Bayesian phylogenetic methods overcome limitations of traditional subgrouping[*]

David Goldstein

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Traditional subgrouping has long been a cornerstone of historical linguistics. In recent decades, however, Bayesian methods have played an increasing role in linguistic phylogenetics, which has prompted debate about the relationship between the two approaches. These discussions have largely focused on the results of Bayesian analyses, which have been especially controversial within Indo-European. While these debates have reinvigorated interest in phylogenetic research, they have also tended to obscure the broader methodological advantages of Bayesian inference. To correct this imbalance, I identify and discuss three critical limitations of traditional subgrouping that this framework overcomes. These advantages underscore the necessity of integrating Bayesian inference into linguistic phylogenetics.

1 Introduction

> They say that Understanding ought to work by the rules of right reason. These rules are, or ought to be, contained in Logic; but the actual science of Logic is conversant at present only with things either certain, impossible, or *entirely* doubtful, none of which (fortunately) we have to reason on. Therefore the true logic for this world is the Calculus of Probabilities, which takes account of the magnitude of the probability which is, or ought to be, in a reasonable man's mind.
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> James Clerk Maxwell apud Campbell and Garnett 1882:81

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Over the past two decades, the relationship between traditional subgrouping and Bayesian phylogenetics has been the focus of considerable scholarly attention (Greenhill and Gray 2012; Pereltsvaig et al. 2015; Chang et al. 2015; Bowern 2017; Greenhill, Heggarty, et al. 2021; Olander 2022a; Piwowarczyk 2022; Ringe 2022). Two characteristics of this ongoing discussion are particularly noteworthy. First, comparisons between the two frameworks focus primarily on the results of individual studies and to a far lesser extent on the mechanics of inference. Second, these methods are often pitted against one another as competitors (Pereltsvaig et al. 2015; Piwowarczyk 2022; Ringe 2022). Olander (2022a:3), for instance, introduces his recent volume on Indo-European phylogenetics as "an attempt at reinvigorating the traditional methodology," since outside of Indo-European studies it "seems to be losing ground to computationally based analyses."

Both tendencies have hindered a productive integration of Bayesian methods into Indo-European linguistics. The focus on outcomes has fostered the view that Bayesian phylogenetics is useful only to the extent that it replicates traditional subgrouping. When Bayesian results diverge from established classifications, they are often dismissed as erroneous; when they align, they are sometimes regarded as redundant. This outcome-oriented evaluation neglects the fact that the validity of the results depends not only on the method but also on factors such as data quality, model specification, and the selection of prior distributions. In addition, this view fails to appreciate the full scope of Bayesian inference, which facilitates the estimation of rates of change, the modeling of uncertainty, and principled comparison between models of linguistic evolution (Greenhill, Heggarty, et al. 2021:228). The Bayesian framework thus accommodates a broader range of questions than traditional subgrouping.

Equally limiting is the tendency to frame traditional subgrouping and Bayesian phylogenetic methods as competitors. It is certainly imperative to be aware of the advantages and disadvantages of any method, so the two frameworks should be compared. Comparison must not, however, imply a single best method. If historical linguistics is "the art of making the best use of bad data" (Labov 1994:11), it behooves us to use a variety of methods. Indeed, scholars who use computational phylogenetic methods have repeatedly argued that they should complement—and not replace—traditional methods (Ringe, Warnow, et al. 2002:66; Gray et al. 2009:479, 482; Greenhill and Gray 2012:534; Goldstein 2020:3; Greenhill, Heggarty, et al. 2021:246).

Despite these appeals, Bayesian phylogenetic methods have yet to gain meaningful traction within Indo-European linguistics. As Olander (2022a:2–3) observes, the findings of computational phylogenetic studies are often overlooked or dismissed by Indo-Europeanists. This resistance may stem in part from the framing described above, in which Bayesian methods appear to lack a distinct purpose within the field. Another contributing factor may be the enduring authority of the traditional method. For example, Ringe, Warnow, et al. (2002:66) assert that "traditional subgrouping is logically coherent and methodologically unobjectionable." If the traditional framework is viewed as sufficient, the rationale for adopting computational methods may seem unclear—or even unnecessary.

The methods of traditional subgrouping are actually not beyond objection, as they suffer from at least the three following shortcomings. First, the foundation of the traditional framework is Leskien's Principle (Campbell and Poser 2008:155; Clackson 2022:21),[1] which holds that subgroups be inferred from shared innovations and not shared archaisms. This principle is intuitively sensible, but fails to make clear that the empirical criteria for inferring a subgroup are actually more stringent. Evidence for a subgroup comes not merely from shared innovations, but rather from shared innovations that occurred once (in the most recent common ancestor of the languages in the alleged subgroup). If a shared innovation occurred more than once, it provides no evidence for a subgroup. Identifying innovations that can confidently be assumed to have occurred only once remains a fundamental difficulty (Ringe, Warnow, et al. 2002:66). Second, there is no agreement on the number of such innovations that suffice to establish a subgroup. This problem dates back to the nineteenth century and leaves researchers free to adopt their own thresholds, with the result that topological claims risk being nothing more than personal preferences. Finally, traditional subgrouping is unequipped to draw inferences in the face of conflicting phylogenetic signals. Different sets of shared innovations often support incompatible tree topologies, but it is impossible to draw inferences from such conflicting data in the traditional framework. These limitations point to the need for a richer methodological toolkit in linguistic phylogenetics. Below I explain how Bayesian methods are well equipped to address each of these challenges.

The remainder of this paper is structured as follows. A brief overview of Bayesian phylogenetic methods is offered in section 2. Sections 3, 4, and 5 then discuss the three challenges introduced above. Section 6 brings the paper to a close with concluding remarks. Throughout my discussion, I draw examples primarily from the ancient Greek dialects, where the methodological challenges identified above are especially pronounced.[2] They are by no means unique to Greek, however, as they are present in all of the major subgroups of Indo-European (as illustrated by the contributions to Olander 2022b).

2 A sketch of Bayeisan phylogenetic inference

At the heart of Bayesian phylogenetics is the following question: what is the probability of a unobservable phenomenon, given data that we can observe?[3] Unobservable phenomena in a phylogenetic context include the tree topology, branch lengths, and rate parameters. The observable data are

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[1] Leskien's Principle is also known as *Brugmann's Principle* (Chrétien 1963:67), since Brugmann (1884:231) argues that subgroups can only be inferred from shared innovations. The principle does not originate with Leskien, as he notes (p. vii) that Schleicher's inferences are based on it.

[2] The need for methodological expansion has long been recognized in Greek dialectology (Coleman 1963; Skelton 2015; Scarborough 2023).

[3] I have simplified the presentation of Bayesian phylogenetic methods to make it maximally accessible. For more detailed introductions, see Lewis 2001; Holder et al. 2003; Lewis 2014; Oaks 2015; Nascimento et al. 2017; Huelsenbeck 2019; Lartillot 2020; Hoffmann et al. 2021; or Greenhill, Heggarty, et al. 2021.

linguistic properties and in theory can be any aspect of language. In practice, however, most Bayesian phylogenetic studies rely on lexical cognate relationships.[4] It is worth pointing out—since this fact is often ignored—that in such studies the data are strictly speaking not observed: cognate relationships are hypotheses treated as observations.

The probability of these unobservable aspects of linguistic history is estimated with Bayes' Rule, which can be thought of as a formula for updating one's beliefs based on new evidence. It consists of four main components. The first is the *prior*, which represents our initial assumptions or expectations before seeing the data. The second is the *likelihood*: it measures how well the observed data align with the prior assumptions. The third is the *marginal likelihood*, or the overall probability of the data under all possible scenarios.[5] Finally, the *posterior probability* is our updated belief after taking into account the new evidence. These four components are related by the following equation:

$$\text{Posterior probability} = \frac{\text{Likelihood} \times \text{Prior}}{\text{Marginal likelihood}}$$

The ultimate objective of Bayesian analyses is the posterior probability, which represents a balance between our initial beliefs and the observed data (Huelsenbeck 2019:183–184). Posterior probabilities quantify one's degree of belief in particular parameter values (Huelsenbeck 2019:181; Clayton 2021:35–45). This interpretation stands in contrast to the frequentist view of probability, where it denotes the long-run frequency of an outcome across repeated experiments.

Prior distributions have attracted a lot of attention and are often considered both a strength and a weakness of Bayesian inference (Huelsenbeck 2019:181). Since prior distributions can be difficult to specify, they may vary among researchers, which raises concerns about subjectivity. At the same time, this flexibility is a real strength of the framework: prior distributions enable scholars to incorporate accumulated domain knowledge directly into a model. It is important to understand that the influence of prior distributions diminishes as the amount of observed data increases.

In contrast to other phylogenetic methods, Bayesian analyses do not return point estimates (i.e., single best values), but rather full probability distributions. For example, rather than producing a single tree, a Bayesian analysis generates a set of trees—the posterior distribution—as illustrated from an analysis of ancient Greek in Figure 1. This set is not a random assortment: each tree is sampled in proportion to its posterior probability, which means that more probable trees appear more frequently.

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[4] More specifically, they are based on root-meaning traits (Chang et al. 2015:200–204), which is one type of lexical cognacy among at least four. To the best of my knowledge there has been no investigation of how phylogenetic inferences vary according to definition of cognacy.

[5] In practice, the marginal likelihood is often intractable due to high-dimensional integrals. This computational challenge is one reason why Bayesian phylogenetic methods are typically coupled with Markov chain Monte Carlo (MCMC), on the basis of which values from the posterior distribution are sampled according to their relative probability.

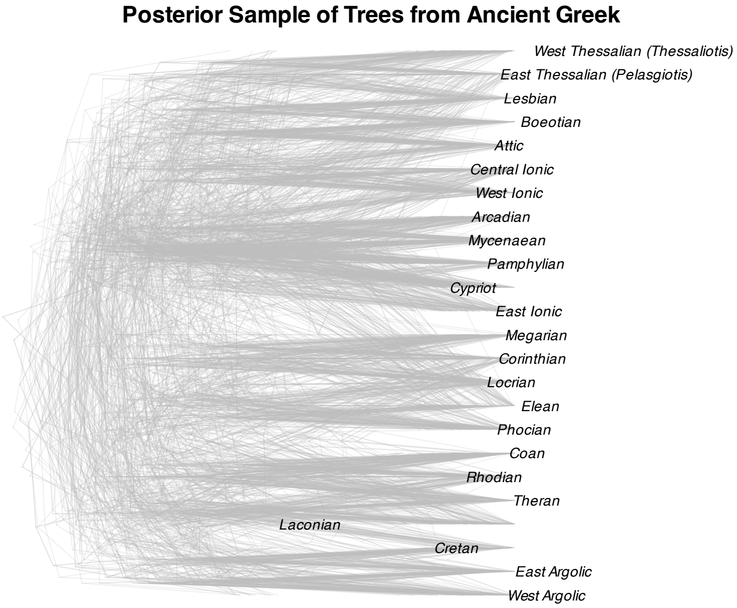

Figure 1: Densitree representation of 150 phylogenetic trees sampled from a posterior distribution. Each tree represents a single plausible evolutionary history of the Greek dialects inferred by the model. The density of a branch reflects the consistency of that relationship across the posterior sample: darker lines indicate stronger support, while lighter fan-shaped areas reflect greater uncertainty. Shallow dialectal relationships show relatively high concordance across samples, whereas the deeper branches corresponding to earlier periods of Greek reveal substantial disagreement. This pattern suggests that while the model detects stable subgroupings among some dialects, the earlier historical relationships are unclear.

Figure 2 presents a posterior distribution of the origin age of the Romance languages based on Goldstein 2024. The x-axis represents millennia before the year 2000. For example, 1.9 kya corresponds to 100 CE. Two features of the distribution are especially informative, its central location and its overall spread. The median estimate is 1.53 kya (497 CE), but the posterior density spans more than a millennium, which reflects considerable uncertainty in the estimated origin age.

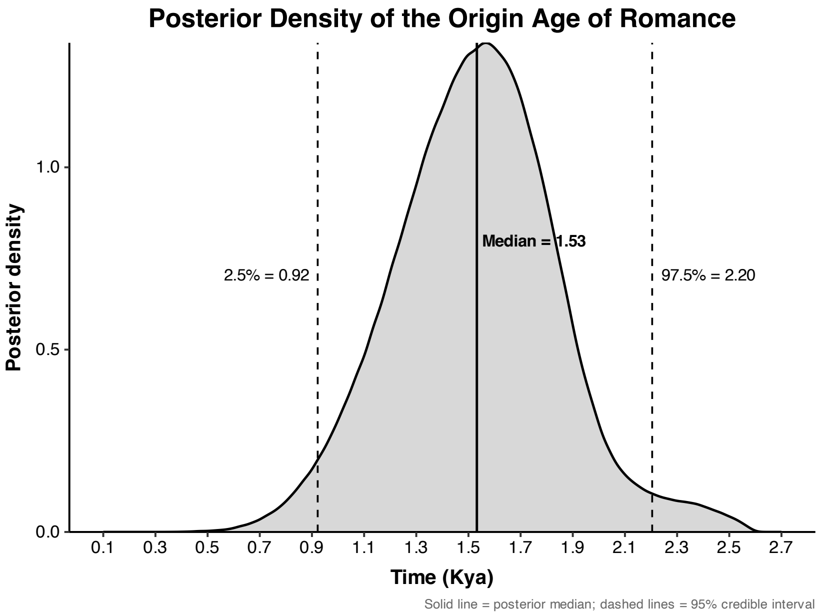

Figure 2: Posterior density estimate for the origin age of the Romance languages under a Bayesian phylogenetic model. The shaded area represents the range of plausible ages supported by the data and model. The solid vertical line marks the posterior median estimate (1.53 kya), while the dashed lines indicate the 95% credible interval (CrI), which range from 0.92 to 2.20 thousand years ago. Bayesian credible intervals directly reflect the uncertainty in the estimated parameter given the data and priors. The distribution's shape captures how strongly the data constrain the estimated age: a narrow peaked density suggests high certainty and a flatter or wider curve indicates more uncertainty.

3 The challenge of shared innovations

As noted above in section 1, Leskien's Principle holds that subgroups must be inferred exclusively from shared innovations (Leskien 1876:vii). Shared archaisms (also called *shared retentions*) are irrelevant.[6]

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[6] Some scholars propose a third category in addition to innovations and retentions, namely *selections* or *choices* (e.g., Adrados 1976; López Eire 1978:293–296; Dunkel 1981; Adrados 1997; Méndez Dosuna 2007:448; García Ramón 2018:68, 79). This category refers to cases where a selection is made from pre-existing alternatives. For example, the ancestors of the prepositions ποτί and προτί are reconstructed to Proto-Greek (or earlier) by some (Risch 1955:66; López Eire 1978:295), but most dialects exhibit just one (the Homeric *Kunstsprache* is exceptional in this regard). The reduction of the two ancestral prepositions to one exemplifies the process of selection. There is no compelling evidence, however, that the mechanism of change differs from that of innovation more generally. Selection therefore reduces to innovation and need not be postulated as a separate category (Scarborough 2023:45).

Leskien's Principle enjoys near-universal acceptance among historical linguists[7] and is standard in many textbooks (Hock 1991:579; Crowley et al. 2010:112; Ringe and Eska 2013:256; Campbell 2020:238). Parallel formulations are found in evolutionary biology (Hennig 1966:120; Baum et al. 2013:85; Sober 2015:178) and anthropology (Nunn 2011:26).

Leskien's Principle has not gone entirely unchallenged, however. García Ramón (2010:222), for instance, argues that the preservation of patronymic adjectives in Boeotian and Thessalian constitutes evidence of a "prehistoric connection" between these two dialects (see also Watkins 1966:30; Wallace 1984:121; Hyllested et al. 2022:241 n. 21). Such arguments for inferring subgroups from shared archaisms, however, have typically met with dismissal (e.g., Hoenigswald 1990:443; van Beek 2022a:186 n. 28).

The notion of a shared innovation is less straightforward than it *prima facie* appears, since it encompasses two fundamentally different phenomena, *synapomorphy* and *homoplasy* (Wiley et al. 2011:5, 14; Baum et al. 2013:85, 93).[8] The distinction depends on the number of times the shared innovation occurs. If it arises once, it is a synapomorphy. If it arises independently more than once, it is homoplasy. To illustrate, consider a single binary character in three languages representing the presence (state 1) or absence (state 0) of a linguistic feature. In Figure 3, state 0 is shown in black and state 1 in gray. If we assume that the gray state is an innovation, we must ask whether it arose once or multiple times. If it occurred only once, it constitutes a synapomorphy and supports the inference that the two languages with gray tips share a most recent common ancestor that had already undergone the innovation, as illustrated in Figure 4. The transition from black to gray would then occur along the branch leading to the gray internal node.

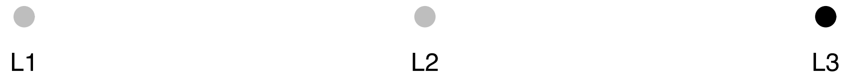

Figure 3: Tip states for single a binary character in three languages (L1, L2, L3). Gray indicates the innovative state and black indicates the ancestral state. The key question is whether it arose once or independently more than once, i.e., whether it reflects synapomorphy or homoplasy.

If the innovation occurred more than once, then other histories have to be considered, in particular the following two. First, the two gray languages could still share a most recent common ancestor, with the transition from black to gray occurring independently after they diverged (Figure 5). Alternatively, the two gray languages may not form a subgroup and the transition from black to gray would have

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[7] See, e.g., Porzig 1954a:54–55; Dyen 1975:22–23, 33–34; Risch 1979:271–279; Hall 1996:161; Otsuka 2006:429; Shen 2006:82; Rubin 2007:91, 93; Horrocks 2010:17; Huehnergard et al. 2011:262; Lama 2012:116, 119; Chousou-Polydouri et al. 2013:7; François 2015:176; Scarborough 2023:43; Ringe 2016:278; Moore 2017:88, 113; Kalyan et al. 2018:9; De Cia et al. 2020:2; Hyllested et al. 2022:226.

[8] In historical linguistics these two phenomena are often referred to as *non-trivial change* and *trivial change* (e.g., Hale 2007:229–233; Eska 2017:1265), respectively. Homoplasy is also known as *parallel* (*independent*) *innovation* (e.g., Ringe, Warnow, et al. 2002:67).

happened along the branches leading to each gray tip (Figure 6). Despite the simplicity of this example, it illustrates a crucial point: topological inference in the traditional framework is only possible when synapomorphy can be distinguished from homoplasy.

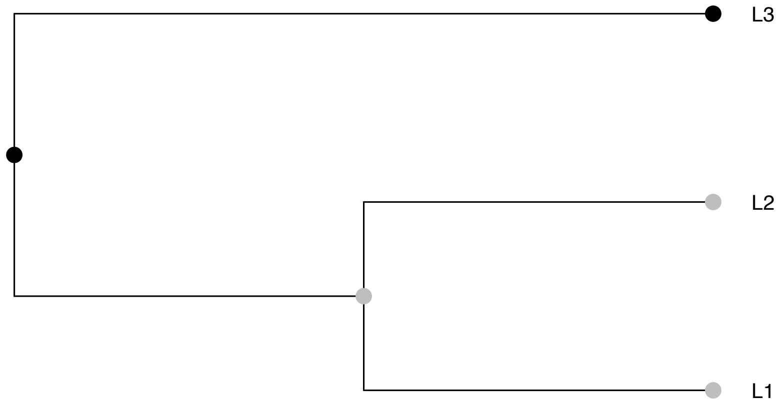

Figure 4: A hypothetical phylogeny illustrating synapomorphy. The innovative gray state is present in L1 and L2 as well as in their most recent common ancestor (the gray internal node). The innovation is assumed to have occurred once along the branch leading to that ancestor.

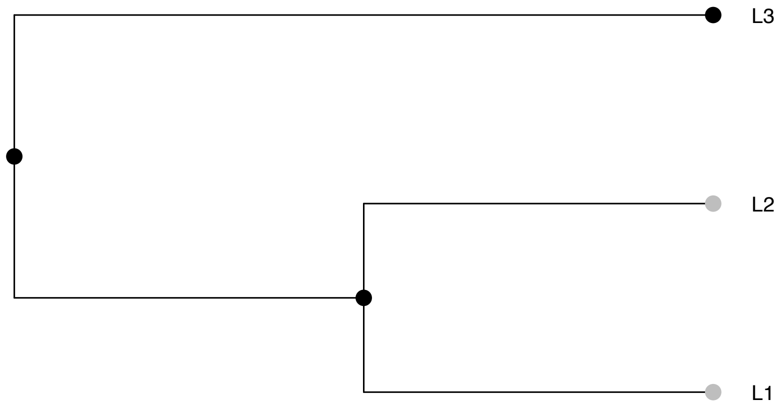

Figure 5: A hypothetical phylogeny illustrating homoplasy. Although L1 and L2 form a subgroup, their most recent common ancestor retains the ancestral (black) state. This implies that the innovation occurs independently in both L1 and L2, rather than once in their shared ancestor.

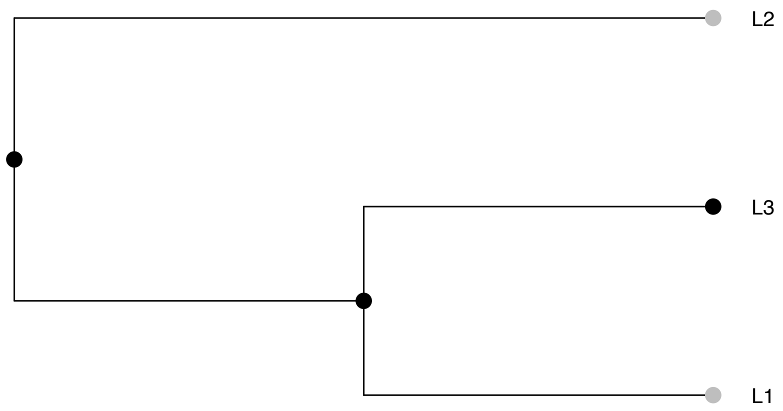

Figure 6: A hypothetical phylogeny illustrating homoplasy. The innovations in L1 and L2 take place independently.

3.1 Identifying homoplasy through relative chronology

Synapomorphy can in some cases be distinguished from homoplasy with a relative chronology of sound changes (Meillet 1922:24; Clackson 2022:24–25). A well-known example in the history of Greek is the second compensatory lengthening, which has been shown to be homoplastic (Risch 1955:68). The change involves the loss of a coronal nasal [n] before a sibilant followed by the lengthening of a preceding vowel:

(1) Second compensatory lengthening
*[pantja] > [pansa] > [paːsa] πᾶσα ‘all’

This change is attested in several dialects, including Attic (Sihler 1995:§§56, 228.2), Ionic (Sihler 1995:§§56, 228.2), Laconian (Striano Corrochano 1989:§§11.212, 11.222, 11.231), and Boeotian (Blümel 1982:§§117–121). On account of this chronology, the second compensatory lengthening in Attic-Ionic cannot be inherited from a common ancestor shared with Laconian and Boeotian. It therefore must have occurred more than once (Chadwick 1956:42; Schwyzer 1959:287; Bartoněk 1968:153; Bubeník 1983:59; Rix 1992:§63; Sihler 1995:§§56, 228.2; Hajnal 2007:137 n. 6).

In addition to relative chronology, heuristics have been developed for distinguishing synapomorphy from homoplasy (Clackson 2022:25). For instance, the more unusual a shared innovation is, the less likely it is to be homoplastic (Ringe, Warnow, et al. 2002:65–66; Hale 2007:226 n. 23, 295–300; Ringe 2016:279; Eska 2017:1270). Morphological innovations are on the whole more likely to be synapomorphic than sound changes or lexical replacements (e.g., Brugmann 1884:237; Meillet 1924:6; Ringe, Warnow, et al. 2002:68).

3.2 The shared-innovation problem in Aeolic

For all their utility, relative chronology and heuristic diagnostics do not always allow us to distinguish synapomorphy from homoplasy with confidence. This difficulty is especially pronounced among the Greek dialects, which are characterized by high diversity (i.e., a large number of dialects) and low disparity (i.e., a high degree of similarity among them). Such a configuration creates fertile ground for innovations to arise independently across the dialects (Brugmann 1884:253; Coleman 1963:62–63; Capano et al. 2023:358).

The challenge of distinguishing homoplasy from synapomorphy is particularly acute with the Aeolic question, that is, whether Lesbian, Thessalian, and Boeotian constitute a genuine subgroup. One of the shared innovations advanced in support of an Aeolic subgroup is the dative plural ending -εϲϲι, which is attested in all three dialects and stands in contrast to the inherited suffix -ϲι (García Ramón 1990:133; Scarborough 2023:110). Boeotian and Thessalian, for instance, exhibit forms such as ανδρ**εϲϲι** ‘to men’ (Scarborough 2023:112), whereas other dialects, such as Attic, preserve the older form ἀνδρά**ϲι**.

The interpretation of this innovation is far from settled.[9] Some scholars contend that as a morphological innovation the creation of -εϲϲι is unlikely to have occurred multiple times independently and is therefore a synapomorphoy of Aeolic (e.g., Cassio 2018:195; van Beek 2022a:186; van Beek 2022b:129; Scarborough 2023:110–117). The challenge to this view is that -εϲϲι is attested outside of Aeolic as well, for instance, in Elean, Locrian, and Corinthian (see Ruijgh 1958; García Ramón 1990; Capano et al. 2023). Since it is implausible that the innovation occurred so early as to be inherited in these dialects (e.g., from Proto-North Greek), it likely arose multiple times. Its repeated emergence can at least partly be explained by the effects of sound change, which introduced allomorphic variation in the dative plural of athematic nouns that may have motivated the morphological reformation (García Ramón 1975:84; Morpurgo Davies 1976:181; García Ramón 1990:133; Scarborough 2023:110, 117).

Considered from this broader perspective, the emergence of -εϲϲι within Aeolic becomes more difficult to assess. It could have developed once in Proto-Aeolic and arisen independently in other dialects. Or it could have been homoplastic within Aeolic itself, as García Ramón (1975:83–84) maintains. Parker (2008:447) takes an even stronger stance and describes the creation of -εϲϲι as “an easy analogical change that occurs in various dialects, and as such is valueless as a basis for subgrouping.” He is of

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[9] There is also considerable debate as to how exactly the new ending arose (e.g., García Ramón 1990; Cassio 2018).

course correct that the analogical change occurred in other dialects, but if it is such an "easy" change, one would expect it to occur in most (if not all) dialects—which did not happen.

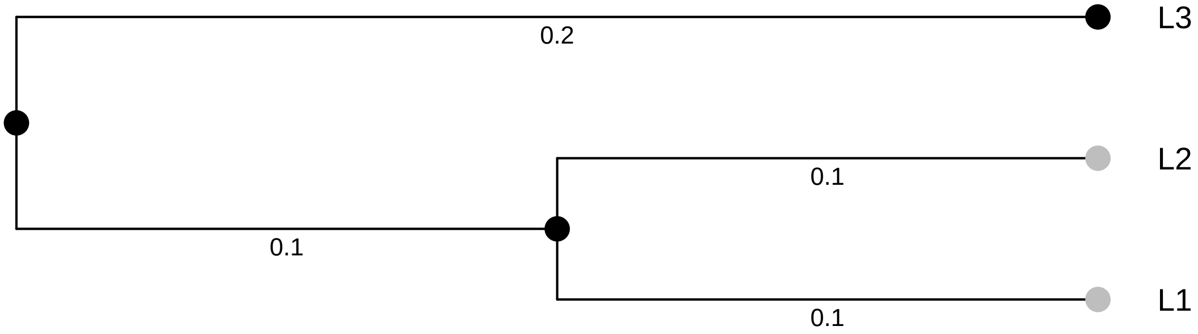
Further investigation of this question lies beyond the remit of this study, since my interest in this example is methodological. The history of -εσσι illustrates the binary logic of traditional subgrouping. If the innovation occurred once within Aeolic, it supports an Aeolic subgroup. If it occurred more than once, it does not. In other words, scholars are essentially required to assign a probability of either zero or one to the hypothesis that a shared innovation is a synapomorphy. This all-or-nothing framework is problematic, particularly in cases such as -εσσι, where it is unlikely that the number of occurrences can be established with such certainty. As Ringe, Warnow, et al. (2002:68) observe in their discussion of phonological change and subgrouping, "the possibility of parallel development can never be absolutely excluded." We therefore need a method that permits inference even when synapomorphy and homoplasy cannot be definitively distinguished (Hoffmann et al. 2021:121).

Bayesian inference provides such a method. As introduced in section 2, the likelihood in Bayes' Rule quantifies the degree to which the observed data align with prior assumptions. In a phylogenetic context, the likelihood is the probability of the data at the tips of the tree given a specific configuration of parameters (i.e., tree topology, branch lengths, and transition-rate matrix). Crucially this calculation integrates over all possible unobserved states at the internal nodes and root of the tree (see Yang 2014:102–113; Harmon 2019:126–131; Goldstein 2020:154–163). As a result, the posterior probability of any given tree topology incorporates uncertainty about unobserved ancestral states.

As an illustration, consider again the binary character and three languages introduced in section 3. Assume the tree topology and associated branch lengths shown in Figure 7, where L1 and L2 form a subgroup. The likelihood is defined as the probability of observing the character states at the tips of the tree, given this topology, the specified branch lengths, and a model of the rate of change between the ancestral black state and the innovative gray state (the specifics of which are abstracted away from here).

Since the ancestral states at the internal nodes are unobserved, the likelihood is computed by summing over all possible state combinations (Hoffmann et al. 2021:123). As a result, the posterior probability of the phylogeny in Figure 7 is not conditional on any single character history. In this way, Bayesian phylogenetic methods allow for inference under uncertainty, since we are not forced to commit to a single hypothesis—such as homoplasy (Figure 7a) or synapomorphy (Figure 7b).

(a) Homoplasy



(b) Synapomorphy

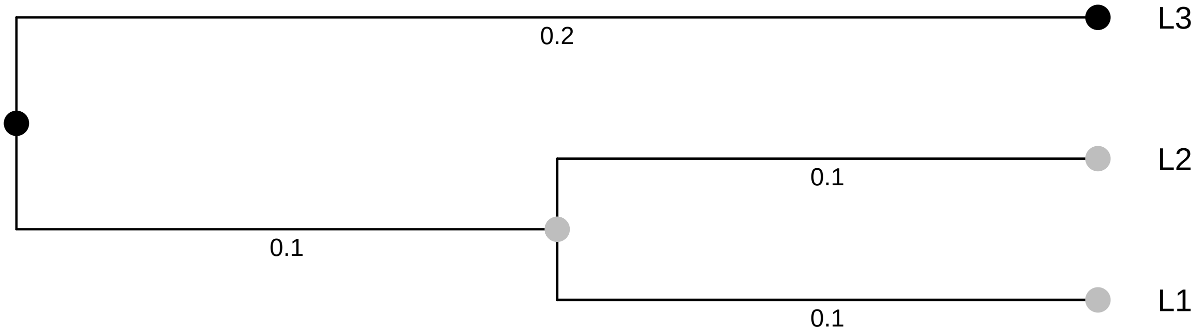


Figure 7: Illustration of the role of ancestral states in likelihood calculations. In Bayesian phylogenetic inference, the likelihood of observing the data (tip states) is computed by summing over all possible configurations of ancestral states. Panels (a) and (b) represent two such configurations, each of which contributes to the total likelihood under the model.

4 How many synapomorphies suffice?

Although it is almost universally agreed that subgroups should be inferred from shared innovations, there is no consensus on how many synapomorphies suffice to establish a subgroup. In his recent overview of subgrouping methodology, Clackson (2022:25–26), for instance, leaves the question open. Much of the debate is centered on whether a single synapomorphy can suffice. Kölligan (2023:318–319) argues that "one indisputable case is sufficient," a position that Hoenigswald (1966:6 n. 13) seems to endorse as well. Brugmann (1884:253), however, maintains that synapomorphies need to be plentiful and drawn from different domains (i.e., phonology, morphology, syntax, and the lexicon).

Examples of these opposing attitudes are plentiful in the literature. Van Beek (2022a:182), for instance, recognizes a North Greek subgroup (comprised of West Greek and Aeolic), although he concedes that there are "few (if any) old innovations that are characteristic for all North Greek dialects." By contrast, Kim (2018:252) in his assessment of the evidence for Greco-Armenian argues that Greek ἦμαρ and Armenian *awr* 'day' is the only (near-)word equation that the two languages share, which he considers "hardly sufficient grounds for setting up a subgroup." When individual scholars are free to choose their own thresholds for synapomorphies, are topological claims anything more than personal preferences?

The contention that a subgroup can be inferred from a single synapormorphy is not without its problems, not least because ruling out the possibility of homoplasy or horizontal transfer is difficult, even in cases where the shared innovation appears "non-trivial." As explained above in section 3.1, homoplasy can be demonstrated with relative chronology, but there is no method for proving synapomorphy. Consequently, claims of synapomorphy are intrinsically more uncertain than claims of homoplasy. When a subgroup is inferred from a single synapomorphy—even an allegedly indisputable one—the inference is not robust.

Given the lack of progress on this issue for over a century, it is worth considering an alternative approach. In a Bayesian context, the question of how many synapomorphies suffice is bypassed. Rather than asking how much evidence is needed to postulate a subgroup, it estimates the probability that a group of languages forms a clade. Calculating the credibility of a subgroup is straightforward. It is the proportion of trees in the posterior tree distribution (such as that in Figure 1 above) in which the subgroup occurs. It is worth emphasizing that the advantage of the Bayesian approach is not simply that it avoids a difficult methodological question. It is rather that it answers the question we are typically most interested in: given the data and a set of assumptions about linguistic change, what is the probability that a particular set of a languages forms a clade? This question cannot be answered in the traditional framework.

5 The problem of conflicting evidence

The final issue concerns the analysis of conflicting phylogenetic evidence. I focus on a specific type of conflict, namely cases in which different alleged synapomorphies support mutually incompatible subgrouping hypotheses. This issue has been a central challenge in the investigation of the diversification of ancient Greek, as Finkelberg (1994:2) aptly observes:

> The whole history of the study of the Greek dialects bears witness to the fact that a clear-cut classification can only be achieved by emphasizing one set of of linguistic features in a given dialect at the expense of others.

Her insight highlights a seldom-acknowledged weakness of traditional subgrouping.

To illustrate the problem, consider first one of the most frequently discussed innovations in the history of Greek, the assibilation of [ti] to [si] (Risch 1955:66–67; Chadwick 1976:104–105, 111; Risch 1979:272–273, 274; Hall 1996:161; Hajnal 2007:145; Parker 2008:443–444; Ringe 2016; Sowa 2017:713; Janko 2018):[10]

(2) a. Boeotian
τιθη**τι** 3SG.PRS.ACT.IND ‘place’
b. Attic
τίθη**ϲι** 3SG.PRS.ACT.IND ‘place’

Evidence for this sound change is attested in Attic, Ionic, Arcadian, Cypriot, and Mycenaean. It is also found in Lesbian, although its presence there is often attributed to language contact. In the remaining dialects, assibilation is generally absent.

This sound change plays a crucial role in the widely accepted model of the Greek dialects presented in Figure 8. Known as the Porzig–Risch topology—after the seminal work of Porzig (1954b) and Risch (1955)—this topology posits an early split between two major groups: South Greek and North Greek. Among the synapomorphies used to justify the South Greek node, assibilation is arguably the most important.

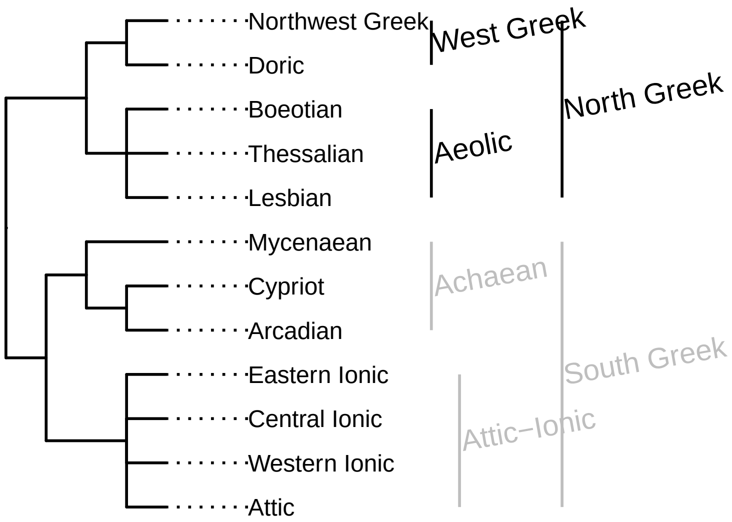


Figure 8: The Porzig-Risch topology (adapted from van Beek 2022a:190). Its central claim is the early division into North and South Greek.

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[10] The morphosyntactic glosses follow the Leipzig Glossing Rules.

Other alleged synapomorphies point to different subgrouping hypotheses. One such feature is the conjugation class of contract verbs. In Lesbian and Thessalian as well as Arcadian, Cypriot, and arguably Mycenaean, they are conjugated athematically, whereas in other dialects they are conjugated thematically:[11]

(3) Athematic conjugation

  a. Arcadian (Dubois 1986:§92.d)
  ποιε-νϲι 3pl.prs.act.ind ‘do’ (*I.v. Magn.* 38.34)

  b. Thessalian (Blümel 1982:172–175)
  ϲτραταγε-ντοϲ masc.gen.sg.part ‘be a general’ (Larissa, ca. 130/129 BCE; Tziafalias et al. 2017:423)

(4) Thematic conjugation (Attic)
ϲτρατηγοῦντοϲ < ϲτρατηγέ-**ο**ντοϲ masc.gen.sg.part ‘be a general’

The thematic vowel -*o*- of the Attic form is absent in Arcadian and Thessalian. If athematic conjugation of contract verbs is a synapomorphy of Aeolic and Achaean (i.e., Arcadian, Cypriot, and Mycenaean), then these dialects would form a subgroup, as Rau (2022) has recently argued. The resulting topology is presented in Figure 9.

Since these two putative synapomorphies support incompatible topologies, the question naturally arises: how should the conflict be resolved? It could certainly be the case that one of them is the result of horizontal transfer or homoplasy. Indeed, Rau (2022) argues that assibilation spread by diffusion. Given that assibilation is a typologically common sound change, one might contend that it is homoplastic, in which case the morphological innovation in example (3) would carry greater weight for inferring subgroup relationships.

The more fundamental issue is that traditional subgrouping cannot accommodate conflicting innovations. In order to draw inferences, one must resolve the conflict by reinterpreting one set of innovations as the result of borrowing or homoplasy. This reflects the same basic limitation encountered in section 3: traditional subgrouping demands a level of certainty that the data often cannot support. By contrast, the strength of the Bayesian approach lies in its ability to draw inferences despite uncertainty. There is no need to privilege one set of innovations over another, as the analysis incorporates the entire dataset—including characters with conflicting phylogenetic signals. Any such conflict is represented in the posterior distribution of trees. Consider again Figure 1, where distinct subgroups are visible near the tips but the earliest regions remain largely unresolved. This pattern reflects stronger agreement

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[11] The interpretation of the evidence for *uerba uocalia* is notoriously difficult, not least because the evidence is so paltry. For discussion and earlier literature, see Risch 1955:71–72 and Scarborough 2023:136–142. Athematic conjugation of contract verbs is also attested sporadically in some West Greek dialects (Scarborough 2023:136 n. 23).

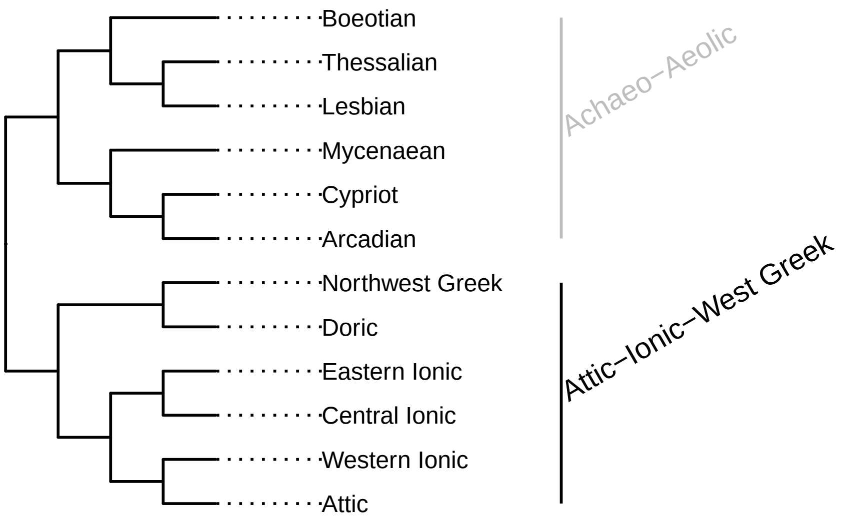

Figure 9: An alternative topology of the Greek dialects posits an initial split between the ancestor of the Achaean and Aeolic dialects and that of the Attic-Ionic and West Greek dialects. This hypothesis is thought to be supported by evidence from the athematic conjugation of contract verbs.

among the sampled trees for the recent history of the dialects and a weaker signal for the earliest divergence events.

6 Conclusion

This study has identified three major limitations of traditional subgrouping, each of which underscores the need for Bayesian inference in linguistic phylogenetics. Although the issues discussed are distinct, they all stem from a common source, namely the inability of traditional methods to accommodate uncertainty. A shared innovation must be either accepted or rejected as a synapomorphy with certainty. When such confidence is justified, the simplicity of traditional subgrouping is an advantage. But in many cases, this binary decision-making imposes assumptions that are too strong for the available evidence. It is time to acknowledge that linguistic phylogenetics is as much a statistical endeavor as a linguistic one and that addressing its challenges requires methods designed to reason under uncertainty (Edwards 1966; Yang 2014:vii). Bayesian approaches offer precisely this capacity, which enables more nuanced and robust inferences about the evolutionary relationships among languages.

Abbreviations

I.v. Magn.	Otto Kern, ed. (1900). *Die Inschriften von Magnesia am Maeander.* Berlin: Spemann.

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