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Contrasting models of morphosyntactic reconstruction. A comparison of results of comparative-historical and phylogenetic methods for the Indo-European family

Gerd Carling & Chundra Cathcart

Morphosyntactic reconstruction has a long history within Indo-European studies, dating back to work by Neogrammarian scholars such as Berthold Delbrück and Karl Brugmann. Non-quantitative morphosyntactic reconstruction employs a number of methodologies, including allowing syntactic reconstruction to be guided by comparative morphological reconstruction — essentially assuming that the evolution of morphosyntactic categories is closely connected by form and function. Another method is the majority rules principle, which inherently relies on an assumption that most morphosyntactic categories are relatively stable throughout the branches of a family tree. Since this is obviously not the case, this method encounters a problem often referred to as the “correspondence problem” (Roberts, 2007), and here, data from precursor languages, from which a change can be traced to its daughter languages, play an important role in tracing and reconstructing change. Thirdly, we have the method of comparative construction grammar, where syntactic frames are reconstructed around lexical cores, which in turn can be reconstructed (Barðdal, 2014).

We present results from a computational method of reconstruction of morphosyntactic features, where we reconstruct features at unobserved nodes of the Indo-European family tree, including Proto-Indo-European. The method is based on a dataset of Indo-European morphosyntactic data (118 features within the domains of alignment, agreement, word, order, nominal and verbal morphology, coded as 1=present/0=absent/NA) from ancient, medieval, and contemporary languages of the family (Carling, 2016/2017). Using a stochastic gain-loss model of trait evolution, we assume that characters are born and die according to GAIN and LOSS rates of some value (Pagel, 2000). We employ a posterior tree sample inferred from lexical data using Bayesian phylogenetic software; clade and ancestry constraints are used to ensure that the branching structure generally agrees with comparative-historical insights into Indo-European subgrouping. On the basis of this sample and data attested for the observed languages in our tree, we infer gain and loss rates for each feature, as well as feature values at unobserved nodes (i.e., protolanguages) via a Markov chain Monte Carlo procedure (Cathcart, Carling, Larsson, Johansson, & Round, submitted).

We contrast the results of our model at unobserved nodes within the Indo-European family tree, in particular at the root (Proto-Indo-European), with earlier theories and discussions on Indo-European morphosyntactic reconstruction and evolution (Bauer, 2000), focusing on a selected number of features, such as word order, alignment system, case system, gender system, and agreement in verbal morphology. We find that our results generally agree with received comparative-historical wisdom, such as that features pertaining to SOV word order is reconstructed. However, some unexpected features are reconstructed, such as the presence of feminine gender marking. We discuss the implications of these results — i.e., the reconstruction of a form vs. a category — for the method we use.

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