependent x model represents the case where the number of conjugation classes is dependent on the conjugation class membership feature, while the Dependent y model represents the opposite case where the conjugation class membership feature is dependent on the number of conjugation classes. Akaike weight calculations allow choice between related models. Table 5.6 summarizes results of each model in terms of AIC and Akaike weights. Figure 5.7 provides a heatmap visualization of the results.

Correlation	Model	AIC	Akaike weight
2 classes, transitivity	Independent	182.976	0
2 classes, transitivity	Dependent x&y	163.35	**0.638**
2 classes, transitivity	Dependent x	165.308	0.24
2 classes, transitivity	Dependent y	166.66	0.122
2 classes, phonology	Independent	156.581	**0.435**
2 classes, phonology	Dependent x&y	159.415	0.106
2 classes, phonology	Dependent x	156.853	0.38
2 classes, phonology	Dependent y	159.993	0.079
3 classes, transitivity	Independent	149.928	0.023
3 classes, transitivity	Dependent x&y	145.363	0.228
3 classes, transitivity	Dependent x	143.254	**0.655**
3 classes, transitivity	Dependent y	147.149	0.093
3 classes, phonology	Independent	123.533	**0.341**
3 classes, phonology	Dependent x&y	124.982	0.165
3 classes, phonology	Dependent x	123.631	0.325
3 classes, phonology	Dependent y	124.93	0.17
4 classes, transitivity	Independent	171.533	0.011
4 classes, transitivity	Dependent x&y	164.01	**0.455**
4 classes, transitivity	Dependent x	164.088	0.438
4 classes, transitivity	Dependent y	167.111	0.097
4 classes, phonology	Independent	145.137	0.003
4 classes, phonology	Dependent x&y	137.79	0.125
4 classes, phonology	Dependent x	135.669	0.362
4 classes, phonology	Dependent y	134.989	**0.509**

Table 5.6: AIC and Akaike weights for four models of correlated evolution

Support for the Dependent x&y model (two-way correlation) is found for the coevolution of two and four conjugation classes with transitivity-based membership. Dependence of the number of conjugation classes on the class membership feature (Dependent x model) is evident for the relationship betweeen three conjugation classes and transitivity-based membership. Dependent y model support indicates evidence that the evolution of phonology-based membership is dependent on the four or more conjugation classes feature. For the association between phonology-based membership and two or three conjugation classes, a higher relative weight for the Independent model suggests no clear evidence of coevolution.

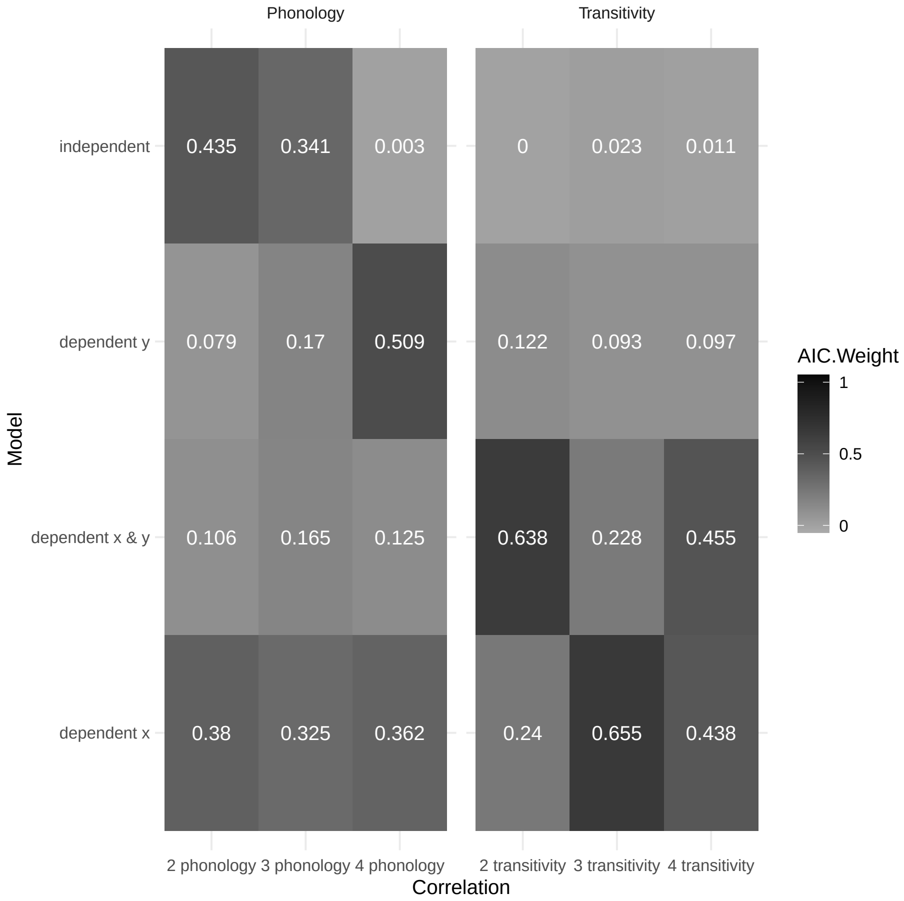


Figure 5.6: Heatmap of Akaike weights for six sets of Independent vs. Dependent model comparisons, `fitPagel` method – Akaike weights (§5.1.2) provide evidence of support for one (or more) model(s) out of a set of competitors. Each column of the heatmap represents a different hypothesized correlation. Darker shaded cells indicate a higher probability of preference for the indicated model.

Turning now to the results of the `fitPagel` modeling and Akaike weight model comparison (Table 5.6; Figure 5.7) we can draw several parallels with the BayesTraits reconstruction models in §5.2. The results are summarized as follows.

Like the discrete models above, the Independent model, indicating a lack of correlated evolution (either two-way or one-way), was preferred for the interactions between two or three conjugation classes and phonology-based membership. It should be noted that in both cases, the Dependent x model performed only slightly worse than the Independent model, indicating the possibility that the evolution of two and/or three conjugation classes is dependent on the presence or absence of phonology-based membership. Moreover, the low probability assigned to the Dependent x&y and Dependent y models indicates that the dependence of phonology-based conjugations on two or three conjugation classes is not supported.

For the correlations between two conjugation classes and transitivity-based membership, the highest probability is assigned to the two-way correlation model, a finding that is in concert with the discrete Dependent model result. Moreover, the model that assumes the two conjugation class feature is dependent on transitivity-based membership (Dependent x model) is twice as likely as the model that assumes the converse (Dependent y model). This finding is potentially reflected in the relatively higher estimated rates involving fluctuations in the gain and loss of two conjugations in the presence of transitivity-based membership found in the Dependent model above. There was no support for the Independent model, indicating strong evidence for correlation between the two features.

With respect to the interaction between three conjugation classes and transitivity-based membership, we find a slight divergence from the Meade & Pagel model, although the overall indication of some degree of coevolution is consistent with previous findings. The highest Akaike weight for the Dependent x model indicates support for the hypothesis that the evolution of three conjugation classes is dependent on transitivity-based membership. This again paralells earlier findings, as does the similarity in this regard between this set of models and the set of models investigating the relationship between two conjugation classes and transitivity-based membership.

The interaction between four conjugation classes and transitivity again shows evidence of coevolution, with the probability being roughly evenly split between the Dependent x&y and Dependent x models. As with the other transitivity-based membership models, a low Akaike weight indicates little support in favor of dependence between transitivity-based membership and four conjugation classes alone or of independence between the two traits. This finding is consistent as well with the earlier model results.

Finally, the `fitPagel` model of coevolution of four conjugation classes and phonology-based membership supports the hypothesis that phonology-based membership is dependent on four conjugation classes. Interestingly, while there is some additional support for the dependence of four conjugations on phonology-based membership, two-way coevolution is not supported. Independence between the two traits is not predicted. Note the difference in the Akaike weight profile of the dependent models for this interaction as compared with the three transitivity-based membership models. In the transitivity models, either Dependent x&y or Dependent x are assigned the highest probability. This interaction provides the only example of the prominence of the Dependent y model.

5.3.1 Discussion

Put together, the results of correlated evolution modeling and the main reconstruction results in Chapter 4 allow us to draw important generalizations about the evolution of the verb conjugation class system in Pama-Nyungan. At the core of the system are two verb conjugation classes with a strong correlation between class membership and transitivity. The evolution of larger numbers of conjugations (beyond three) is associated with the introduction of phonology as a conditioning factor on membership alongside transitivity, indicating the role of stem phonology as a secondary characteristic in determining which verbs belong to which conjugation class. More specifically, we find evidence in favor of the following implicational relations between number of conjugation classes and membership features:

1. There is a strong correlation between two conjugation class systems and transitivity-based membership. This correlation is bidirectional, in that the gain of either feature is conditioned by the presence of the other. The converse is also true, the absence of either feature is correlated with the loss of the other. This could indicate that a loss of transitivity as a conditioning factor on conjugation membership leads to loss of conjugations.

2. The existence of three conjugation class systems relies on the presence of transitivity as a conditioning factor on membership. Results from Chapter 4 indicate that languages with more than three conjugation classes are unlikely to lose distinctions and move to a state of having three classes. Results of correlated evolution modeling indicate that languages that lack transitivity-based membership are similarly unlikely to gain a third conjugation class.

3. The introduction of stem phonology as a membership feature is heavily reliant on the presence of a four or more conjugation class system. The loss of conjugation classes from a state of four to less than four, though uncommon in the model, is strongly correlated with the absence of a correlation between membership and stem phonology.

These findings are also borne out by the typological observations of the modern Pama-Nyungan languages (Chapter 3). Most of the languages included in the current sample show correlation between conjugation class membership and transitivity, while many further show a correlation with both transitivity and phonology. The Warluwaric languages are unique in the language sample in having a conjugation class system in which a correlation between stem phonology and class membership is observed in the absence of transitivity as an additional conditioning factor. Breen (2004: 236-237) argues that the source of the four conjugation classes commonly found in Warluwaric is not a continuation of those found in the prehistory of Pama-Nyungan proper, but rather the interaction between stem-final segmental material and present participle or present tense suffix, in combination with ordinary phonological processes common across the Pama-Nyungan languages. This finding provides a clear explanation for the differences between the Warluwaric phonology-based system and the rest of the Pama-Nyungan languages. As discussed in §3.2.9, Breen (2004: 239) hypothesizes that if an early stage of Warluwaric likely lacked conjugations, with the phonology-based system being an innovation within the subgroup. Alternatively, if we assume Warluwaric did inherit the Pama-Nyungan conjugation classes in some capacity, these were overtaken by the emergence of the phonology-based system and replaced entirely, such that Breen could find no evidence of the expected reflexes of the Pama-Nyungan conjugation system at the time of description.

Chapter 6

Effects of tree topology on reconstruction

The Bayesian ancestral state reconstructions discussed in Chapter 4 used a set of (~4,000) trees as the input topology, with a single topology sampled at each iteration of the model. This chapter briefly discusses the implications of this approach before turning to a more detailed exploration of the effect of tree topology on reconstruction results by reconstructing grammatical traits on single trees that represent distinct topological possibilities present in the larger tree sample. This approach allows us to test different hypotheses about the internal structure of the Pama-Nyungan family by comparing the fit of representative topologies to observed morphological data that was not used in their inference.

Figure 6.1 depicts the frequency with which each tree was observed across samples from a representative ancestral state reconstruction model run. Note that individual trees are sampled more or less frequently from run to run due to the method of randomly selecting a candidate tree at each iteration of the model.

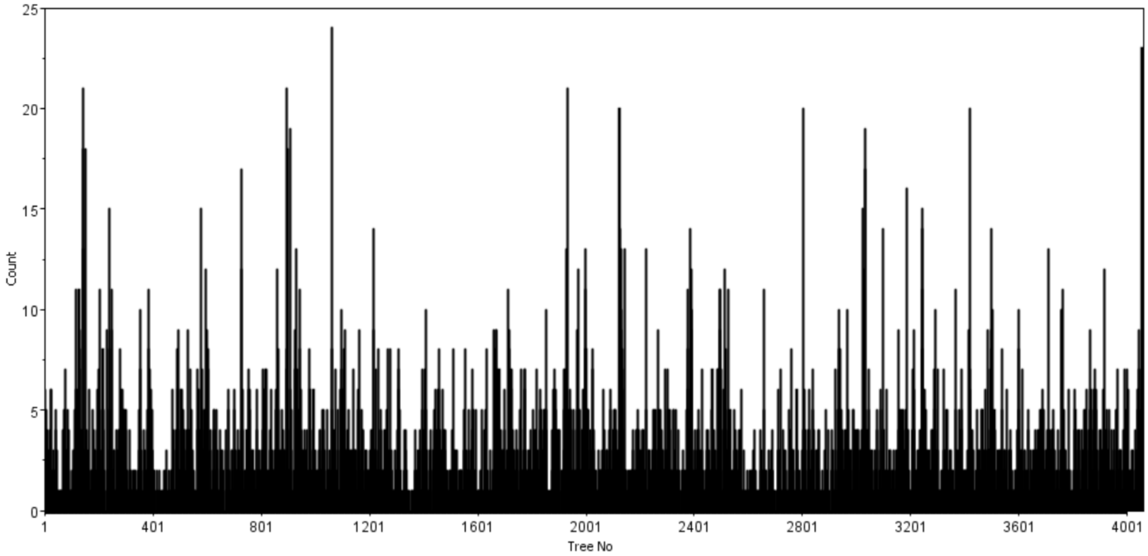


Figure 6.1: Histogram of tree sampling frequency; Presence of conjugation classes character, baseline unrestricted model

In practice, sampling from a set of trees allows us to generalize over uncertainty about the exact internal structure of the Pama-Nyungan phylogeny. Each tree may differ from or resemble others in the set at any of the possible branching nodes. A given node in the phylogeny will be sampled proportionally to the number of trees it appears in; a node that appears in every tree will appear in every iteration of the model, while a less well-supported node will be sampled less frequently on average. We can visualize the distribution of different tree topologies by overlaying them on top of one another using the DensiTree software package (Bouckaert & Heled 2014). What we find is that there is agreement across possible trees with respect to lower-level constituency, i.e., the grouping of small numbers of languages together into subgroups. We can also roughly identify the existence of three larger groupings, while the exact membership in these groups and the way they combine with one another is not well resolved in the sample of trees. In the overlay plot in Figure 6.2, density indicates the support for a given constituency, i.e., how many trees it appears in. Areas of low support are indicated by a less defined grouping or by conflicting groupings with similar levels of support, while overlapping branches indicate areas of uncertainty and subgrouping conflicts.

Figure 6.2: Overlay of ∼4,000 possible Pama-Nyungan tree topologies

Bayesian phylogenetic tree inference results in a set of possible trees with different topologies. Overlaying visualizes relative support for different internal structures. Figure 6.2 overlays ∼4,000 inferred topologies (Bowern & Atkinson 2012; Bouckaert, Bowern & Atkinson 2018) that were used for ancestral state reconstruction (Chapter 4). Areas of the overlay tree with higher density indicate stronger support, i.e., that a given branching exists in a large proportion of trees in the set. Note the stronger support for lower level structure, with more uncertainty higher in the tree. There is a good deal of uncertainty about the dating of internal splits in the phylogeny, which is represented in the overlay as less dense areas mapping the same basic subgrouping that extend to the left (older) or right (younger) of the denser parts of the plot.

Because each difference in tree topology potentially changes the distribution of character states, we may also want to consider the effect of individual tree topology on ancestral state reconstruction. Building on Pagel & Meade's (2004) finding that the maximum probability of a reconstruction is bounded by the maximum posterior probability of the node in the tree sample, varying the input tree or set of trees potentially leads to differences in reconstructions. This approach focuses on the regions of the overall phylogeny where information from inferred trees is not deterministic, using tests of phylogenetic signal and model plausibility based on morphological traits as diagnostic evidence for resolving these areas of uncertainty. The rest of this chapter focuses on the effect of specific topological differences on reconstruction model fit and results via an exploration of differences in the genetic affiliation of the Karnic languages in the context of the larger Pama-Nyungan phylogeny.

6.1 Identifying topologies

In order to investigate the role tree topology plays in inferring the ancestral state of grammatical features, we begin by identifying the relevant topologies we would like to consider in model comparisons. Here the goal is twofold; 1) identification of areas of uncertainty in the Pama-Nyungan phylogeny inferred from lexical cognates and investigation of the ability of closed-class morphological features in discerning between conflicting subgroupings, and 2) determining whether or not loss of conjugation classes has utility as a metric for diagnosing the existence of a clade.

The subgroup containing the Karnic languages, including Arabana, Pitta Pitta, Diyari, Ngamini, Yandruwandha, and Wangkumara provides a vehicle for drawing distinctions between topologies. This subgroup is homogenous in terms of its typological profile (all Karnic languages lack verb conjugation classes) and well supported as a clade in the tree sample. Karnic also represents a point of contention between the tree inference findings of Bowern & Atkinson (2012), which reconstructed a "Central" macro-group that included Karnic (albeit with low support), while Bouckaert, Bowern & Atkinson 2018 did not find evidence for this grouping. Moreover, we can leverage the lack of verb conjugation classes in the Karnic language in order to explore the possibility that the languages without conjugation classes form should be grouped together in the larger tree (i.e., do the languages that lack conjugation classes form one monophyletic group while the languages with conjugation classes form another). This latter consideration ties in with the notions of parsimony and homoplasy, which are discussed in detail in §6.2.2.

We will include Pakaantyi in this set for the current exploration, as it also lacks conjugations, and the clade containing Karnic and Paakantyi has a very high posterior probability in the tree sample ($> 99\%$). Figure 6.3 provides the maximum clade credibility (MCC) tree for the tree sample:[1]

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[1] For this and other trees in this chapter, certain subgroups tangential to the discussion are collapsed in the interest of legibility.

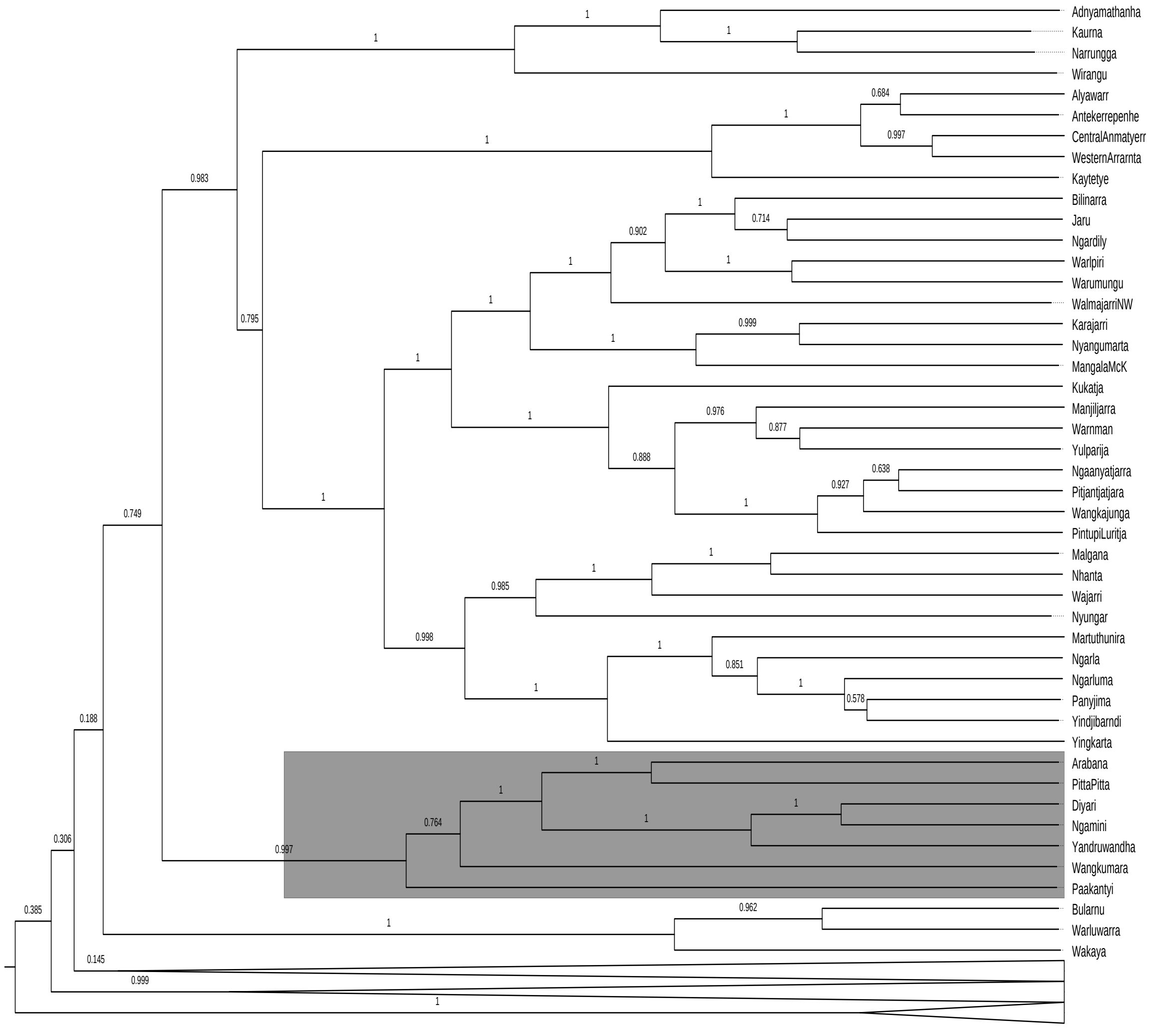


Figure 6.3: Maximum clade credibility tree among ∼4,000 inferred Pama-Nyungan trees – The maximum clade credibility (MCC) method selects the tree from a set of trees that maximizes the product of the posterior probabilities of the included clades. Nodes in the tree are labled with their posterior probabilities. The Karnic languages plus Paakantyi, which patterns with Karnic > 99% of the time, are highlighted.

Importantly, what is not well resolved is the location of the Karnic + Paakantyi clade within the larger Pama-Nyungan phylogeny across the set of inferred trees. This allows us to identify distinct topologies that differ with respect to where Karnic appears for use in a comparative study. Note that the MCC tree in Figure 6.3 associates the Karnic languages with the Central Pama-Nyungan languages, with a reasonably high sample posterior probability of 0.75 (i.e., this clade is present in ∼75% of trees in the sample). Nonetheless, there is a degree of uncertainty as to whether or not Karnic is monophyletic with the Central languages, and if so, what the shared ancestry is between Karnic and certain Central subgroups. This lack of resolution can be visualized (Figure 6.4) by overlaying the constituency of the Karnic + Paakantyi clade for each tree in the sample.

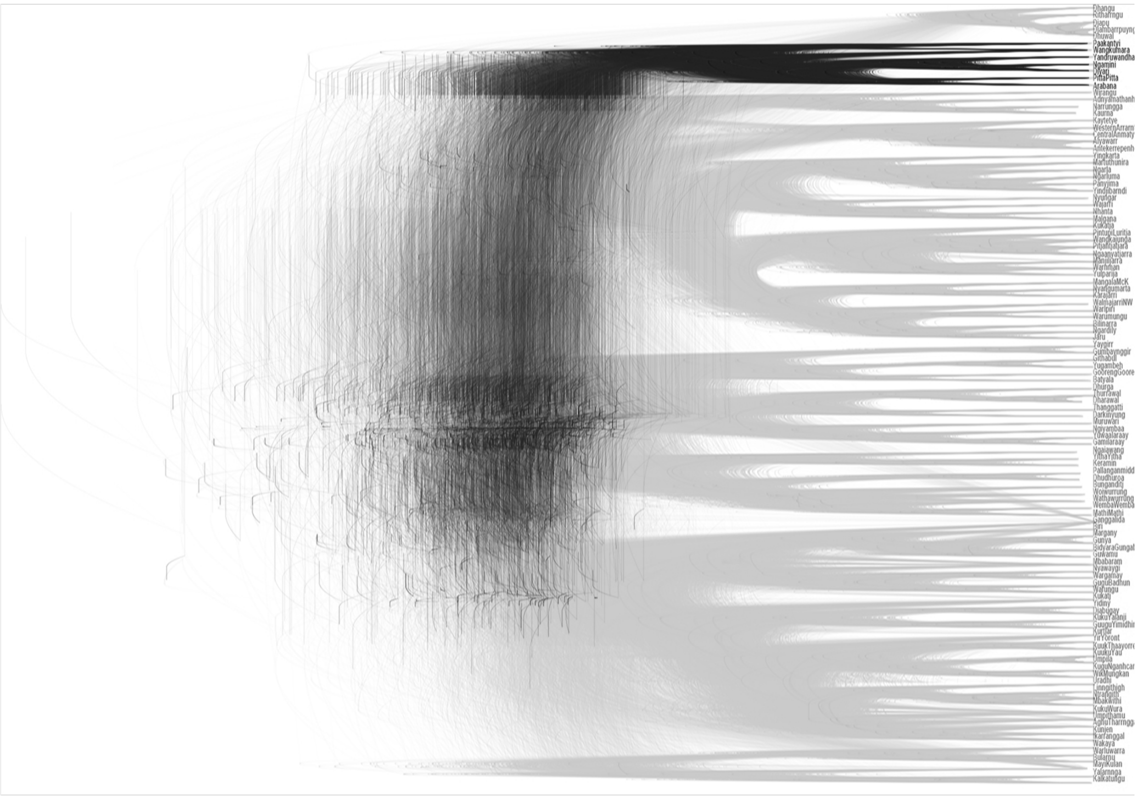


Figure 6.4: Overlay of Karnic subgroup (plus Paakantyi) across ∼4,000 inferred Pama-Nyungan trees

The current study will make use of four individual trees for model comparison, summarized here. Three of these include Karnic as part of Central Pama-Nyungan, while the remaining tree assumes Karnic does not form a clade with the Central languages. The *Monophyletic* tree, shown in Figure 6.5, includes Karnic and Pakaantyi as sharing a common ancestor with the larger Central subgroup. This topology is in concert with the MCC tree (Figure 6.3) with respect to the genetic affiliation of

Karnic.

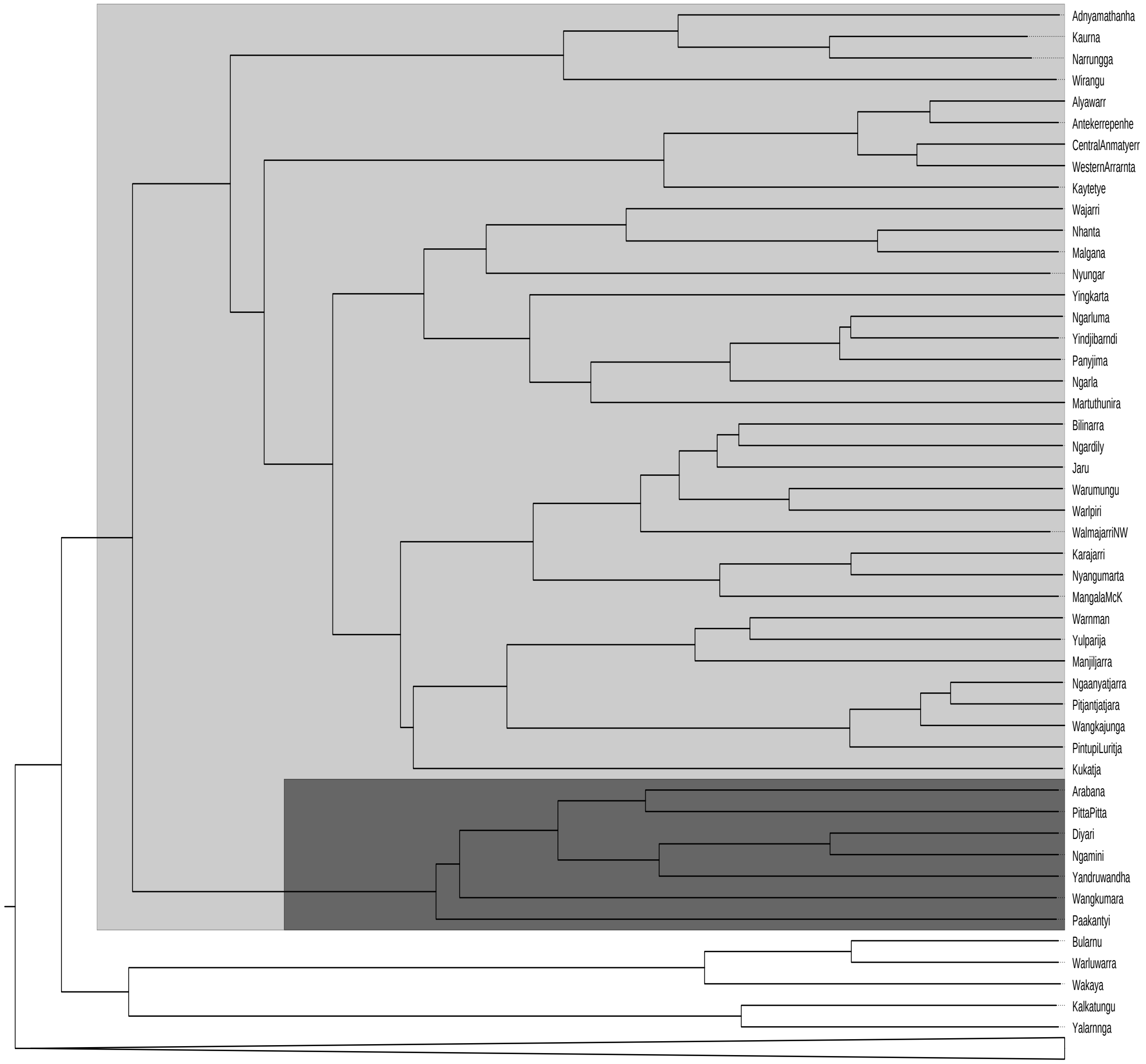


Figure 6.5: Monophyletic Karnic/Central Pama-Nyungan tree – In the *Monophyletic* tree, Karnic (darking shading) forms a clade with the Central Pama-Nyungan macro-group (lighter shading). This represents the highest posterior probability for the placement of Karnic in the tree, as found in the MCC tree in Figure 6.3.

In the *Karnic/Kalkatungic* tree, Karnic shares a common ancestor with the Kalkatungic languages Kalkatungu and Yalarnnga, and it is the resulting clade that forms a subgroup with the Central languages. Interestingly, Yalarnnga (Blake 1971; Sullivan 2005), like the Karnic languages, is not described as having conjugation classes, while Kalkatungu (Blake 1979b) appears to have at two well-defined conjugations, plus additional minor closed conjugations. This topology is shown in Figure 6.6.

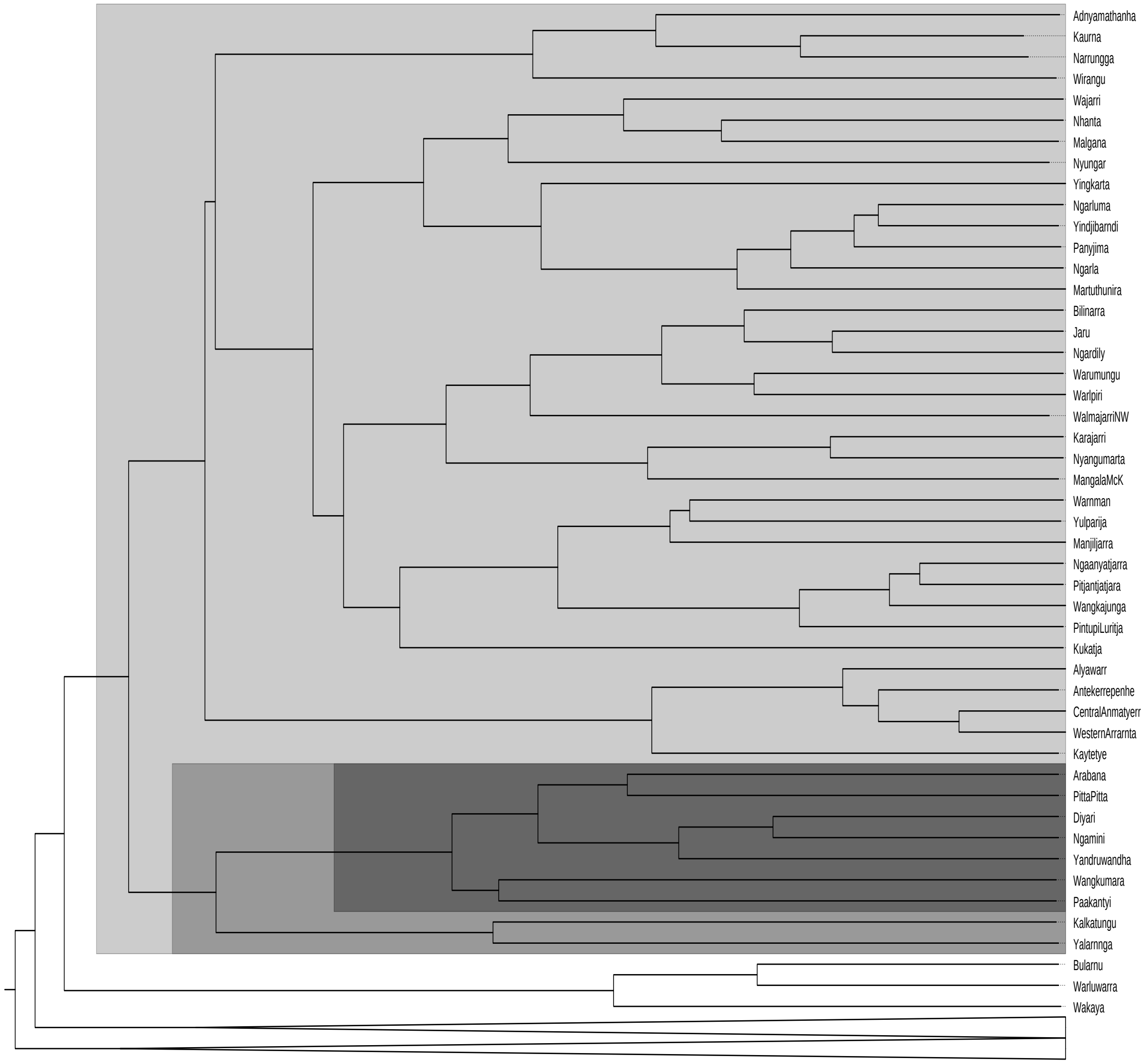


Figure 6.6: Karnic/Kalkatungic tree – In the *Karnic/Kalkatungic* tree, the Kalkatungic languages join with Karnic (darkest shading) before the resulting clade (lighter shading) joins with the Central subgroup (lightest shading).

In the last of the topologies under consideration that places Karnic within the Central Pama-Nyungan clade, the *Yolngu/Central* tree (Figure 6.7), the Yolngu languages Dhangu, Ritharrngu, Dhuwal, Djambarrpuyngu, and Djapu share a common ancestor with the Central languages. The Karnic languages subsequently form a clade with this expanded Central subgroup. The Yolngu languages are characterized by the preservation of intricate patterns of inflection in their verbal morphology.

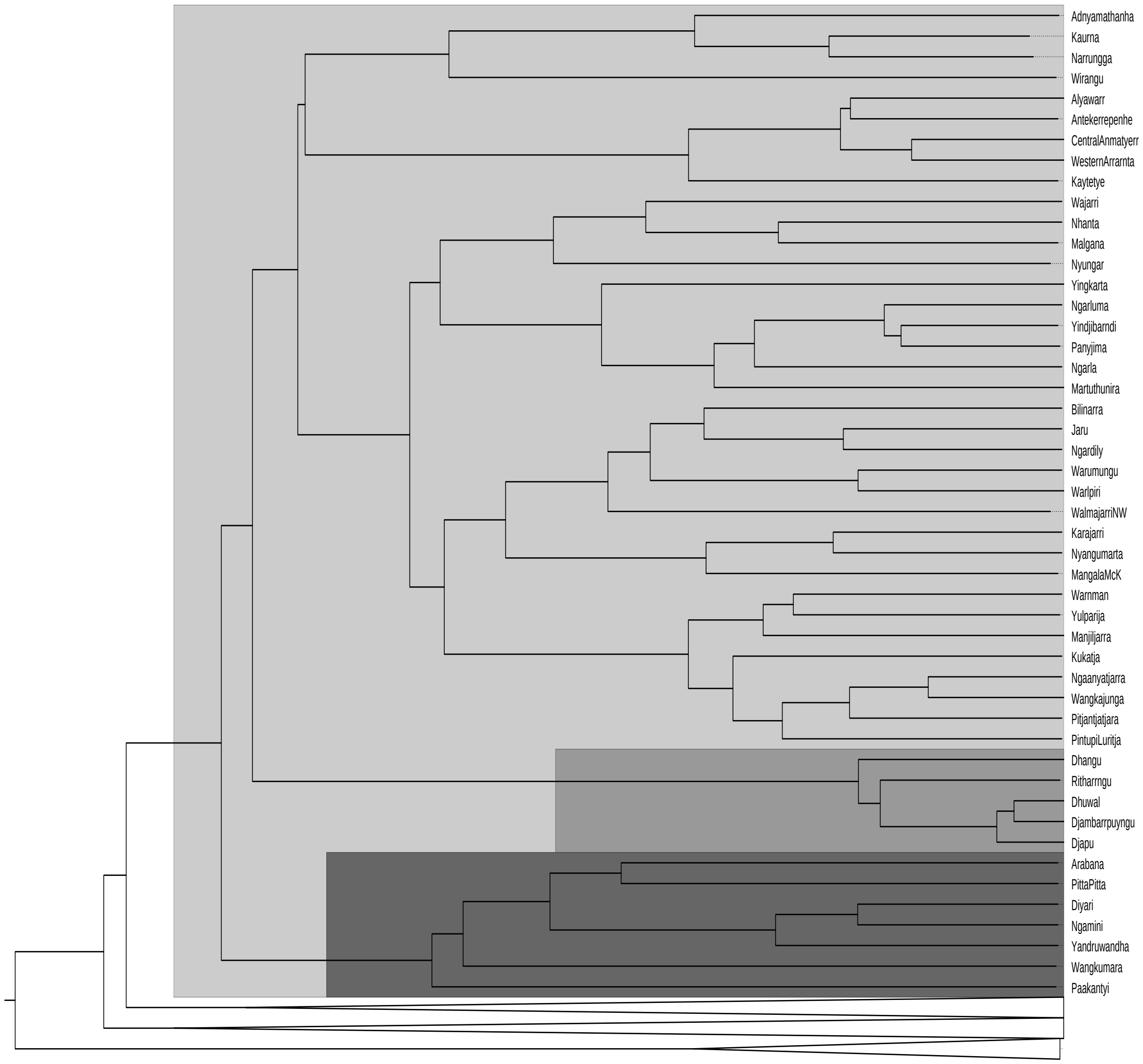


Figure 6.7: Yolngu/Central tree – The Yolngu languages (lighter shading) join with the Central macro-group in the *Yolngu/Central* tree. Karnic (darkest shading) subsequently forms a clade with this subgroup (lightest shading).

While the inclusion of Karnic with the Central group is a common feature of many of the trees in the sample, the possibility that the two subgroups are nonmonophyletic is also represented. The *Nonmonophyletic* tree (Figure 6.8) an example of this possibility, placing Karnic far outside the Central subgroup.

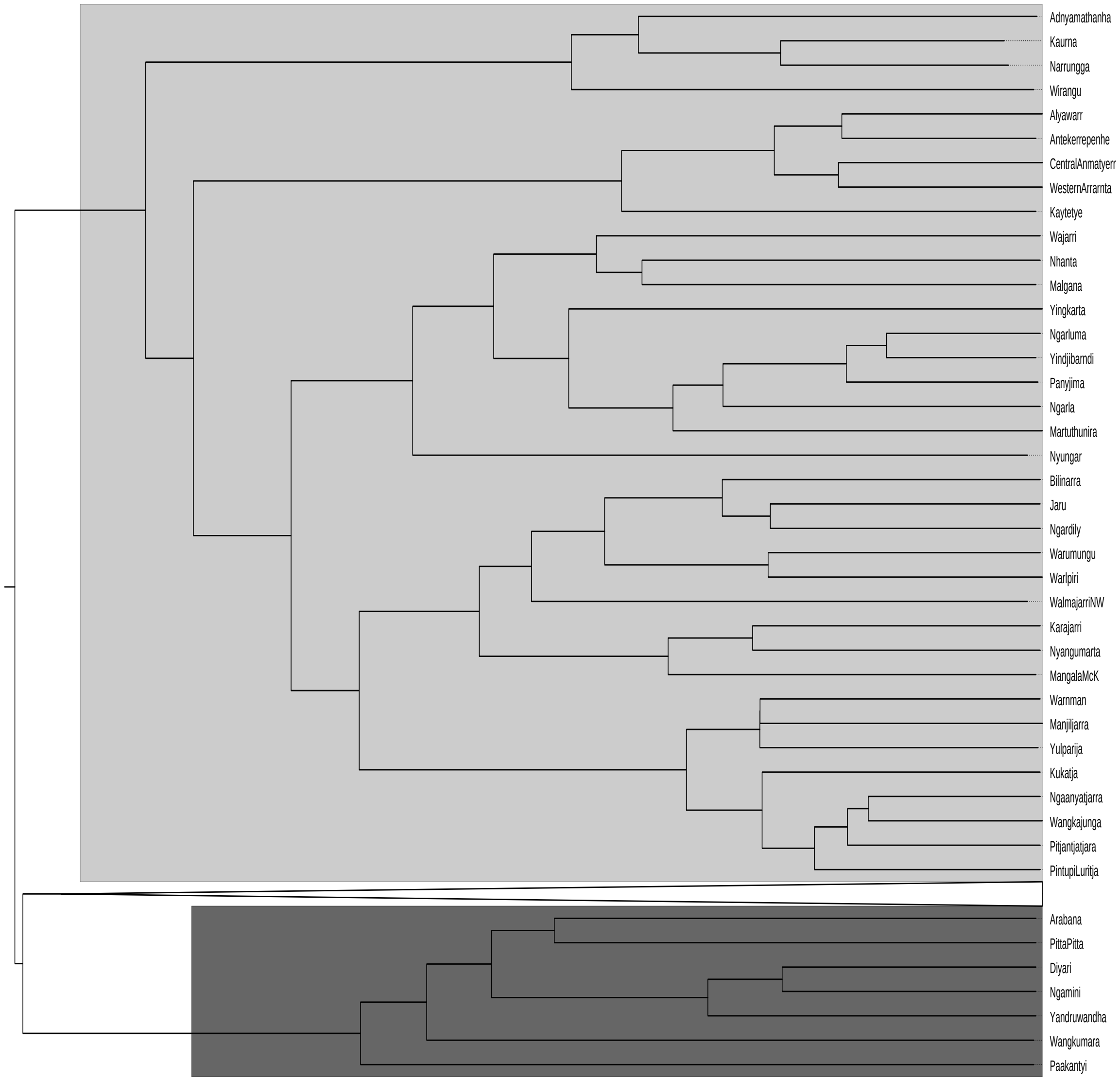
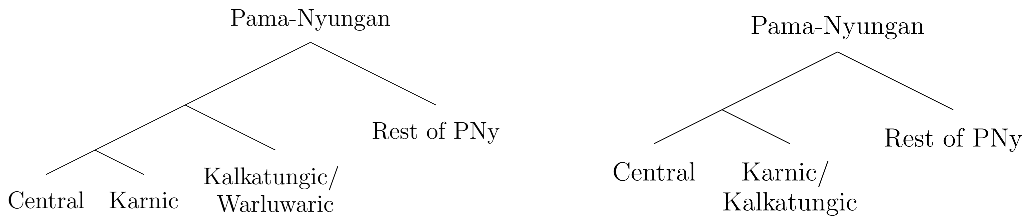
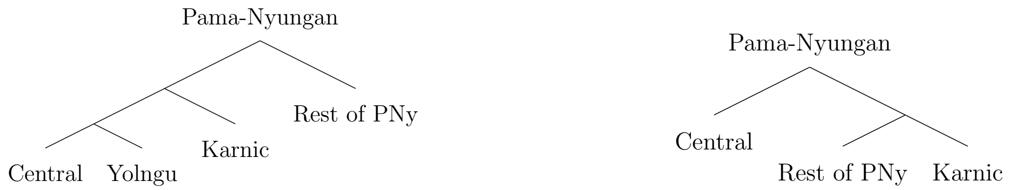


Figure 6.8: Nonmonophyletic Karnic/Central Pama-Nyungan tree – The *Nonmonophyletic* tree does not assume a common ancestry between Karnic (darker shading) and Central Pama-Nyungan (lighter shading) before the root node.

Note that each candidate tree introduces differences in the distribution of character states and the evolutionary history of verb conjugation classes across the phylogeny. Like the MCC tree in Figure 6.3, the Monophyletic tree (Figure 6.5) assumes multiple instances of loss of verb conjugation classes within the common ancestry of the Central Pama-Nyungan languages. The Karnic/Kalkatungic tree (Figure 6.6) introduces an additional gain or loss event, leading to the observed state of the modern Kalkatungic languages. We might expect this tree to be less likely than the Monophyletic tree from a parsimony standpoint. The same could be said for the Yolngu/Central tree (Figure 6.7), which requires either catastrophic collapse of the conjugation system in Karnic and Arandic or rapid proliferation of conjugation classes in the Yolngu languages, both of which are generally unsupported by previous findings (Chapter 4). The Nonmonophyletic tree (Figure 6.7) is interesting, as it removes the earliest instance of loss of conjugations from the Central branch of Pama-Nyungan while simultaneously introducing loss of conjugations earlier than expected elsewhere in the tree. The four topologies under consideration are schematized in Figure 6.9:



(a) Monophyletic **(b)** Karnic/Kalkatungic



(c) Yolngu/Central **(d)** Nonmonophyletic

Figure 6.9: Four Pama-Nyungan trees with different placement of Karnic

6.2 Comparing topologies

Each of the topologies presented in §6.1.1 were tested for strength of phylogenetic signal the goodness of fit of ancestral state reconstruction models. Specific choice of models for comparison was informed by model fit to the full set of possible topologies discussed in Chapter 4. The best fitting model(s) for each character were chosen as diagnostics for this study. Models were run with the same settings as in Chapter 4 to allow valid comparisons. Models were run for 50 million iterations (5 million burn in) with hyperprior optimization of prior selection. The chains were sampled every 5,000 iterations for a total of 10,000 samples per run, and were manually checked for convergence/sufficient mixing of the parameters between samples. Results are given as the average over five independent model runs. The specific models under consideration are as follows. For Character 1, the presence or absence of verb conjugation classes, three different models were used, due to the lack of evidence supporting a single model over the others when tested on the full set of trees. These include the Baseline model, which allows gain and loss of conjugations at potentially different rates, the Restricted model, which allows gain and loss at an equal rate, and the NoGain model, which does not allow the innovation of conjugation classes at any point in the tree. For Character 2, the number of conjugation classes, The No Jump/No Innovation model was chosen. Recall that this model does not allow gain or loss of more than one conjugation class in a single evolutionary step, while also restricting the innovation of conjugation classes at any point in the tree. Finally, the unrestricted Dependent model was used for Character 3, transitivity and/or phonology as a basis for determining verb conjugation class membership. This model assumes correlated evolution between the two membership feature possibilities, while allowing either feature to be gained or lost as a contributing factor on membership (and the other feature) at any evolutionary step.

6.2.1 Phylogenetic signal

Chapters 2 and 4 introduced useful diagnostics for quantifying strength of phylogenetic signal of trait data on a given phylogeny for both binary and multistate traits. Recall that we can take phylogenetic signal to represent evidence for or against the hypothesis that the observed character data is likely to have arisen from processes of language evolution, rather than randomness. Phylogenetic signal for binary traits (Characters 1 and 3) was evaluated for each of the candidate topologies using Fritz & Purvis' (2010) *D* statistic, while Blomberg, Garland & Ives' (2003) *K* measure was used for the multistate Character 2. A *D* value near (or below) zero for binary traits or *K* near or above 1 for multistate traits represents strong phylogenetic signal (thus rejection of the randomness hypothesis). Tables 6.1 and 6.2 present the results of phylogenetic signal evaluation for our four candidate topologies.

CHARACTER	TREE	*D* statistic	P(Brownian)
Character 1	Monophyletic	−0.563	0.96
Character 1	Karnic/Kalkatungic	−0.585	0.97
Character 1	Central/Yolngu	−0.613	0.97
Character 1	Nonmonophyletic	−0.571	0.96
Character 3a	Monophyletic	−0.726	0.99
Character 3a	Karnic/Kalkatungic	−0.746	0.99
Character 3a	Central/Yolngu	−0.76	0.99
Character 3a	Nonmonophyletic	−0.674	0.98
Character 3b	Monophyletic	−0.429	0.85
Character 3b	Karnic/Kalkatungic	−0.46	0.87
Character 3b	Central/Yolngu	−0.562	0.91
Character 3b	Nonmonophyletic	−0.674	0.84

Table 6.1: *D* statistic computation for Characters 1 and 3 across four topologies

Looking at Table 6.1, we see that there is strong phylogenetic signal for all characters and all topologies for the two binary characters. As we saw in Chapter 4, the strength of the signal is slightly less for the phonology-based conjugation class membership feature for all topologies under consideration, but values are all below zero, indicating the highly-conserved nature of these traits.

Character	Tree	K	Variance_{Obs}	Variance_{rdm}	P-value
Character 2	Monophyletic	1.14	0.00057	0.002	0.0001
Character 2	Karnic/Kalka	1.04	0.00072	0.002	0.0001
Character 2	Central/Yolngu	1.04	0.0006	0.002	0.0001
Character 2	Nonmonophyletic	1.04	0.0007	0.002	0.0001

Table 6.2: *K* test of phylogenetic signal for Character 2 across four topologies

We find strong evidence of phylogenetic signal for all four topologies with respect to the distribution of feature states for Character 2 (Table 6.2), both in terms of the K metric and the significant difference in the variance of the data as compared with the variance observed in a random permutation test. While these findings do not allow us to make any strong claims about the preference of one topology over another based on strength of phylogenetic signal, we can use them to validate further consideration of the different trees as input to ancestral state reconstruction models.

6.2.2 Measures of Homoplasy

Another possibility for comparing topologies is to consider how parsimonious each candidate tree is with respect to acconting for the evolution of a character. HOMOPLASY, which occurs when a feature state arises multiple times in the evolutionary history of a character, provides a vehicle for such a parsimony comparison. Homoplasy takes two main forms, namely PARALLEL EVOLUTION, which occurs when related languages share a feature state that is not shared by their common ancestor, and BACK-MUTATION, the return to a feature state that existed in the evolutionary history of the character previously.[2] This section explores the notion of quantifying homoplasy in the Pama-Nyungan verb conjugation class data with respect to the four Pama-Nyungan topolgies outlined in §6.1.

The most common measure of homoplasy is the CONSISTENCY INDEX (CI), along with the related RETENTION INDEX (RI), both of which are discussed briefly here. Given a set of related taxa, the consistency index (c; Kluge & Farris 1969) of some character with respect to tree t is the ratio of the minimum number of changes necessary (m) to map observed character data to any possible tree to the number of changes necessary to map the data to t (s_t):

$$c = m/s_t \tag{6.1}$$

A CI of 1 indicates that the reference tree and maximally parsimonious tree are the same, i.e., no homoplasy, while decreasing values of CI represent increasing amounts of homoplasy and thus increasingly poor fit of the tree to the data. There is no stipulated lower bound for CI, though Kitching et al. (1998; Klingenberg & Gidszewski 2010) show that the measure will not reach zero, even in cases where there are high degrees of homoplasy.

Farris (1989: 417) proposes the related measure RI, which is calculated as the quantity number of changes in the maximally unparsimonious tree minus number of changes in the reference tree divided by the quantity number of changes in the maximally unparsimonious tree minus number of changes in the maximally parsimonious tree:

$$RI = (\Delta_{max} - \Delta_{obs})/(\Delta_{max} - \Delta_{min}) \tag{6.2}$$

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[2] Warnow et al. (2005) provide a broad discussion of the relevance of homoplasy in models of linguistic evolution.

Farris further proposes the rescaled consistency index (RC), which is the product of CI and RI. Both RI and RC have the benefit of ranging between one and zero, allowing for potentially more meaningful comparison than CI in certain contexts.

Computation of CI and RI for the Pama-Nyungan verb conjugation class feature data with respect to four references trees was performed using the R package `phangorn` (Schliep 2011). Results are presented in Table 6.3:

Character	Tree	CI	RI	RC
Character 1	Monophyletic	**0.063**	**0.634**	**0.039**
Character 1	Karnic/Kalkatungic	0.059	0.61	0.035
Character 1	Central/Yolngu	0.056	0.585	0.032
Character 1	Nonmonophyletic	0.056	0.585	0.032
Character 2	**Monophyletic**	**0.125**	**0.569**	**0.071**
Character 2	Karnic/Kalkatungic	0.121	0.554	0.067
Character 2	Central/Yolngu	0.118	0.538	0.063
Character 2	Nonmonophyletic	0.121	0.554	0.067
Character 3a	**Monophyletic**	**0.063**	**0.659**	**0.042**
Character 3a	Karnic/Kalkatungic	0.059	0.636	0.038
Character 3a	Central/Yolngu	0.056	0.614	0.034
Character 3a	Nonmonophyletic	0.053	0.591	0.031
Character 3b	Monophyletic	0.048	0.412	0.02
Character 3b	Karnic/Kalkatungic	0.048	0.412	0.02
Character 3b	Central/Yolngu	0.048	0.412	0.02
Character 3b	Nonmonophyletic	0.048	0.412	0.02

Table 6.3: CI, RI, and RC for 3 characters across four topologies

From Table 6.3, we see that the Monophyletic tree scores slightly higher on each of the measures for each of the characters (with the exception of Character 3b, where all trees resulted in the same values of CI and RI). Note also that the Nonmonophyletic tree resulted in the greatest amount of homoplasy for Characters 1 and 3a, while the Central/Yolngu tree provides the worst fit for Character 2. Though it isn't clear to what degree these small differences are significant, the Monophyletic tree provides the overall best fit for across the characters in terms of homoplasy, which may tentatively suggest preference for the Monophyletic tree based on the morphological data that comprises the current study.

6.2.3 Visualizing effects of varying tree topology

A third possibility for investigating the effect of varying tree topology is to visually inspect the posterior sample of MCMC models fit using the four reference topologies outlined in §6.1, using the same model selection and setup as was defined for the homoplasy diagnostics in §6.2.2. This section explores the effect of tree topology on posterior likelihood, as well as the interaction between estimated transition rates and posterior likelihood.

Character 1: Presence of verb conjugation classes

The No Gain model was used for Character 1. This model has a single transition rate, representing loss of conjugations. Figure 6.10 visualizes the distribution of posterior log likelihood (Lh) separated by tree number. Better likelihood values are associated with Tree 1 (Monophyletic) and to a lesser extent Tree 4 (Nonmonophyletic). Tree 2 (Karnic/Kalkatungic) and Tree 3 (Central/Yolngu) lead to worse likelihood values, indicating worse fit to the data.

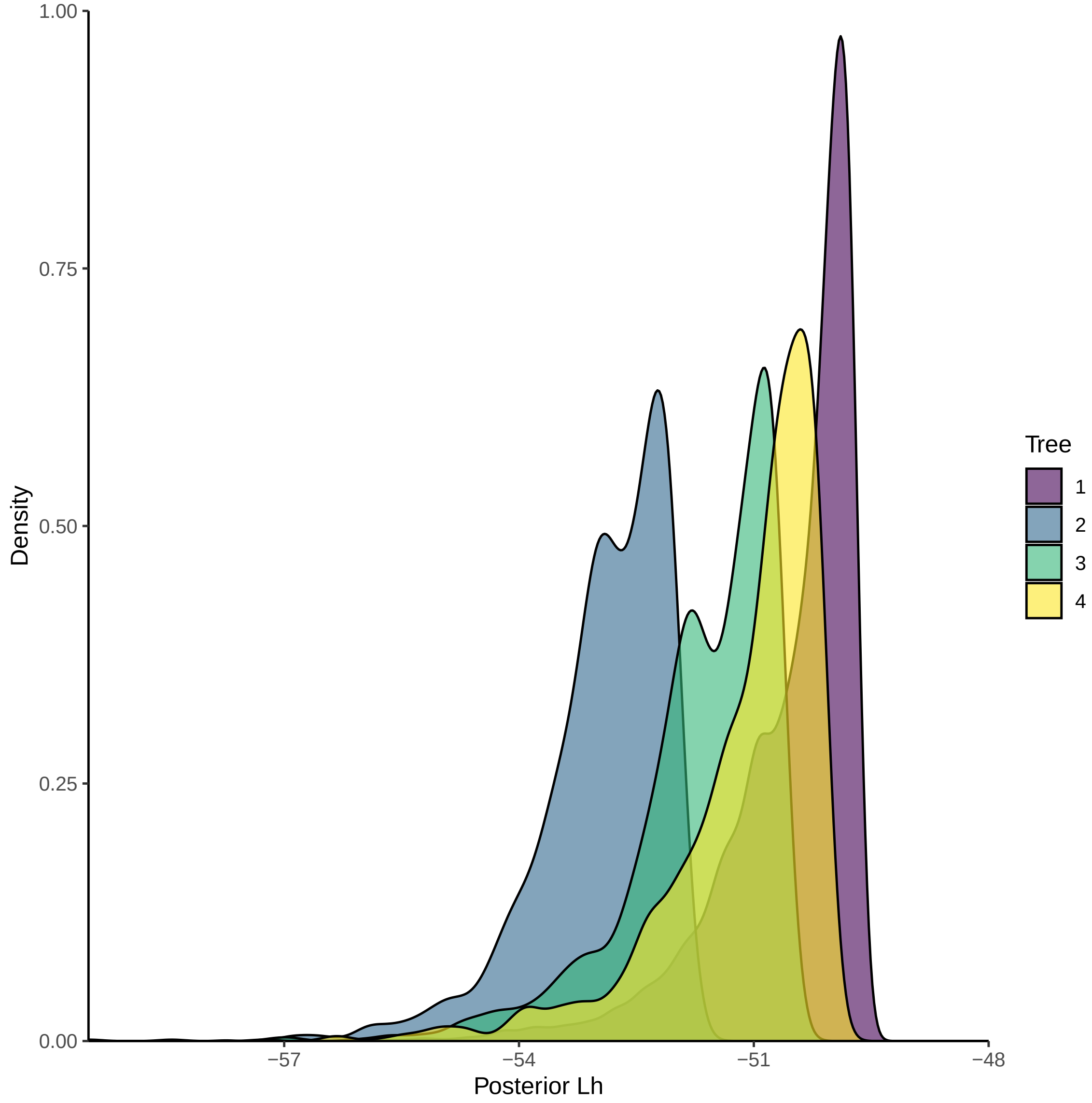

Figure 6.10: Density of posterior likelihood by topology for Character 1

We can also look at the effect of tree topology on the interaction between estimated rates and posterior likelihood. In Figure 6.11 (and subsequent boxplots), the y-axis is the log likelihood of each model for each parameter, while the plot for each tree indicates the mean value of the relevant transition rate on the x-axis. Comparing the median values for likelihood for each rate and tree combination (Figure 6.11), we again see that in the No Gain model of Character 1, Trees 1 and 4 are associated with better fit to the data, while Trees 2 and 3 perform worse. Moreover, note that roughly 75% of the Tree 1 and Tree 4 likelihood values are better than the Tree 3 values, while Tree 2 provides a poor explanation of the data. Mean transition rate value by tree is less informative for this model, as all of the means are grouped together in a small range. Moreover, note that while Trees 1 and 4 are associated with the best fit to the data, the poorly performing Tree 2 has a mean transition rate value closer to Tree 1 than Tree 4 is to Tree 1.

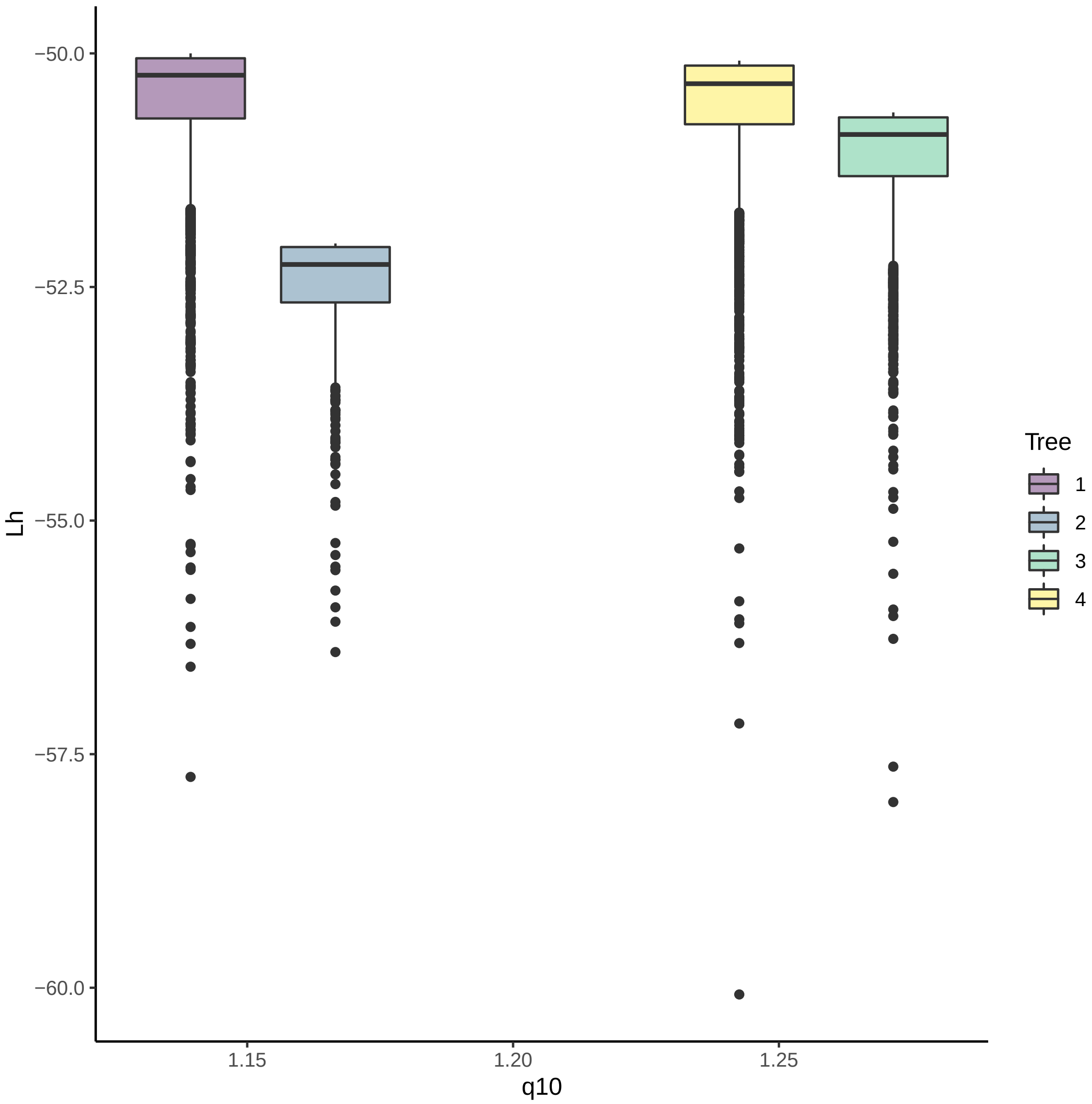

Figure 6.11: Boxplot of posterior likelihood versus estimated transition rate by topology for Character 1

Character 2: Number of verb conjugation classes

For Character 2, results of the No Jumps/Innovation model using the number of conjugation classes data and four reference topologies are presented. Recall that this model removes rates associated with the gain and/or loss of more than one conjugation class in a single evolutionary step, as well as the innovation of conjugation classes from a state of absence. Figure 6.12 plots the density of posterior likelihood values by tree topology. Note that Trees 1 and 4 again provide the best fit to the data, though the distinction between them is less pronounced that in the No Gain model of Character 1. Trees 2 and 3 again provide worse results.

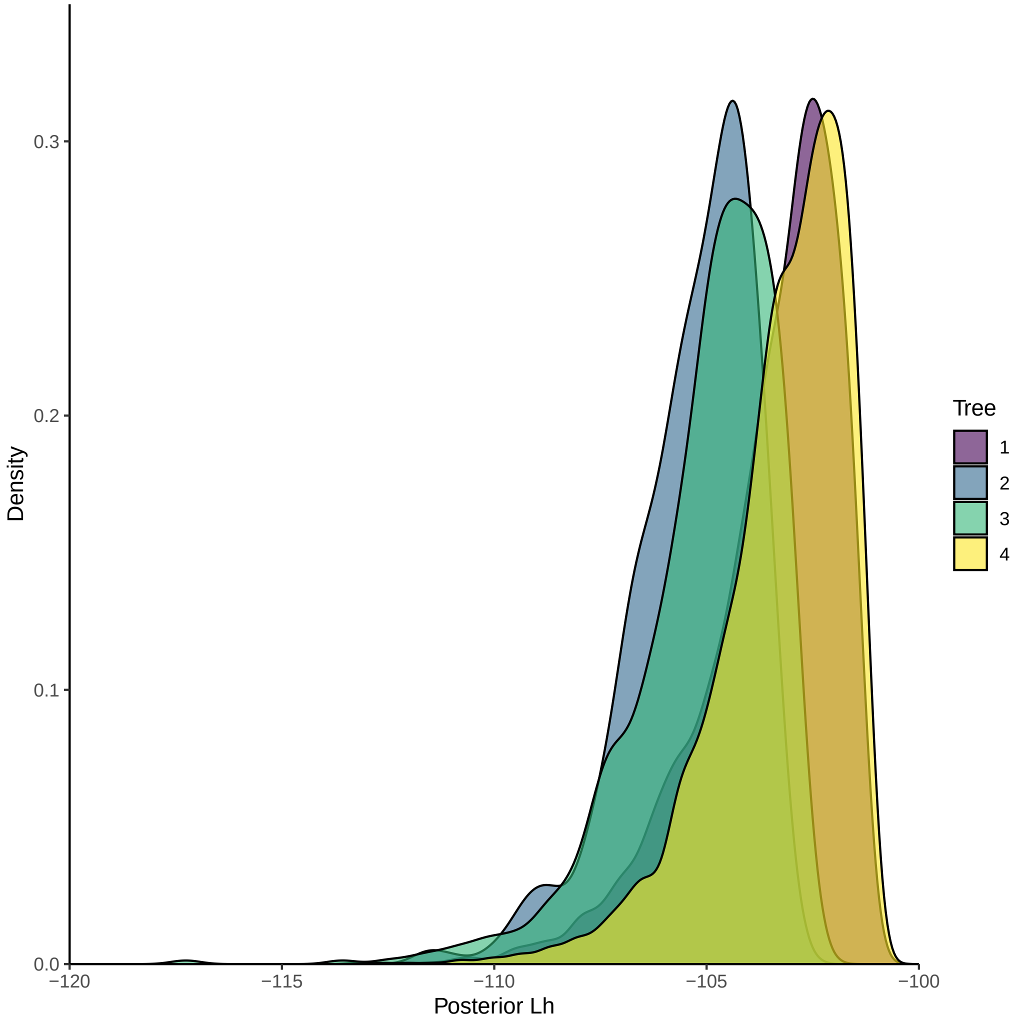

Figure 6.12: Density of posterior likelihood by topology for Character 2

Figure 6.13 visualizes the interaction between estimated transition rates and posterior likelihood by tree topology. For each rate, we again see better fit of Trees 1 and 4 to the data as compared with Trees 2 and 3. Between the latter pair, note that Tree 2 performs slightly better for each of the rates in the Character 2 model relative to the other trees as compared with the results for Character 1.

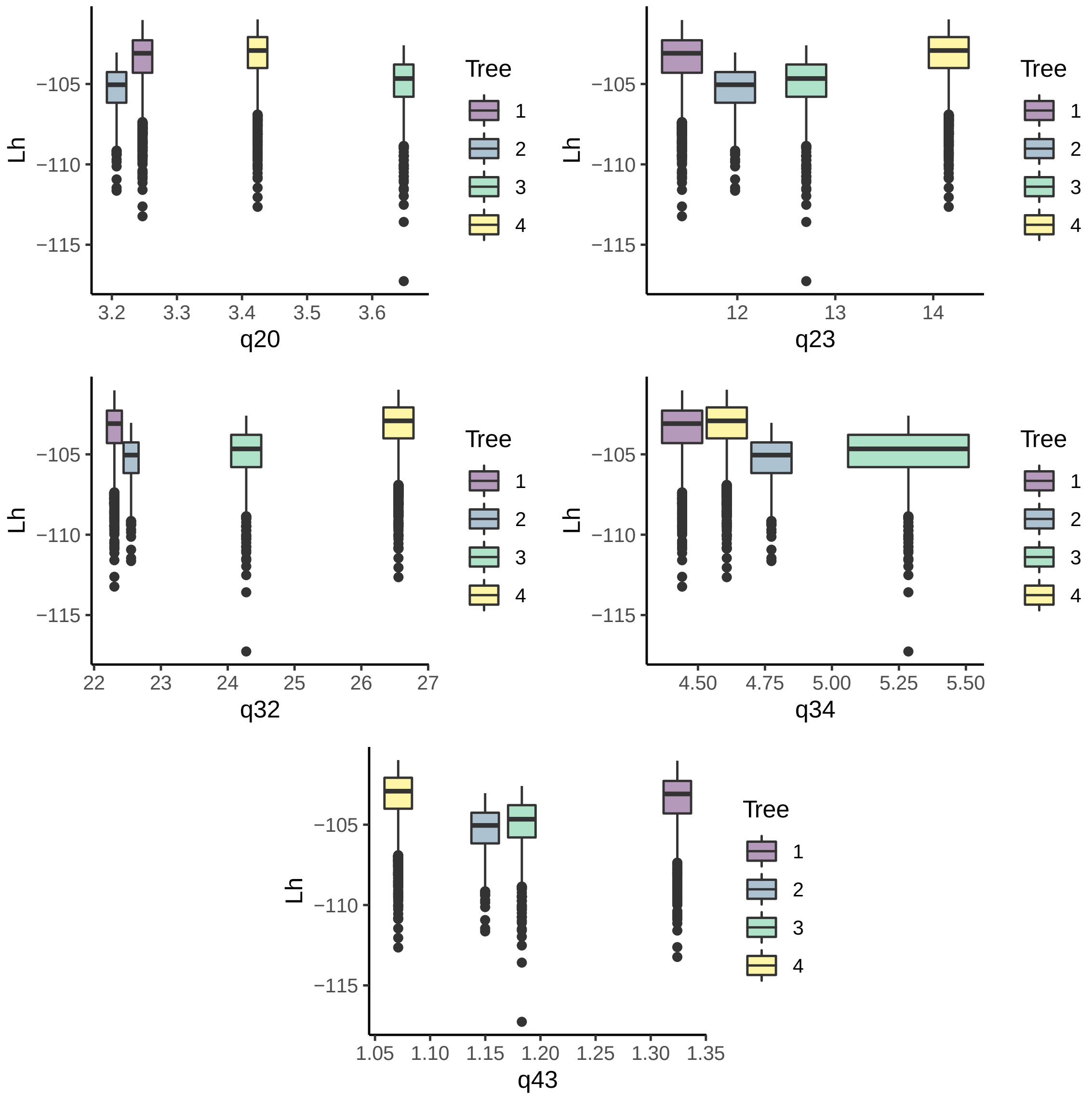

Figure 6.13: Boxplot of posterior likelihood versus estimated transition rate by topology for Character 2

Character 3: Verb conjugation class membership features

Model selection for Character 3 identified the dependent model without restrictions on the eight permissible transitions as the best fit to the data. This model assumes correlated evolution between transitivity- and phonology-based membership in verb conjugation classes. Figure 6.14 visualizes the effect of tree topology on the posterior likelihood of the model. As with models of Character 1 and 2, we see that Tree 1 leads to better likelihood values than the other trees, though note that Tree 4 does not outperform Trees 2 and 3 as in previous models. Trees 2, 3, and 4 show a great deal of overlap in their density curves.

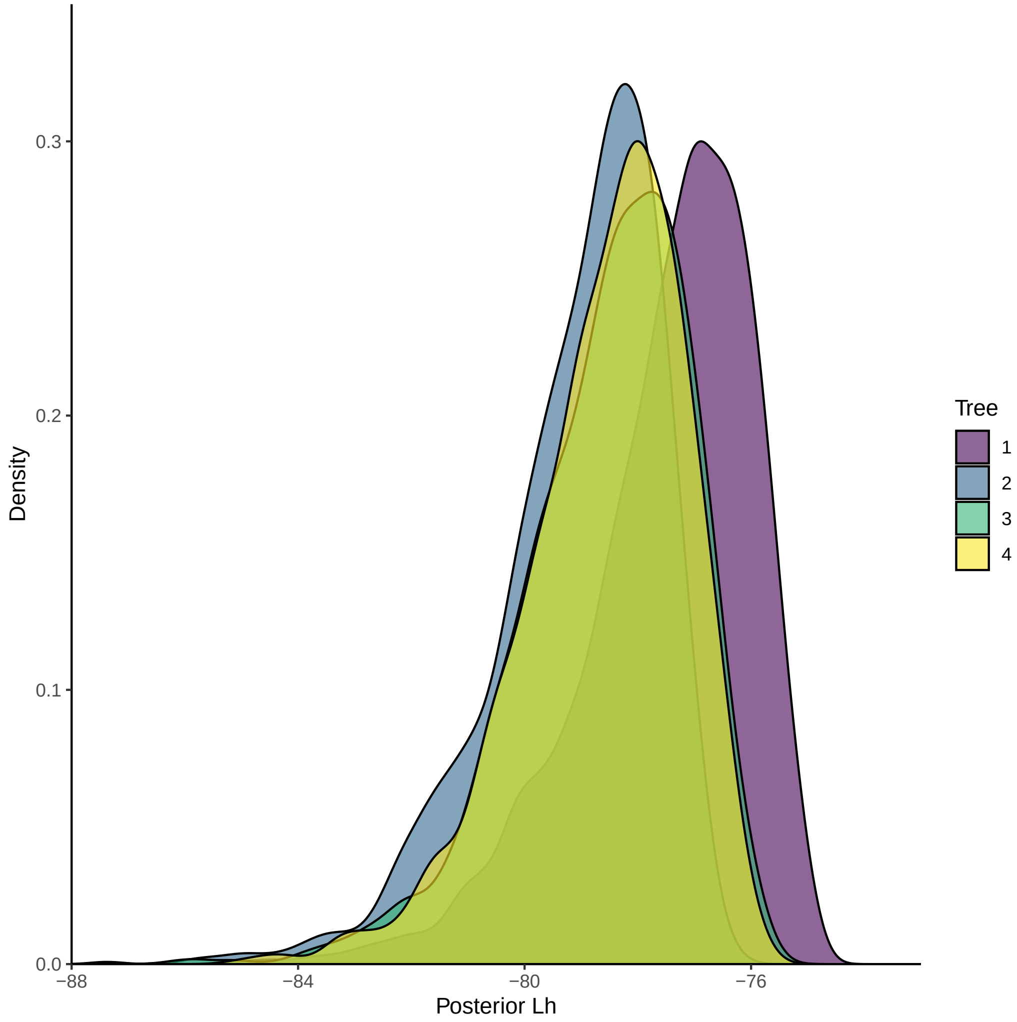

Figure 6.14: Density of posterior likelihood by topology for Character 3

Turning to the effect of topology on the interaction between estimated transition rate and posterior likelihood by topology, we see a slightly different pattern in the results from those of models of Characters 1 and 2. First, note that while Tree 1 is associated with better likelihood values, the grouping of the four trees is much tighter than in previous models. Moreover, Tree 4 no longer resembles Tree 1 in terms of its likelihood values. Instead Trees 2, 3, and 4 are roughly equivalent in terms of model fit, though Tree 2 provides slightly worse fit to the data than the others.

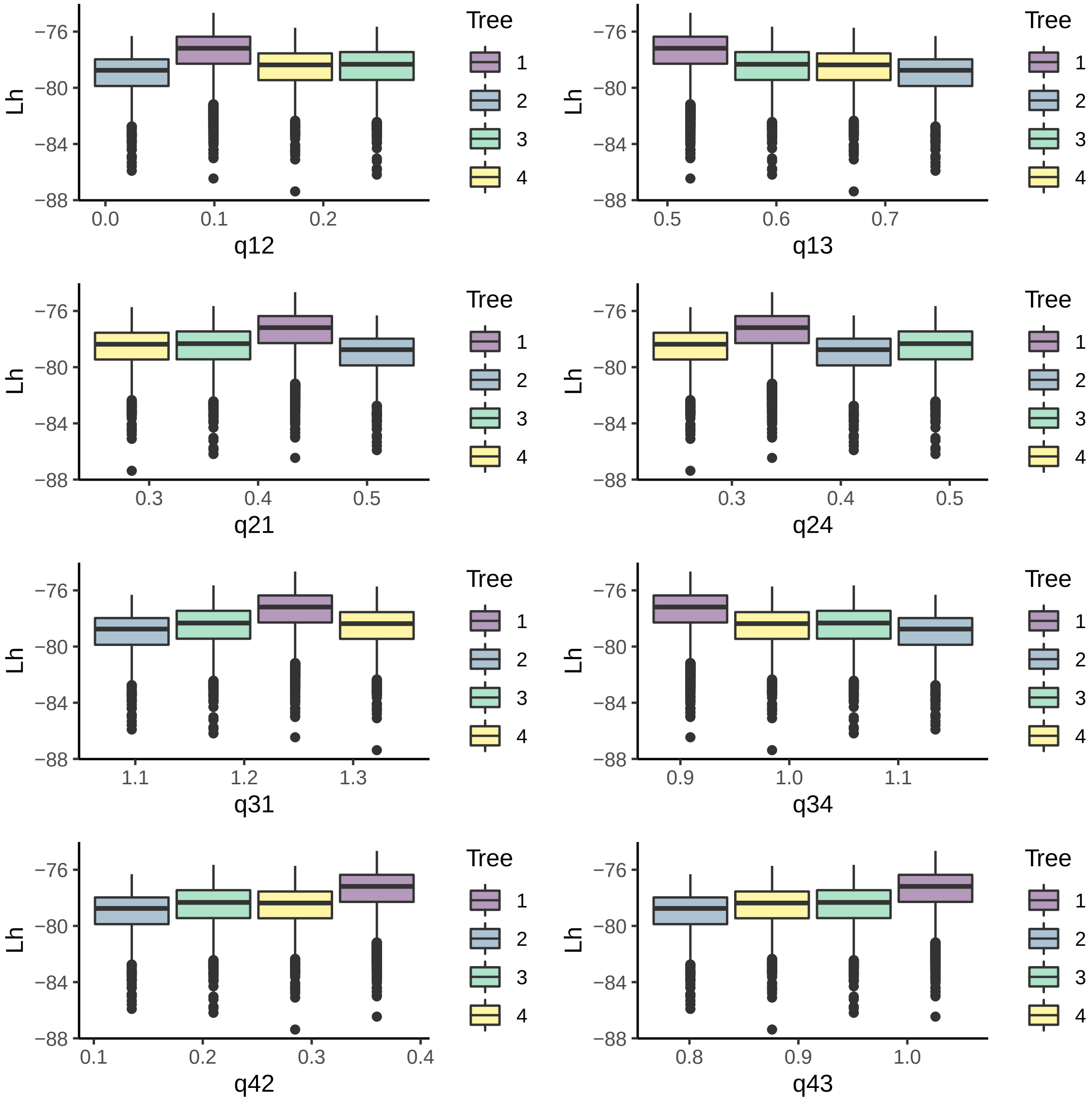

Figure 6.15: Boxplot of posterior likelihood versus estimated transition rate by topology for Character 3

As with the measures of homoplasy presented in §6.2.2, the visualization of the effects of tree topology on model likelihood allows us to again draw conclusions about subtle differences between tree topologies with respect to how well they explain the data. In each of the comparisons offered in this section, the Monophyletic tree (Tree 1) was associated with better model likelihoods, both in absolute terms and when the individual estimated transition rates were taken into account. This result is in agreement with the results of §6.2.2. For Characters 1 and 2, we also see that the Nonmonophyletic tree (Tree 4) provides an equally good fit to the data as Tree 1, a result that differs from the homoplasy measurement results. Finally, note that the Karnic/Kalkatungic (Tree 2) and Central/Yolngu (Tree 3) trees do not fare especially well in terms of their effect on model likelihood for any of the verb conjugation class characters.

6.3 Discussion

Reconstruction of unattested linguistic evolution, both Bayesian tree inference models or traditional comparative method approaches to reconstructing genetic relationships between languages, is often characterized by areas of certainty and areas of inconclusiveness. The ancestral state reconstruction models outlined in Chapter 4 provide an elegant solution in allowing us to generalize over these uncertainties by sampling from a potentially large set of trees at each iteration. At convergence, we expect to sample a putative node in the phylogeny roughly in proportion to its representation in the set of trees.

In the context of the reconstruction of the internal structure of the Pama-Nyungan languages, tree inference using lexical cognate data (Bowern & Atkinson 2012; Bouckaert, Bowern & Atkinson 2018) has provided appreciable resolution of the lower subgrouping structures in the tree, representing the more immediate relationships between various sets of languages that make up the larger family. This contrasts with the higher-level structure of the tree, representing how these well-defined subgroups relate to one another, which in many cases is still uncertain. This chapter proposes several methods for discerning between possible higher-level relationships between subgroups, taking the genetic affiliation of the Karnic languages as a case study.

The first of these methods is comparing the amount of phylogenetic signal in the data for each of the candidate topologies, which in this case did not lead to any strong claims about the preference of one tree over another. This finding is due to the fact that the highly conserved morphological data showed strong phylogenetic signal on each topology. While this is not a conclusive answer to the appropriate placement of Karnic in the tree, it does validate the use of these topologies in MCMC models, which were subsequently employed in determining the effect of individual tree topology on other parameters of the model, including posterior likelihood (i.e., how well the model fits the data) and the estimated transition rates.

A single candidate model was chosen for each character based on the findings of model selection tests in Chapter 4. For all three characters, the tree that assumes a direct common ancestor between Karnic and the Central Pama-Nyungan languages was associated with the best model likelihoods, indicating slight preference for this tree over the other candidates. The tree that placed Karnic as a distant relative of Central Pama-Nyungan also fit the presence of conjugation classes and number of conjugation classes well, but failed to distinguish itself with respect to the conjugation class membership features character.

An additional metric for comparing topologies considers the amount of homoplasy, the appearance of a feature state multiple times in the evolutionary history of the feature, as diagnostic of the appropriateness of a phylogeny. Here, common measures of homoplasy including consistency index, retention index, and rescaled consistency index were considered. Results of homoplasy quantification again showed slight preference in favor of the Karnic/Central Pama-Nyungan Monophyletic tree.

The results of all three methods of topology comparison were subtle in their suggestion of one tree over the others, though it should be noted that the data and specific choice of candidate topologies are likely to have an effect on the relative distance between possible trees. In other words, it is hard to interpret how strong the evidence in favor of the Karnic/Central Pama-Nyungan tree is in relation to the other trees, given that the proposed measures are dependent on the theoretical best and worst fit of any possible phylogeny. Nonetheless, we have seen the utility of the various diagnostics on offer in investigating topological differences and uncertainties in the larger phylogeny. Moreover, note that the candidate tree that fared the best in this mini-study also finds some support in the inclusion of Karnic and Central Pama-Nyungan as a clade in the maximum clade credibilty tree presented in Figure 6.3.

Chapter 7

Summation and discussion

In closing, I offer a brief summation of the main findings of the thesis and their contribution to our understanding both of language-family specific typological features of the Pama-Nyungan languages, as well as the utility of computational phylogenetic methods for investigating the evolutionary trajectory of closed-class morphological systems more generally.

First, I have presented the experimental design (Chapter 3) for and results (Chapter 4) of the application of robust statistical models of evolution in the reconstruction of the ancestral state of the Pama-Nyungan verb conjugation class system. As evidenced by the survey outlined in §3.2, the typology of modern Pama-Nyungan verbal inflection is quite varied. Some languages (e.g., Arandic, Karnic, and Thura-Yura) feature a single set of tense, aspect, and mood suffixes, while others (e.g., Yolngu) feature intricate patterns of inflection that number in the double digits. Languages also differ with respect to how the verbal lexicon is divided into conjugation classes. We may observe a general pattern in which languages with two distinct classes tend to group verbs based on their valence, with one conjugation consisting of mostly intransitive verbs, and the other mostly transitive. Conjugation classes in languages with richer inventories still often show this pattern of grouping together verbs with similar argument structures, while they also in many cases tend to collect stems with specific phonological profiles, usually based on the final vowel or the number of syllables in the stem.

In his influential work on the topic, Dixon (1980, 2002) reconstructs a set of seven conjugation classes for the ancestor of Pama-Nyungan, a claim with which the current study is incompatible. It is important to keep in mind that the outcome of linguistic reconstruction may be conditioned by the assumptions of the model. Dixon's approach strongly favors the hypothesis that morphology becomes more regular, more opaque over time, and furthermore, that the return of distinctiveness cannot and does not occur with any appreciable frequency. This precludes the incrementation of the number of conjugation classes in a language, and as such must propose a large set of classes in antiquity. In the context of the Pama-Nyungan languages, this is perhaps an overstatement of a weaker claim for which there is additional evidence in the findings of the probabilistic reconstruction on offer, namely that languages without verb conjugation classes are unlikely to innovate them. This is not the same as the innovation of new inflectional patterns and subsequent reassignment of verb stems into new conjugation classes.

We have also seen (Chapter 5) that the observed tendency for verbs with similar argument structures or stem phonology to be grouped into the same conjugation class(es) is more than epiphenominal. Instead, evidence supports the notion that the evolution of the number of conjugation classes in Pama-Nyungan languages is highly correlated with these feature-based delineations. This is perhaps unsurprising if we consider sound morphological theory to be informed by typology. This generalization is also present in Dixon's reconstructions, in which he posits a system based on both verb valence and the number of syllables in verb stems.

The findings of the current study suggest a number of conclusions about the evolutionary history of verb conjugation classes in Pama-Nyungan, which are summarized here:

1. The common ancestor of the modern Pama-Nyungan languages likely had two verb conjugation classes, though it should be noted that there is minor additional support for a third conjugation class. Absence of conjugation classes or a system of four or more classes are not supported.

2. Membership in these two ancestral verb conjugation classes was likely based on verb valence, with one class favoring monovalent verbs and the other dyadic/triadic verbs. This result finds support in the state of the modern Pama-Nyungan languages as well; two conjugation class systems tend to show a strong association between verb valence and conjugation class membership.

3. Verb conjugation classes were both gained and lost throughout the evolutionary history of Pama-Nyungan. Moreover, we find support for the existence of threshholds of stability in the conjugation class systems. Languages that have reduced their verbal systems to a single set of inflectional tense, aspect, and mood suffixes are unlikely to return to the ancestral state and innovate conjugation classes anew. Languages with four or more conjugations are also unlikely to return to a state of having less than four. That is not to say that languages with richer sets of inflectional patterns do not collapse distinctions over time, rather that four conjugations seems to be a boundary that is difficult to cross for processes of paradigm leveling and reduction.

4. There is a strong correlation between the evolution of the number of verb conjugation classes in a language and how membership is determined. Results support an evolutionary pathway in which the maintenance of valence-based conjugation classes is supplemented by organization of stems into classes based on their phonological properties as the number of classes grows beyond two. Little to no support was found for the opposite trajectory, in which languages

> first develop a phonological basis for the separation of verbs into conjugation classes, followed by the introduction of verb valence as an additional factor in determining membership. These findings are consistent with the idea that stem phonology is a secondary characteristic of conjugation class membership, serving to disambiguate when more than one conjugation class has mostly transitive or intransitive verbs. This is again supported by the typological data. In the current sample, only the Warluwaric languages showed a tendency towards stem phonology as a determining factor of conjugation membership while defying categorization as a transitivity-based system.

Finally, Chapter 6 introduced the notion of using morphological data to shed light on areas of uncertainty in the internal structure of the Pama-Nyungan phylogeny, adding to the incremental stochastic resolution of the relationships between the well-defined language subgroups that comprise the larger family. Specifically, I investigated the question of whether or not the existence of a shared closed-class typological feature can be diagnostic of a clade. Measures of phylogenetic signal and homoplasy and comparison of the results of ancestral state reconstruction models were employed in the exploration of the the effect of controlled modulation of the tree topology on the fit of the phylogeny to the data. While results were not strongly conclusive, they do indicate a preference for grouping the Karnic languages together with the Central Pama-Nyungan macro-group, a finding which is in line with earlier probabilistic reconstructions. More generally, this mini-study supports the validity of this approach to resolving higher-level phylogenetic relationships.

The findings of this study have a number of implications for historical linguistic reconstruction and our understanding of how morphology may change over time. Regarding reconstruction, note that while this thesis has singled out Dixon's hypotheses about the prehistory of the Indigenous Australian languages due to their relevance to the topic of investigation, the reconstruction of two (or three) conjugation classes at an early stage of Pama-Nyungan provides a counterexample to the bias against innovation and/or homoplasy in traditional approaches using the comparative method. In other words, Dixon is motivated by the foundational assumption that any identifiable conjugation class in the modern languages necessarily represents a reflex of an earlier conjugation. By contrast, phylogenetic modeling affords us the flexibility to test different possibilities, including that of Dixon in addition to various hypotheses that allow innovation and simplification (i.e., loss of conjugation classes) to exist in parallel. It should also be pointed out that both approaches share the limitation that the hypothesis space is limited to what is observed in the data; reconstruction of more conjugation classes than are found in the largest inventory in the modern languages are not taken into consideration.

From a theoretical standpoint, the reconstruction of two conjugation classes has implications for our understanding of how morphology may change over time. If this reconstruction is accurate, then we must assume that conjugation class inventories were expanded in some branches of Pama-Nyungan, while others collapsed distinctions to the point of losing them entirely. This result paints a different picture than, e.g., studies of Romance (Maiden 2005), which suggest the stability of paradigm structure and inflection classes over time, with minor, predictable changes. Of course, it should be noted that the Pama-Nyungan languages provide a very different object of study than the modern Romance languages, both in terms of the overall number of languages and the amount of variation they demonstrate.

Related to this is the finding that incrementation of an existing conjugation class inventory, possibly via splitting of existing classes, appears to be much easier than innovating conjugation classes *de novo*. On the surface, we might argue from parsimony that having multiple sets of inflectional endings for different verbs is hard to introduce or maintain when a single set of affixes will suffice. Put more precisely, we see pressure against the creation of a second form paradigm for use with certain verbs that already have an existing form paradigm, especially when we consider that differences in the range of morphosyntactic properties covered by the content paradigms of verbs belonging to different conjugation classes are not a defining characteristic of languages with multiple conjugations.

Looking at the Pama-Nyungan data, we see that two-conjugation systems invariably show a correlation between verb valence and conjugation class membership, which may provide a crucial clue to understanding why this initial innovation of conjugations is difficult in the Pama-Nyungan context. Morphological change that targets individual forms via analogy or merger is typically slow. If valence is the defining feature being targeted for drawing distinctions and clustering verbs into groups, we would expect this process to take much longer than one based on phonology. Phylogenetic reconstruction model results also indicate a pressure against the rapid expansion or loss of the conjugation class system in terms of the overall number of conjugations. Once this initial hurdle is overcome, the idea of having contrasting form paradigms for different sets of verbs is more likely to continue propagating through the system. A possible next step in the Pama-Nyungan context involves proliferation of the number of conjugation classes based on phonological properties of the stem. Note that phonology starts to become a conditioning factor on conjugation class membership when the number of conjugation classes grows to four or more, and that the only languages in the sample that have purely phonology-based conjugation class distinctions also have four conjugation classes, namely the Warluwaric languages.

For languages that have lost conjugation classes as a feature, re-innovation is unlikely to occur, a finding which is reinforced by the observation that presence or absence of conjugation classes is a defining characteristic of subgroups of the modern languages. Though there are a few exceptions, closely related languages generally tend to resemble one another in terms of having or lacking verb classes, indicating that the loss of the feature must have occurred much earlier in the evolution of the modern languages. We can also conclude based on the internal structure of the Pama-Nyungan family that different subgroups must have lost conjugation classes at different stages in their development and at different time-depths in order to account for the distribution of the data that we observe in the modern languages. If we take the internal structure of the Pama-Nyungan family to resemble the phylogeny presented throughout the thesis, the putative Central Pama-Nyungan macro-group shows an interesting trajectory whereby early splits involving the Karnic, Thura-Yura, and Arandic languages coincided with loss of conjugations as a feature in those subgroups. By contrast, later splits involving the Wati, Ngumpin-Yapa, and Marrngu languages correspond to expansion of the verb conjugation class inventory and correlated introduction of stem phonology as a conditioning factor on class membership. Reconstructing the time-depth of these various gain and loss events remains a question for continued scholarship on the topic.

Appendix

Full coding profile and sources for sampled languages

LANGUAGE	C1	C2	C3a	C3b	SOURCE
Adnyamathanha	0	0	0	0	Simpson & Hercus (2004)
Kaurna	0	0	0	0	Simpson & Hercus (2004)
Narrungga	0	0	0	0	Simpson & Hercus (2004)
Wirangu	0	0	0	0	Simpson & Hercus (2004)
Alyawarr	0	0	0	0	Yallop (1997)
Antekerrepenhe	0	0	0	0	Breen (1982)
CentralAnmatyerr	0	0	0	0	Hale (n.d.)
WesternArrarnta	0	0	0	0	Wilkins (1989)
Kaytetye	0	0	0	0	Turpin & Alison Ross (2011)
Wajarri	1	2	1	0	Marmion (1996)
Nhanta	1	3	1	0	Blevins (1999)
Malgana	1	2	-	-	Gargett (2011)
Nyungar	0	0	0	0	Douglas (1976)
Yingkarta	1	2	1	0	Dench (1988)
Ngarluma	1	4	1	0	Kohn (2001)

Yindjibarndi	1	4	1	1	Wordick (1982)
Panyjima	1	2	1	0	Dench (1981)
Ngarla	1	2	1	0	Westerlund (2015)
Martuthunira	1	3	1	0	Dench (1995)
Bilinarra	1	4	-	-	Nordlinger (1990)
Jaru	1	4	1	1	Tsunoda (1981)
Ngardily	1	4	-	-	Cataldi (2011)
Warlpiri	1	4	1	1	Dixon (2002)
Warumungu	1	4	1	0	Simpson & Heath (1982)
WalmajarriNW	1	4	1	1	Dixon (2002)
Karajarri	1	4	1	0	Sharp (2004b)
Nyangumarta	1	4	1	1	Sharp (2004a)
MangalaMcK	1	3	-	-	McKelson (1974)
Warnman	1	4	1	-	Burgman (2010)
Yulparija	1	4	1	1	Burridge (1996)
Manjiljarra	1	4	1	1	Marsh (1976)
Ngaanyatjarra	1	4	1	1	Glass & Hackett (1970)
Pitjantjatjara	1	4	1	1	Bowe (1990)
Wangkajunga	1	4	1	-	Jones (2012)
PintupiLuritja	1	4	1	1	Hansen & Hansen (1976)
Kukatja	1	4	1	1	Platt (1972)
Arabana	0	0	0	0	Hercus (1994)
PittaPitta	0	0	0	0	Blake (1979a)
Yandruwandha	0	0	0	0	Breen (n.d.)
Diyari	0	0	0	0	Austin (1981)
Ngamini	0	0	0	0	Breen (ms)

Wangkumara	0	0	0	0	McDonald & Wurm (1979)
Paakantyi	0	0	0	0	Hercus (1982)
AghuTharrnggala	0	0	0	0	Jolly (1989)
Kunjen	1	2	-	-	Sommer (1970)
Ikarranggal	0	0	0	0	Sommer (1999a)
Umpithamu	0	0	0	0	Sommer (1999b)
KukuWura	0	0	0	0	Godman (1993)
Linngithigh	1	4	-	-	Hale (1966)
Mbakwithi	1	4	1	0	Crowley (1981)
Ntrangith	0	0	0	0	Hey (1903)
Uradhi	1	4	1	1	Crowley (1983)
KuguNganhcara	1	3	1	1	Smith & Johnson (2000)
WikMungkan	0	0	0	0	Kilham et al. (2011)
KuukuYau	1	3	1	0	Thompson (1988)
Umpila	1	3	1	0	Thompson (1988)
KuukThaayorre	1	2	1	0	Gaby (2006)
YirYoront	1	4	1	0	Alpher (1973)
Kurtjar	1	4	-	-	Black & Gilbert (1996)
Djabugay	1	2	1	0	Patz (1991)
Yidiny	1	3	1	0	Dixon (1977)
GuuguYimidhirr	1	3	1	0	Haviland (1979)
KukuYalanji	1	2	1	0	Patz (2002)
Kukatj	1	2	1	0	Breen (1988)
Biri	0	0	0	0	Terrill (1998)
BidyaraGungabula	0	0	0	0	Breen (1973)
Guwamu	0	0	0	0	Breen (1973)

Gunya	1	2	1	0	Breen (1981a)
Margany	1	2	1	0	Breen (1981a)
Nyawaygi	1	4	1	1	Dixon (1983)
Wargamay	1	2	1	0	Dixon (1981)
GuguBadhun	1	2	1	0	Sutton (1973)
Warungu	1	3	1	0	Tsunoda (2011)
Mbabaram	1	2	1	0	Dixon (1991)
Kalkatungu	1	2	1	0	Blake (1979b)
Yalarnnga	0	0	0	0	Breen & Blake (2007)
MayiKulan	1	2	1	0	Breen (1981b)
Dhangu	1	4	1	-	MacLellan 1992
Dhuwal	1	4	1	0	Heath (1980a)
Djambarrpuyngu	1	4	1	0	Wilkinson (1991)
Djapu	1	4	1	0	Morphy (1983)
Ritharrngu	1	4	-	-	Heath (1980b)
Ganggalida	1	2	1	0	Keen (1983)
Darkinyung	0	0	0	0	Jones (2008)
Thanggatti	0	0	0	0	Lissarrague (2007)
Dharawal	0	0	0	0	Eades (1976)
Thurrawal	0	0	0	0	Mathews (1901)
Dhurga	0	0	0	0	Eades (1976)
Gamilaraay	1	4	1	0	Ash, Giacon & Lissarague (2003)
Yuwaalaraay	1	4	1	0	Ash, Giacon & Lissarague (2003)
Ngiyambaa	1	3	1	1	Donaldson (1980)
Muruwari	1	4	1	1	Oates (1988)
Githabul	0	0	0	0	Geytenbeek & Geytenbeek (1971)

Yugambeh	0	0	0	0	Sharpe (1988)
Batyala	1	3	-	-	Bell (2003)
GoorengGooreng	1	2	1	0	Brasch (1975)
Gumbaynggir	0	0	0	0	Eades (1979)
Yaygirr	1	2	-	-	Crowley (1979)
Keramin	0	0	0	0	Horgen (2004)
YithaYitha	0	0	0	0	Horgen (2004)
Ngaiawang	0	0	0	0	Horgen (2004)
Bunganditj	-	-	-	-	Mathews (1903)
Wathawurrung	0	0	0	0	Blake et al. (1998)
Woiwurrung	-	-	-	-	Blake (1991)
WembaWemba	0	0	0	0	Hercus (1992)
MathiMathi	0	0	0	0	Blake et al. (2011)
Dhudhuroa	0	0	0	0	Blake & Reid (2002)
Pallanganmiddang	-	-	-	-	Blake & Reid (1999)
Bularnu	1	4	0	1	Breen (n.d.)
Warluwarra	1	4	0	1	Breen (1971)
Wakaya	1	4	0	1	Breen (1974)

Character coding and sources for 111 Pama-Nyungan languages

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