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The Added Value of a Comparative Phylogenetic Reconstruction in Indo-European and Beyond

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The most fundamental use of phylogenetic methods is to infer a cladistic tree structure. Besides the use of different methods for the phylogenetic inference (parsimony, likelihood), contemporary phylogenetic research also discusses on which linguistic features an inference should be based. What happens if we substitute (or complement) the basic vocabulary data with other data types, such as sound changes or morphosyntactic features? By a comparative phylogenetic reconstruction model, i.e., a reconstruction of the transition rates and probability of presence at the root and hidden nodes of features in a phylogenetic tree, we may reconstruct the probability of the presence of different features back to a proto-language, and using a world tree even further back, to Early language. However, how reliable is this reconstruction? How does this reconstruction relate to other types of reconstruction, using, e.g., the comparative method or diachronic typology? Alternatively, is there any other information that can be extracted from a comparative phylogenetic reconstruction?

This paper introduces and outlines comparative phylogenetic reconstruction: the advantages, the constraints, and the ways in which these models support or contradict earlier attempts towards reconstruction. Further, this paper indicates how comparative phylogenetic reconstruction can be used to scale up questions about the origin of morphosyntactic categories, general evolutionary trends, as well as aspects of lineage and areality in the diffusion of morphosyntax.

1 Background: language reconstruction by the comparative and phylogenetic methods

The reconstruction of language families and language classification is an old and well-established discipline. Ultimately referring back to the earliest attempts to draft language trees in the mid-nineteenth century (Schleicher 1853), the discipline of comparative reconstruction has had nearly two centuries to expand and develop. The scientific progress of the method has expanded by adding more data, more languages, and more families. Likewise, the accuracy of the method has developed by refining some of the basic principles of reconstruction, including models for better understanding principles of change (e.g., analogy, grammaticalization, language contact, sociolinguistic principles of language change), or models for reconstructing beyond the attested material (e.g., the laryngeal theory). The development of the comparative method in the late twentieth and early twenty-first centuries has been impacted by progress in comparative typology. By adding typological comparison (Kulikov and Lavidas 2015; Viti 2015), the comparative method has emerged as a powerful and precise instrument of language reconstruction. The typological method has contributed by further argument in cases where the comparative method itself has provided uncertainty.

In recent decades, a new method has been added to the toolkit of linguistic reconstruction: the phylogenetic method (Cathcart 2018; Jäger 2019; Carling and Cathcart 2021b). This method emerged from models developed within evolutionary cladistics and approaches the problem of reconstruction probabilistically. In this model, a linguistic feature is defined as a character, the gain and loss of which is computed by a model that infers a phylogeny. The estimated probability of the presence of a feature at the internal nodes and the root of the tree depends to a high degree on the structure of the tree inferred in the model (Jäger 2019; Carling and Cathcart 2021b). In this model, the tree is a fixed constant. In an alternative model (Goldstein 2021), ancestral states are rather inferred over a set of trees to overcome the problem of trying to do reconstruction in the face of phylogenetic uncertainty.

The three reconstruction methods—the comparative method, the typological method, and the phylogenetic method—have developed to be complementary to each other (see figure 1 for an overview). While the comparative method still is unchallenged when it comes to reconstructing phonemes, morphemes, lexemes and syntagms (Weiss 2015), it has shortcomings when it comes to linguistic classification and distinguishing shared innovations from archaisms. The typological method is unchallenged when it comes to observing and explaining pattern similarity between languages, independent of linguistic affiliation (Haspelmath 2001;

Croft 2003). The phylogenetic method, on the other hand, depends on the comparative and typological method. The comparative method is a prerequisite to code lexical data sets used for phylogenetic inference (Dunn 2015), whereas the typological method is a necessary precondition for defining features to infer in phylogenetic reconstruction (Jäger 2019; Jäger and Wahle 2021; Carling 2024). In this paper, I look at some of the theoretical and methodological preconditions for comparing different reconstruction methods against each other. The paper will also deal with the options for reaching beyond a single language family by reconstructing with the phylogenetic method.

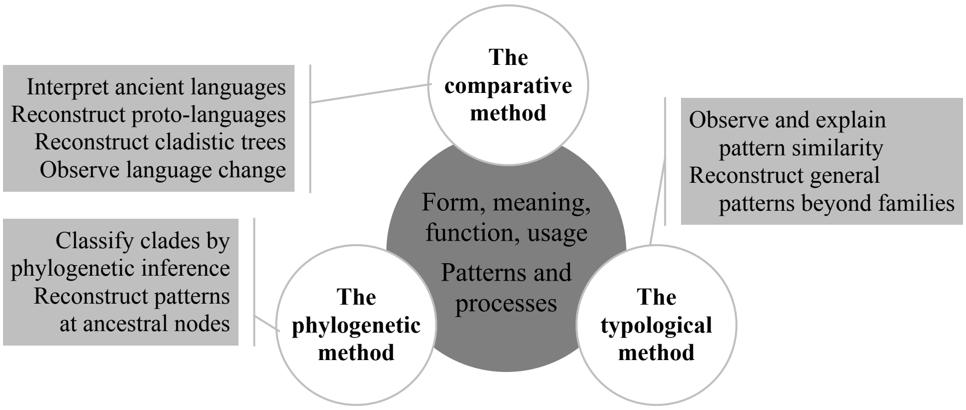

Fig. 1. The reconstruction methodology package, visualizing the relations between the comparative, the typological, and the phylogenetic method

2 Theoretical implications of reconstruction by the comparative and the phylogenetic methods

The comparative method uses structures and features of languages to reconstruct a state to a common language, known as a *proto-language*. A reconstruction leads to a fixed point, where branches of a family tree meet (i.e., the point from which they are all perfectly visible). This is referred to as the Archimedean point, and the reconstruction to this point is linear, as it considers all the branches of the tree but is restricted to data points available in the branches of the tree (Eichner 1988). However, the comparative method itself does not prevent a reconstruction beyond the proto-language state. Rather, a reconstructed language can be the basis for reaching beyond this state, by using typology and internal reconstruction (Gamkrelidze and Ivanov 1984; Robbeets and Savelyev 2020). One expects the reliability of a reconstruction by the comparative method to decrease with time-depth, as the uncertainty of reconstructed changes in form and meaning increase. There is a phenomenon that runs counter to the expectation, however, which is known as Korhonen's paradox. According to the paradox, the perfection and systematicity of an inferred reconstruction potentially increases with an escalating uncertainty due to an increasing distance from the present. In other words, the more uncertainty is in the data, the better the reconstruction. This scenario was noticed by the Uralist Mikko Korhonen (Korhonen 1974), who observed that the further back in time he projected his reconstruction of states of the Uralic family, the more regular his proto-languages became (Eichner 1988).

In a phylogenetic model, a reconstruction always leads to an Archimedean point, that is, a common state at an unobserved node (such as the roots of a tree). This state is fixed and does not allow for variation or layering into further states, in contrast to early and late stages of a proto-language (Carling and Larsson 2024). A phylogenetic reconstruction gives probabilities of features at unobserved nodes, which in turn can be compared to reconstructions achieved by the comparative method (Carling and Cathcart 2021b; Skirgård 2021). On the other hand, a phylogenetic tree can be extended to include more languages and families, including macro-families or even world trees (Jäger 2018; Jäger and Wahle 2021). In such macro-structures, it is necessary to distinguish *deep* and *shallow* or *family-based* reconstructions, that is, whether the reconstruction leads to the root of an established language family or beyond that, such as to macro-families or even the earliest stages of language evolution (Bentz et al. 2018; Carling 2024). These are reconstructions that serve different purposes. While a reconstruction of a language family aims to define a proto-language and focus on change and evolution within the family, a deep reconstruction aims to focus on general trends, such as the evolution of speech, cultural evolution, or evolution of meaning or function in general.

3 Tree inference and comparative phylogenetic reconstruction

The basis for a phylogenetic reconstruction is cladistic tree inference. The tree structure—including branch lengths, branching structures, chronological age of the root—plays a role for the result coming out of the reconstruction. In phylogenetics, the underlying tree and its structure is normally estimated from lexical data, in particular abstract cognate relationships among basic vocabulary items (Dunn 2015). An ongoing discussion is whether other data types, including sound changes, cognate word-forms, or morphological and morphosyntactic data, could be used to infer cladistic trees (Ringe, Warnow, and Taylor 2002; Olander 2022; Goldstein et al. 2024) to achieve a more representative cladistic model. However, tests with sound change data (Ben Hamed, Darlu, and Vallée 2005) or morphosyntactic data indicate that these tend to give unrepresentative cladistic trees, often with an impact of non-genetic features, such as areal pressure (Carling et al. 2018).

A further question of a cladistic tree inference includes where the ancient languages are to be positioned. Either the ancient languages—in case these exist—are treated as equals to the modern languages (Gray and Atkinson 2003), or they are placed in trees using ancestry and clade constraints, a feature that impacts not just the tree chronologies, but also the phylogenetic reconstructions (Chang et al. 2015; Carling and Cathcart 2021b; Goldstein 2024). In phylogenetic inferences, these are all factors that are built into the models in order to achieve a maximally reliable reconstruction.

4 How do we interpret the results?

A phylogenetic reconstruction infers a set of features, typically designed as multistate features, against a phylogenetic tree and computes the rates of change of features among states along the tree. The model assumes that a linguistic variable changes according to evolutionary rates, which can be estimated from the data in combination with the tree. The feature evolution is normally computed by a continuous-time Markov model and the rates can be used to reconstruct the probability of presence of features at internal nodes and the root of the tree (Cathcart 2018; Jäger 2019; Carling and Cathcart 2021a, 2021b; Jäger and Wahle 2021).

The results of a phylogenetic reconstruction can be used for various purposes. The probability of presence of a specific feature variant at the root or an internal node of a tree can be compared to the results of a reconstruction achieved by other methods, such as the comparative method (Carling and Cathcart 2021b; Skirgård 2021). The rates of gain and loss of features (Figure 2) reflect either the probability of a feature variant to be gained or lost (1 → 0, 0 → 1) or to change (a → b) over a defined time span, or alternatively, the probability for a feature variant to remain in a state before changing to another state over a defined time span. The inference depends on the coding of the features.

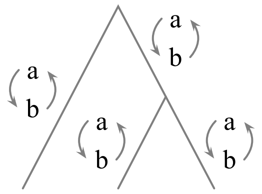

Fig. 2. The probabilities of gain and loss of feature variants are computed as rates of change between states of the phylogenetic tree

If features variants are coded as /a, b, c/ the result is in the form of transitions between these features. If the features are binary coded (i.e., yes/no or 1/0) the result is a gain or a loss of the specific feature. If the features are multistate (e.g., a, b, c, none), the result is either a transition between /a, b, c/ or a gain/loss of /a, b, c/.

The results of transitions or gain/loss rates of features are to be considered in relation to the probability of presence at the root for this feature. This is an important aspect of evolutionary dynamics: a transition between two variants of a feature or the gain or loss of a feature requires that the feature variants be present in the data. The phylogenetic model cannot reconstruct feature variants not observed at the tips of the tree. For instance, if a data set of word orders are inferred as SVO, SOV, V2, VSO for the reason that these are the features present in a family, it is not possible for the model to reconstruct OSV or OVS, either for the protolanguage or in the transition rates. In general, the evolutionary dynamics can be visualized as four different types (figure 3), which also relate to the probability of presence of a feature at the root of the tree.

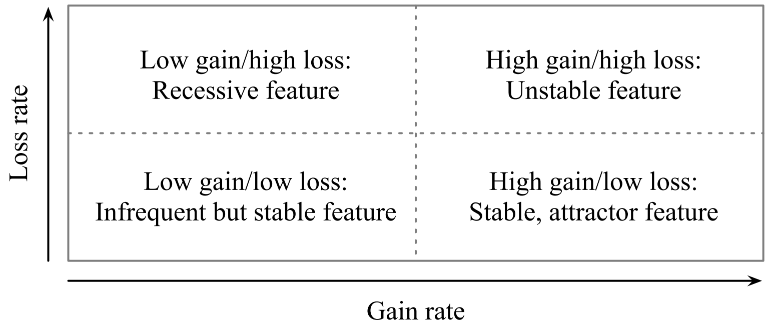

Fig. 3. Model for reading and interpreting evolutionary dynamics of features and feature variants.

1. A feature can have *low gain* and *low loss* rates. This is a feature that has a high degree of stability, but which is not likely to have a high productivity over time.
2. A feature which has *high gain* and *low loss* rate, an *attractor feature* (Carling and Cathcart 2021b:585–7), has a high productivity over time.
3. A feature with *low gain* and *high loss* rates, a *recessive feature* (Carling and Cathcart 2021b:585–7), is likely to disappear over time.
4. A feature of *high gain* and *high loss* rate is an unstable feature which shows a lot of oscillation back and forth between states.

In this scheme, feature types 1 and 2 are more likely to occur at the root of the tree, whereas 3 and 4 are less likely at the root state (Carling and Cathcart 2021b: 585–7).

5 Reconstructions and evolutionary trends—are they useful for anything?

Reconstructions of probabilities at unobserved nodes, gain/loss rates, and transition rates can be used to reconstruct proto-languages and observe language change. However, there are several problems related to the results that have to be considered. The first problem is historical. What is the situation when a phylogenetic reconstruction gives a result that is divergent from the result achieved by the comparative method? The problem is discussed in Carling and Cathcart 2021a and 2021b, where various theories about the Indo-European alignment systems, nominal and verbal morphology, and word order were tested against a phylogenetic model. The phylogenetic model provided clear support for one of the previous models (the canonical model of Delbrück 1893), which reconstructed a highly synthetic, mainly head-final language, with nominative-accusative alignment independent of tense and animacy degree of the first argument, case marking on nouns, no definite article, three grammatical genders (masculine, feminine, neuter), predicative gender agreement, a non-agglutinating case system with fewer than seven cases but with a nominative, accusative, dative, genitive, and vocative, also in pronouns, a synthetic present, no future, full agreement in present tense of verbs but not in the past tense, postpositions, OV infinitive word order, SOV in main and subordinate clauses, possessor-noun, adjective-noun, noun-relative clause, OV participle word order, and *wh*-initial word order. The results of this paper are remarkable from several perspectives. First, that the phylogenetic model is capable of reconstructing a coherent system that can match a typological reconstruction model. Second, that the phylogenetic model—even though exceptions occur—normally is confident about the result.

Carling et al. [under review] further investigates grammatical gender in Indo-European, both in grammar and lexicon, and infers a gender system for the Indo-European proto-language. In addition, the study also expands to include all the world's gender languages, in order to contrast the general results with the result achieved from Indo-European.

First and foremost, the phylogenetic inference of gender in Indo-European (using a global tree of Jäger 2018) reconstructs, with a probability of 80%, a masculine-feminine system at the root of the tree. This result diverges a from the result of Carling and Cathcart 2021b, which gives a higher probability for a neuter case at the root of the tree and thus reconstructs a three-gender system. Furthermore, it is problematic as comparative reconstruction indicates that the feminine may be a secondary addition in Proto-Nuclear-Indo-European (Lundquist and Yates 2018), emerging either from a suffix marking abstracts (Luraghi 2011, 2014), a deictic particle (Pinault 2011), or alternatively the individuating use of the *-*eh*$_2$ suffix (Melchert 2014). The consensus reconstruction for gender in Proto-Indo-European is an animate-inanimate system, to which the feminine was later added (Matasović 2004, Lundquist and Yates 2018). It must be remembered that the comparative and phylogenetic reconstructions are based on different data and different models. The phylogenetic reconstruction is based on typological generalizations about gender systems in all Indo-European languages, in which agreement (Corbett 1991) is used as the main motivation for defining gender. The reconstruction using the comparative method is based on a contrast of morphological devices in various languages, marking gender on the noun, which does not qualify a language to be classified as gender in our data. However, a three-gender distinction in the adjectival paradigm can be securely reconstructed for Proto-Nuclear-Indo-European (Lundquist and Yates 2018). The outlier Anatolian, which branches off first from the Indo-European language, reflects the animate-inanimate system in the comparative reconstruction. Apparently, the state of Anatolian has not caused the phylogenetic model to reconstruct an animate-inanimate system to Proto-Indo-European.

In addition, Carling et al. [under review] adds a typological aspect to the gender scenario. The model reconstructs the gender system of all the world's gender languages (based on a data set of 3,245 languages). Out of 29 language families with gender, 25 are reconstructed with a higher probability of a masculine-feminine system (86%). Only 3 families are reconstructed with a masculine-feminine-neuter system (10%) and only one (Algic of North America) is reconstructed with an animate-inanimate system. Generally, a sexus-based system displays stronger evolutionary dynamics, as other systems have a tendency to transition into sexus-based systems.

This raises a further question for the contrast between a comparative and a phylogenetic reconstruction. If Indo-European, against the phylogenetic reconstruction, was a language with an animate-inanimate gender, how likely is this given that there is only one single family (Algic), for which this pattern is reconstructed? Also, was Indo-European one of the 1% of the world's languages that have an animate-inanimate gender system? The issue touches upon questions of typological plausibility, frequency, and how likely languages are to be atypical or display infrequent features.

6 Conclusion

I have discussed some of the premises and preconditions for a reconstruction by the phylogenetic method. Just as reconstruction by the comparative method, a phylogenetic reconstruction is linear and reconstructs features to a common state in the past. Even more than in the comparative method, a phylogenetic model results in a fixed state. Results do not show any variation, but as they reflect the evolutionary dynamics of features over the tree, the rate tendencies can be used to observe how features relate to each other and how stable they come out. Transition rates must be seen in relation to the probability of presence of features and feature variants at the root of a tree.

A phylogenetic comparative model can support a specific model in a comparative paradigm. As we have seen, a phylogenetic model for Indo-European supports a canonical model of grammar, in which Indo-European is modelled as a synthetic language rich in grammatical categories. Generally, a phylogenetic model seems to entail two previous models of morphosyntactic reconstruction. First, the *majority-wins model*, which suggests that structures of a proto-language are most likely to be preserved in a majority of languages. Second, the *ancient languages most archaic-model*, which suggests that structures of ancient languages are more likely to be similar to the proto-language than structures of modern languages. These are arguments often used in discussions on morphosyntactic reconstruction (Campbell and Harris 2002; Roberts 2007; Carling and Cathcart 2021b; Carling 2024). A phylogenetic model is capable of reconstructing a complete and coherent system for the Indo-European proto-language and therefore follows a canonical model of typology, where traits reconstructed to a proto-language system may remain stable and continue in branches of the tree (Carling and Cathcart 2021b).

A phylogenetic model can be used for global linguistic reconstruction. However, it is always questionable how reliable the result of such a reconstruction is. An interesting outcome is if general tendencies can be observed, where global evolutionary dynamics can be paralleled by results achieved in individual families. Results from a study on gender in all gender families of the world give a result that shows a clear tendency and a preference for a specific system, namely masculine-feminine. A tendency always has exceptions, and the question remains if the reconstruction in a specific language family, such as Indo-European with its animate-animate system, is more or less likely to go against global tendencies.

An important question is if a phylogenetic reconstruction has any added value beyond reconstructions by the typological and comparative methods. First and foremost, a phylogenetic model can make calculations on amounts of data that far outstrip what can be done with the traditional application of the comparative method. Second, these models can systematically tease apart phylogeny and areal bias and thereby confirm or disconfirm earlier theories on reconstructed states. Phylogenetic models can also reflect general principles of change, which are of great value when results of a traditional reconstruction are to be evaluated.

However, the phylogenetic methods have shortcomings. They cannot reconstruct out of the sample, that is, it cannot reach at anything lost or is not present in the data. On the other hand, phylogenetic methods are superior when it comes to handling large amounts of empirical data, which remains an important source for reconstructing previous states of languages.

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