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### Citation

Dunn, M., & Bellamy, K. (2023). Evolution and spread of politeness systems in Indo-European. *Transactions Of The Philological Society*, 121(1), 152-167.  
doi:10.1111/1467-968X.12260

Version: Publisher's Version  
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Downloaded from: <https://hdl.handle.net/1887/3677311>

**Note:** To cite this publication please use the final published version (if applicable).

## EVOLUTION AND SPREAD OF POLITENESS SYSTEMS IN INDO-EUROPEAN

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(Submitted: 11 August, 2020; Accepted: 10 February, 2023)

### ABSTRACT

In this paper, we investigate the phenomenon of pronominal politeness in the Indo-European languages and demonstrate that the processes of change of pronominal systems related to politeness follow two evolutionary regimes, one inside the ‘Standard Average European’ (SAE) linguistic area and another outside of it. Historical processes of language change differ at different levels of linguistic structure. In general, we presume that lower level, unconscious aspects of language change slowly over phylogenetic time, giving rise to patterns of relationship that can often be described as a family tree. Aspects of language that are consciously manipulated by speakers are expected to vary at a faster rate and to diffuse within areas of contact. Politeness is a social phenomenon, so we expect these systems to be highly susceptible to areal norms of interaction. We show that the similarities of SAE politeness systems can be accounted for with a model of convergence due to parallel evolution in a shared (social-demographic) environment, rather than by genealogical relatedness or borrowing. By quantifying and testing factors determining rates of structural change, we offer a novel and realistic approach that can explain similarities between distantly related languages sharing the same environment.

### 1. INTRODUCTION

Politeness is a basic constituent in the maintenance of social order (Brown & Levinson 1987). In order to maintain social order, societies develop a variety of communicative politeness strategies (Mühlhäusler & Harré 1990). These strategies can take various morpho-syntactic forms, a frequent locus being pronominal systems. Pronominal politeness systems are found on almost every continent, but are certainly not ubiquitous in languages of the world (Helmbrecht 2013). The Indo-European (IE) languages, however, are a hotbed of such systems, even though considerable variation in form and extent is visible within the family. This diversity would suggest that the systems have evolved in a complex manner, which genetic relatedness could account for, but, in this instance, we will show that it does not.

In areas where multiple speech communities are in contact for long periods, languages may acquire words, sounds, and elements of grammatical structure from each other (Nichols 1997).

The authors would like to thank the audiences at the EHBEA annual conference in Durham, UK (March 2012) and the KNAW-hosted Quantitative Approaches to Linguistic Typology in Amsterdam (December 2012), as well as Evangelia Adamou and two anonymous reviewers, for discussion and suggestions on earlier versions of this paper. We are also grateful to Evangelia Adamou, Jan Casalicchio, Louise Friis, Guglielmo Inglese, Stefan Norbruis, Tijmen Pronck, Giampaolo Salvi, Xander Vertegeal and David Willis for assistance with checking language data.

A set of languages sharing structural features that cannot be due to retention from a common proto-language, and which are normally geographically contiguous, is known as a linguistic area or Sprachbund (e.g., Haspelmath 2001). Pronominal politeness systems are found in most ‘Standard Average European’ (SAE) languages (Whorf 1956 [1941]), whose core members form a linguistic area in western Europe that has also been termed the ‘Charlemagne Sprachbund’ due to its largely coinciding boundaries with the former Carolingian Empire (van der Auwera 1998; Helmbrecht 2003; Mladenova 2010). This area also coincides with the boundaries of the original European Economic Community (Friedman 2012), suggesting a reality of the cultural area up to the present day.

In addition to their established history of comparative and sociolinguistic approaches, IE languages also have a more recent tradition of study within computational approaches (Dyen et al. 1992; Gray & Atkinson 2003; Bouckaert et al. 2012). Computational phylogenetic methods can be used with linguistic data sets to, for example, infer phylogeny within a language family (Gray & Jordan 2000; Holden 2002; Gray & Atkinson 2003; McMahon & McMahon 2003; Dunn et al. 2005, 2008; Greenhill & Gray 2009; Kitchen et al. 2009; Lee & Hasegawa 2011; Greenhill et al. 2017), make inferences about the evolutionary behaviour of a group of languages (e.g., detecting evolutionary punctuations or other variation in rates of change, inferring dates or geographical locations; Bouckaert et al. 2012, Greenhill et al. 2010, Atkinson et al. 2008), or make inferences about evolutionary processes acting upon other elements of language (Dunn et al. 2011; Dunn et al. 2017) or culture (Holden & Mace 2003; Jordan et al. 2009; Jordan 2011). Language contact has, to date, largely been investigated in terms of (mostly qualitative) loanword studies, but now both contact and admixture can also be modelled with statistical network analyses (Reesink et al. 2009; Bowerman 2010; Nelson-Sathi et al. 2011).

Through the application of Bayesian comparative phylogenetic methods, we show in this paper that (i) pronominal politeness may be considered a distinguishing feature of SAE languages, and that this may be quantified despite the evident formal variation; (ii) existing accounts of the evolution of pronominal politeness do not adequately explain how this dynamic, common feature has come to be shared; and (iii) the evolution of pronominal politeness systems—and perhaps other linguistic features—could be better explained in terms of parallel evolution stemming from shared cultural and communicative needs, rather than as a result of genetic relatedness or borrowing. Indeed, these shared needs could also be considered as constituting a common adaptational environment since pronominal politeness systems are innovated at the local level to serve necessary social and linguistic functions.

## 2. BACKGROUND

### 2.1. *Pronominal politeness systems*

Pronoun systems constitute one of the many overt structural expressions of linguistic politeness. The principal goals of using polite forms generally are to (i) enable the other to be placed with respect to self, (ii) indicate deference through the creation of (greater) social distance, and (iii) establish “distinctions in the speech roles [...] rather than identifying the persons who perform these roles” (Bhat 2007). Pronominal systems encode these speech roles, as well as grammatical information such as person, number and gender, although their social function overrides the denotational aspects of their grammatical functions (e.g., plural used to address a single addressee). The decision to use a particular personal pronoun varies at the individual level, in accordance with the social and structural norms of a given language (Stone 1977; Mülhäusler & Harré 1990).

Politeness distinctions in pronoun systems are found in around a quarter of the world's surveyed languages, with IE languages constituting a considerable proportion of this total

(Helmbrecht 2013). In some systems, a binary politeness distinction is found (i.e., a singular referent can be addressed with either an intimate or polite form), while others possess a ternary distinction, where the plural referent also has intimate and polite forms. Yet these systems display considerable variation in terms of which pronoun is used for deferential purposes. Five types of deferential address can be identified within the IE language family: (i) 2pl for 2sg, e.g., French *vous*, Russian *vy*; (ii) 3sg for 2sg, e.g., Italian *Lei*, Friulian *Lui*; (iii) 3pl for 2sg, e.g., German *Sie*, Danish *de*; (iv) a contracted nominal form, often from a title, e.g., Spanish *Usted*, from *vuestra merced* ‘your grace’; and (v) a reflexive pronoun, e.g., Bengali *āpni* ‘self’. Such variation seems to support the position that pronouns or pronoun paradigms in IE are not inherited from a common source, nor do they constitute instances of wholesale borrowing (Trudgill 2011).

Discussion of the history of pronominal politeness systems in Europe dates back to the late nineteenth century, when Latin origins were proposed (e.g., Châtelain 1880, Dräger 1874, cf. Haspelmath 1998). More recent socio-historical accounts also attribute the introduction of deferential forms of address (specifically 2pl for 2sg) to the Late Roman period, when the imperial power was vested in two men (see notably Brown & Gilman 2003 [1960]; repeated in, e.g., Wallwork 1997; Besch 1998). A seventeenth century Papal origin (Brown & Gilman 2003 [1960]) and an eighteenth century French courtly hypothesis (Mühlhäusler & Harré 1990; Brown 1996) have also been proposed. Moreover, Ferguson (1991) and Mühlhäusler & Harré (1990) linked the emergence of polite pronouns to, *inter alia*, the growth in industrialisation and an increasingly stratified society. In contrast, structural accounts explain the shared presence of pronominal politeness systems in terms of the ‘slant’ of a given language (e.g., Head 1978; Lehmann 2002), which “is the ensemble of structural proclivities which predispose it toward accepting and generalizing certain innovations made by some speakers, but not others” (Joseph 1987: 265).

Contact and borrowing are also cited as triggers for the spread of pronominal politeness systems. The most notable of these is the Standard Average European account (Haspelmath 2001; Mladenova 2010), whereby France and Germany represented the homeland or epicentre of an area of polite pronoun usage, which subsequently radiated out across the continent. French and German, along with Dutch and Northern Italian, have been considered the core SAE languages (van der Auwera 1998).

An important assumption underlying all of these accounts, either explicitly or implicitly, is that the politeness systems have not developed in isolation. Rather, speech communities possessing such systems have been influenced by numerous external factors, such as politics, geography, and environment, as well as physical and material culture (Brown 1996, see also Bowden 1992; Dixon 2010). Intertwined socio-cultural factors cannot be ignored since people are social beings, engaged in purposeful social behaviour in social space (Mühlhäusler & Harré 1990). This behaviour may involve interacting with speakers of other languages, sometimes over long time periods. As such, it makes sense to think about types and rates of linguistic change in these contact situations as not only determined by varying combinations of external factors, but perhaps more as a consequence of parallel evolution stemming from shared socio-cultural and communicative needs (Matthiassen 1985).

## 2.2. Linguistic areas

It is widely accepted that some languages “owe many of their characteristics to the languages with which they have been in contact over time, languages either related to them or not” (Muysken 2008: 2). Where a set of distantly related or unrelated languages shares common lexical, phonological, and/or morphosyntactic features, the phenomenon can be labelled a Sprachbund (literally ‘language union’) or linguistic area (LA) (e.g., Friedman 2012).

Numerous LAs have been proposed across the Americas, Africa, Eurasia, southeast Asia, and the Pacific, including Australia (see contributions in Hickey 2017; see also Muysken 2008, Thomason 2001, Haspelmath 2001). Nonetheless, disagreement exists regarding which languages belong to these linguistic areas, the traits that characterise them, how many traits are required to define a LA, and their precise geographical extent (Heine & Kuteva 2001; Campbell 2006). LAs have therefore also been claimed to be largely artificial constructs that do not reflect natural objects in the real world, to the point where some would consider discarding the notion completely (Stolz 2002: 262; see also Dahl 2001).

The existence of a Standard Average European LA (Whorf, 1956 [1941])—comprising the Romance, Germanic, Balto-Slavic and, more marginally, the westernmost Finno-Ugric languages—is a relatively new insight (Bechert et al. 1990; Bernini & Ramat 1996; Haspelmath 1998; van der Auwera 1998; König & Haspelmath 1999; Haspelmath 2001). It is now clear, however, that “[...] the Indo-European SAE languages are clearly more similar to each other in the relevant respects than would be expected on the basis of their genetic relatedness. The SAE languages belong to no major genetic subdivision of Indo-European” (Haspelmath 1998:273). The languages forming this LA share a varying number of structural features from a principal list comprising: (i) definite and indefinite articles, (ii) relative clauses with a relative pronoun, (iii) ‘have’-perfects, (iv) participial passives, (v) dative external possessors, (vi) non-pro-drop, (vii) intensifier-reflexive differentiation, (viii) relative based equative constructions, and (ix) negative pronouns without verbal negation (Haspelmath 2001). The SAE languages of continental western Europe share the highest number of these features, with peripheral languages sharing decreasing amounts (see Figure 1).

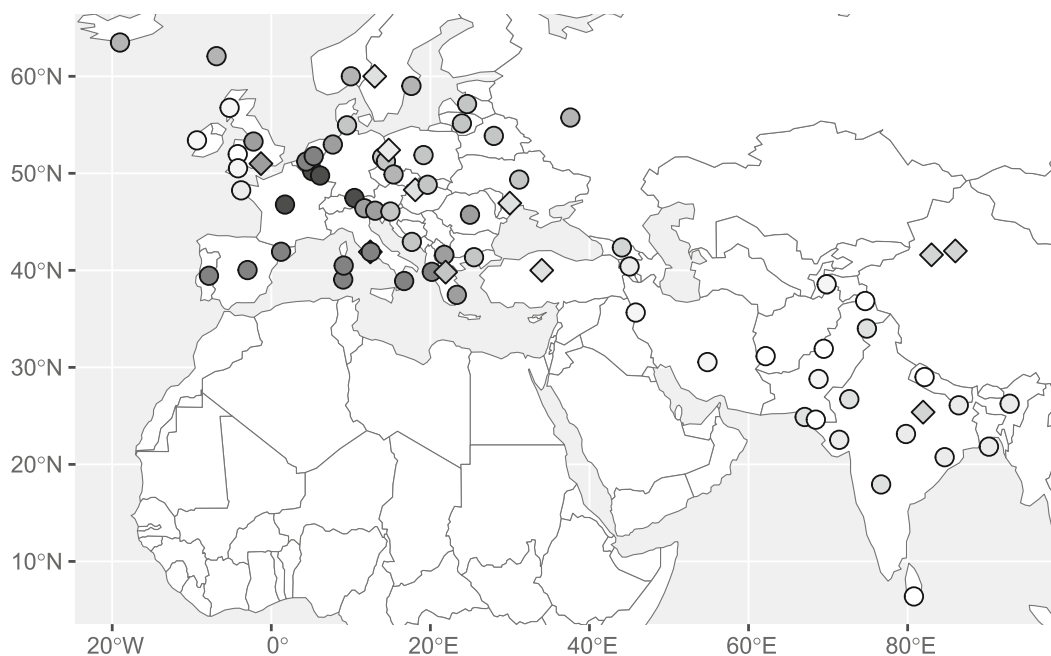


FIGURE 1. Indo-European languages included in the sample. Modern languages are marked with circles, and ancient languages with diamonds. The greyscale fill of the points indicates how many SAE features are present in the language, from 9 (darkest) to 0 (lightest). Tabular versions of this data are included in supplementary materials

These shared features are often attributed to analogical borrowing (Haspelmath 1998), as is evident in the present perfect structures of the SAE core languages, e.g., French *j'ai vu*, Dutch *ik heb gezien*, English *I have seen*. Such constructions are generally not found in peripheral languages such as those of the Slavic and Celtic branches and are unusual typologically. Regarding pronominal politeness systems, a simple binary formal-intimate distinction tends to occur in the core SAE languages, with more peripheral languages (as well as those falling outside of the SAE area) more likely to possess tertiary or other (e.g., deictic) distinctions. However, these binary distinctions vary in form and origin between the core languages, strongly suggesting that they do not stem from a common source.

### 2.3. *Phylogenetic approaches to language evolution*

Phylogenetic trees are a basic tool for understanding diversity in all evolutionary domains (Felsenstein 2004: xix). In the domain of language, linguistic explanations of synchronic patterns of diversity can only be safely made when genealogical factors, such as shared inheritance and innovation, are also taken into account. As products of an evolutionary process, linguistic phenomena cannot be treated as independent observations for the purposes of making statistical generalisations. Phylogenetic comparative methods (unrelated to the 'Comparative Method' from historical linguistics) have been developed to solve this statistical problem. Rather than ignoring the interdependence of observations of linguistic diversity, or trying to reduce it through 'lossy' methods (methods which throw away information) such as sampling, phylogenetic comparative methods build a quantitative model of phylogenetic interdependence into their statistical tests. As a family of methods, phylogenetic comparative methods can address different questions, including those relating to chronological and geographic inference. They can also test hypotheses about expansion sequences or rates of change, infer ancestral states, and test adaptational hypotheses (see references in Section 1). The present paper joins several of these tests, taking an adaptive hypothesis about social determinants of language change to test models of evolutionary rate variation.

## 3. METHOD

The pre-modern range of the Indo-European language family occupies a largely contiguous region from Sri Lanka in the east to Iceland in the west. The SAE area is contained within this region, toward its western edge. The language sample used in this study consists of 78 Indo-European languages, including a number of extinct languages. The languages were sampled reasonably densely and include most languages for which published lexical and grammatical material are available. This sample has good geographic coverage and includes representatives of all branches of the Indo-European family. Three kinds of data are used in the analysis:

- i. *Indo-European phylogenetic tree*, based on a superset of the language sample (94 languages and 197 meaning classes). The data and methods used to generate this tree are derived from Bouckaert et al. (2012) and Chang et al. (2015) and are documented at <https://doi.org/10.5281/zenodo.5556801>.
- ii. *Areal diagnostic data*, from reference grammars, coded as the presence or absence of the nine diagnostic grammatical structures for the SAE area (following Haspelmath 2001); coding data are available in the supplementary materials in the file `analysis/SAE-features.csv`.
- iii. *Pronominal paradigms*, also from reference grammars, collated according to the grammatical categories that they encode, namely:

- a. person (1, 2, 3)
- b. number (single/dual/plural)
- c. inclusivity-exclusivity
- d. gender (masculine/feminine/neuter/common)
- e. formality (informal/mid-formal/formal/super-formal)
- f. proximity (near/mid/far)
- g. animacy (human/non-human)
- h. impersonality

The raw data are available in the supplementary materials in the file `data/pronoun_paradigms.csv`.

Pronoun paradigms were coded against the full set of grammatical distinctions made in the aggregate data set, and gaps were not admitted. Where a distinction is not made in a particular language (e.g., near and far masculine use the same form), the form is simply reproduced in both cells of the table which holds the full dataset of the personal pronouns.

### 3.1. *Indo-European phylogeny*

The traditional visualisation of the historical relationships between Indo-European languages is that of a family tree, where daughter languages ‘branch off’ from their parent, often in clusters, or sub-families such as Celtic or Balto-Slavic, on the basis of shared innovations (Schleicher 1848). The present study uses the genealogical tree of languages to estimate rates of change, and as such we rely on a tree with quantified branch length indicating calendar time between nodes. For this purpose we use a tree produced by Bayesian phylogenetic inference, a quantitative method which produces a tree with the required statistical properties (Dunn and Tresoldi 2021; see also Bouckaert et al. 2012, Chang et al. 2015).

Bayesian phylogenetic inference (BPI) is a model-based method which proposes a phylogenetic hypothesis to account for observational data about a set of related taxa. In linguistic analysis the most common application of Bayesian phylogenetic methods is to model lexical histories—the innovation of new cognate sets and the retention and loss of their reflexes—in order to produce a sample of phylogenetic trees. This is a ‘sample’, rather than a single tree, because the method can only say how much a particular tree is a better or worse fit to the observed data than another. The sample represents possible phylogenetic hypotheses, sampled in proportion to how likely they are. This has an advantage over a single, ‘best’ tree in that the representation of different aspects of the tree within the sample gives an estimate of how much confidence we can have in each detail of the reconstruction.

The philosophy of Bayesian inference is to take what is known and to infer what follows from this; BPI can thus be considered an adjunct to traditional linguistic comparative methods. Cognate identifications from the Linguistic Comparative Method (LCM) are the basic source of data for modelling, and events in the LCM tree can be used as topological constraints on the BPI inference. Bayesian phylogenetic inference quantifies explicit models of these reconstructions and allows us to quantify chronology and other aspects of history. A reproducible workflow for producing a minimally controversial Indo-European tree is published by Dunn and Tresoldi (2021), available at <https://doi.org/10.5281/zenodo.5556801>.

Note too that tree inference is by no means the be-all and end-all of phylogenetic inference. A quantified evolutionary model allows us to investigate many other aspects of evolutionary change. These include phylochronology or phylogeography (the inference of dates and places; see Gray & Atkinson 2003, Atkinson et al. 2005, Bouckaert et al. 2012), inferences about evolutionary processes within a domain that co-evolves with the phylogenetic tree (see, e.g.,

Currie et al. 2010 on political complexity, Jordan et al. 2009 on postmarital residence practices, and Dunn et al. 2017 on patterns of syntactic change), phylogenetic dependency (are two linguistic features evolving in tandem, or are they independent? Dunn et al. 2011), or patterns of rate variation (e.g., does language change show punctuated equilibrium? Atkinson et al. 2008). All these methods test a phylogenetic hypothesis, but the purpose is to infer additional elements of tree history invisible to LCM inference.

### 3.2. Measuring the variation of pronoun paradigms

The structures of pronoun paradigms in the language sample were summarised and compared by a two-step process of abstraction. First, pronoun paradigms were collected from each language, and a complete list of potentially contrastive pronoun functions appearing in all these paradigms was created. Thus, rather than the common, broad categories, such as “first person singular” or “third person plural”, the data codes much less granular categories, such as “first person singular feminine” (which occurs in Tocharian) or “third person plural feminine near” (which occurs distinctively in Kashmiri). In each language, the appropriate form was entered for all these possible functions, with forms repeated where a language does not make a distinction (e.g., English uses the same pronoun *you* for both 2sg FEM and 2sg MASC, as well as all 2pl contexts).

Second, the tabulated pronouns were transformed into a pairwise similarity table: For each language, all the pairs of pronominal functions were compared and the results were coded as either (1), where the pronouns used for this pair of functions were the SAME (e.g., English uses *they/them* for both 3pl FEM NEAR and 3pl FEM FAR), or (0), where the pronouns used for this pair of functions were DIFFERENT (Kashmiri uses *yimi* for 3pl FEM NEAR but *timi* for 3pl FEM FAR). A pairwise similarity table abstracts away from the lexical form used and allows the abstract structure of the paradigms to be compared directly. The pairwise similarity test provides a vector of binary SAME-DIFFERENT codes for each language, which, in the third step, allows the abstract pronoun paradigm structure to be compared between languages, independently of lexical form using a simple distance metric. This process is illustrated with a toy example, below.

Step 1: Collect paradigms for each language, noting terms for every attested 2nd and 3rd person pronominal function. A selection of languages and functions is shown in Table 1: The full list of languages and of potentially distinctive pronominal functions found in the data is given in the supplementary materials.

TABLE 1. Pronominal paradigms showing an etic grid of all pronominal functions. Note that German *Sie* is grammatically a 3pl pronoun, but it has the function of marking formal address in the second person

	2sg informal	2sg masc formal	2sg fem formal	(more functions)
English	<i>you</i>	<i>you</i>	<i>you</i>	
French	<i>tu</i>	<i>vous</i>	<i>vous</i>	
German	<i>du</i>	<i>Sie</i>	<i>Sie</i>	
Tajik	<i>to</i>	<i>tu</i>	<i>šom</i>	
Waziri	<i>de</i>	<i>dər</i>	<i>tə</i>	

Step 2: Compare each pair of cells within a row and code whether the forms are the same (1) or different (0), as illustrated in Table 2.

TABLE 2. Per language comparison of similarity of pronominal forms for each pair of functions

	2sg informal = 2sg masc formal	2sg informal = 2sg fem formal	2sg masc formal = 2sg fem formal	(more pairwise comparisons)
English	SAME (both <i>you</i> )	SAME	SAME	
French	DIFFERENT ( <i>tu</i> ≠ <i>vous</i> )	SAME	SAME	
German	DIFFERENT	SAME	SAME	
Tajik	DIFFERENT	DIFFERENT	DIFFERENT	
Waziri	DIFFERENT	DIFFERENT	DIFFERENT	

Step 3: Calculate a similarity matrix comparing each pair of languages, as in Table 3. For the toy example of only three functions per language given above, the similarity of English to Tajik is 0.0 (completely dissimilar), since every cell has a different value. The similarity of English to French is 0.66 (one difference out of three). The similarity of French to German is 1.0 (completely the same for these three comparisons) since their paradigms make exactly the same functional contrasts.

TABLE 3. Similarity matrix comparing pairs of languages

	French	German	Tajik	Waziri
English	0.66	0.66	0.0	0.0
French		1.0	0.33	0.33
German			0.33	0.33
Tajik				1.0

Finally, this language similarity matrix is transformed into two continuous variables using principal components analysis (PCA).

The full data set of Indo-European pronouns was analysed using the methodology illustrated above. The first (PC1) and second (PC2) components of the PCA clustering of the pairwise similarity data are shown in Figure 2. Note that these components are abstractions measuring the divergence of certain structures internal to these paradigms, and should not be interpreted as cluster diagrams measuring similarity of the overall paradigmatic systems or indeed languages. Note also that these measured differences are meaningful relatively, but are not strictly proportional to the amount of change, since distances depend on the number and nature of the contrasts that emerge from the selection of features made by the researcher, and different researchers could make different selections of features.

The first component (i.e., PC1) accounts for 67.1% of the variance in the data, and PC2 accounts for 19.7% of the data, i.e., 86.8% of the variance between them. As is often the case with PCA, it is possible to give an approximate prose interpretation of these components: PC1 draws out pronoun systems characterised by the conflation of singular and plural in the second person and/or third person. PC2 gives heaviest weighting to features related to having distinct politeness forms that are different in the singular and plural.

### 3.3. Quantifying the SAE linguistic area

Since politeness is a social phenomenon, we expected pronominal politeness systems to be highly susceptible to areal norms of social interaction. We tested whether the SAE linguistic area correlates with evolutionary processes acting within politeness systems. Haspelmath (2001) gives nine grammatical structures which are diagnostic for the SAE area (see Section 2.2). We coded the presence/absence of these from reference grammars for our sample

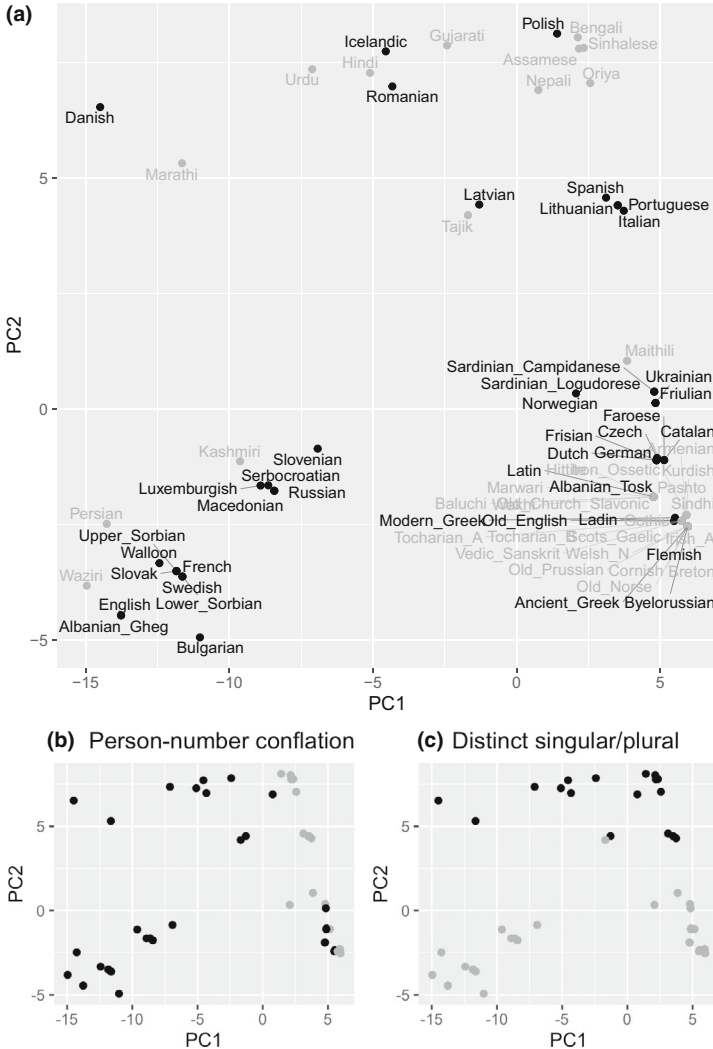


FIGURE 2. Principal components analysis (PCA) of pronoun pairwise similarity measures. Panel (a) shows SAE languages labelled in black, non-SAE in grey. Note the cluster of SAE languages in the bottom left quadrant (PC1 and PC2 both negative), as well as a mixed group of SAE languages in the top half (PC2 positive). PC1 puts negative weight on languages which have conflation of pronominal number in the 2nd or 3rd person, as shown—without labels—in panel (b); PC2 puts positive weight on languages which have distinct politeness forms in both 2sg and 2pl, shown in panel (c)

of 78 Indo-European languages (which includes languages from both inside and outside the putative area). Data were checked against Haspelmath's coding where overlap between the language samples occurs. This coding gives us a nine-point scale for how much each language approaches the SAE areal prototype. Languages can score 0 to 9 on this scale. There is a natural breakpoint between 4 and 5 (see Figure 3), which corresponds well with the usual understanding of the limits of SAE, as shown on the map in Figure 1.

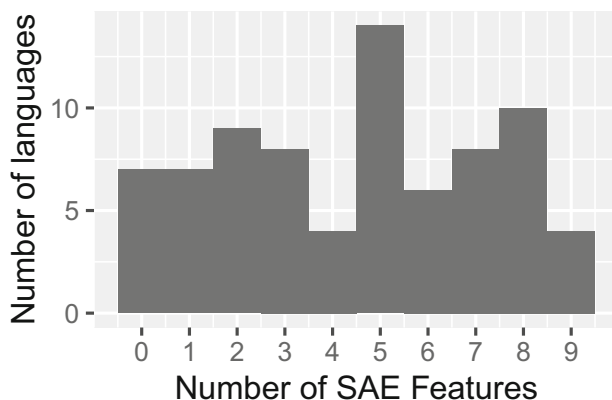


FIGURE 3. Distribution of diagnostic SAE features in the sample. While the count of features varies from 0 to 9, there is a natural division at 5, which can be used as a threshold to define two classes: Membership of the SAE area is defined as languages having 5 or more of the SAE features

### 3.4. Simulating SAE history

The problem of detecting differences in processes of language change is analogous to the situation in biological evolutionary systems, where the rate of diversification of a characteristic varies according to environmental factors. We carried out a hypothesis test for whether trait histories are better explained by a single rate of diversification, or by a two-rate model determined by an environmental classifier. The environmental classification of the taxa (e.g., species or languages) under study is usually only known with certainty at the tips of the tree, where it can be observed directly. The environmental states of taxa in the past are inferred using simulations on the tree.

In our case, we start from a tree with observed languages annotated for whether or not they are within the SAE zone according to a threshold on the SAE prototypicality statistic (Figure 3; see also Section 3.3). Each point along the branches of the tree represents a linguistic variety at an instant in time, which may be within or outside the SAE zone. Using tools developed by O'Meara (O'Meara et al. 2006; Stack et al. 2011), we simulate possible histories in order to estimate plausible parameters of change. This is carried out multiple times over multiple equiprobable trees. Figure 4 shows three sample simulations carried out over a summary tree of the Bayesian tree sample; in the analysis, these simulations are done over the entire sample in order to integrate an estimate of the uncertainty of the phylogeny.

### 3.5. Modelling pronoun evolution

The phylogenetic hypothesis test compares two different models of pronoun evolution. In each case, we are investigating the rate of change of the PCA components that summarise the structure of the pronoun paradigms outlined in Section 3.2. This is modelled as a Brownian process: a series of small random changes whose magnitude is governed by a rate parameter (Hida 1980). In the one-rate model, pronoun diversification rates are assumed to be unaffected by the membership of the SAE linguistic area. In this model, we estimate the fit of a Brownian model of change of the pronoun structure measure to the tree sample, and measure the range of likelihood scores, that is, how well the model fits the data. In the two-rate model, we assume that there are two different rates of change that apply under different environmental regimes,



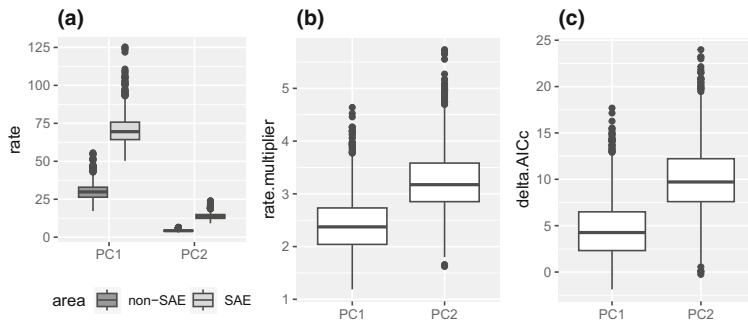


FIGURE 5. (a) Estimated rates of change in the first two principal components (PC1 and PC2) according to the two-rate model for languages inside (grey) and outside (black) the Standard Average European area, (b) relative rates of change inside the SAE area compared to outside, and (c) change in the small-sample Akaike Information Criterion (AICc) showing the improvement of model fit in the two-rate model compared to the one-rate model.

defined by the sample of reconstructed SAE histories (Section 3.4). We estimate the range of parameters that fit best, given that there is one rate of change for the languages of the SAE area and another for the non-SAE languages. As in the first model, the output is the range of inferred values for the rate of change parameter(s) and a likelihood score.

#### 4. RESULTS

The rate of change parameters were estimated according to the one-rate and two-rate models using the O'Meara et al. (2006) method as implemented in the *brownie.lite* package (Stack et al. 2011) in the R programming language (R Core Team 2021). The results are stochastic, so the exact figures reported below may vary slightly. For PC1, the median log likelihood of the two-rate model was  $-275.5$ , higher than the single rate model, which had a median log likelihood of  $-278.7$ ; for PC2, the two-rate model had a median log likelihood of  $-206.9$ , whereas the one rate model had a likelihood of  $-212.7$ . The inferred rates of change for the two-rate models are shown in Figure 5a (rates for SAE and non-SAE languages). Figure 5a shows that the rate of change of PC1 is considerably faster for SAE languages (grey) than non-SAE languages (black); in PC2, the SAE languages are also faster than non-SAE, although the absolute rates are smaller. These same differences in rates are given as a ratio in Figure 5b, showing that the difference in inferred rates of change ('rate multiplier') in the SAE area was approximately 2.3 times faster than the non-SAE rates of change for PC1 and 3.2 times faster for PC2. Figure 5c shows the change in Akaike Information Criterion (AICc) score comparing the better fitting to the worse fitting models (Burnham & Anderson 2002). For PC1, the median change in AICc is 4.256, which corresponds to an evidence ratio of 8.4 to 1 (i.e., the likelihood of the two-rate model is 8.4 times higher than that of the one rate model; see Burnham et al. 2011 for conversion from  $\Delta\text{AICc}$  to evidence ratio). For PC2, the median change in AICc is 9.711, which is an evidence ratio of 128.5 to 1 in favour of the two-rate model. These figures can be interpreted to mean that there is moderate evidence to prefer the two-rate model for PC1, and very strong evidence in support of the two-rate model for PC2. This supports the conclusion that the major dimensions of variation in the structure of pronoun paradigms in Indo-European have evolved faster inside the SAE linguistic area than outside.

While it is known that the rate of structural change of language differs within families (Dunn et al. 2011; Greenhill et al. 2017), the factors determining these rates have never been

quantified or tested. This paper therefore presents a novel but realistic approach to the treatment of areal linguistic similarities. Similarities between distantly related languages sharing an environment can be accounted for with an explicit model of parallel evolutionary change, rather than by borrowing. While a word from one language can be taken over directly by another, a linguistic structure has to be recreated in the target language out of the available linguistic resources. Most so-called structural borrowing in languages might be better thought of in this way (Ross 2007). An account based on multiple innovation sources also supports the socio-cultural approaches to the development of pronominal politeness (see Section 2.1) since they consider the systems to be culture (or language) specific, yet fulfilling the same function.

## 5. CONCLUSIONS

In order to maintain social order, societies develop a variety of politeness strategies. Pronominal systems represent just one of the many linguistic strategies for encoding politeness. In practice, people not only address one another but also simultaneously make choices between the available address forms, thereby conveying indexal information (Stone 1977). These forms vary cross-linguistically, including within the IE family, which contains the major concentration of pronominal politeness systems typologically speaking. Standard Average European languages are a hotbed of pronominal politeness systems that, we have shown, can be quantified despite their observable formal variation. The presence of such synchronic diversity is a strong indication that diachronic processes of change other than genetic relatedness have been at work.

Indeed, it is not always possible to fall back on traditional theories of contact and borrowing to explain the presence of shared features in several languages (i.e., within a linguistic area), which are not inherited from parent languages. Our results suggest that this is the case with pronominal politeness systems inside and outside the SAE area: An alternative explanation is required. Similarities in the less closely related languages sharing an environment can rather be accounted for with an explicit model of parallel evolutionary change, rather than borrowing. The higher rate of change within the SAE languages indicates that the membership of this area influences the mode of evolution: multiple rates of change are identifiable within the model. Since a linguistic area is a social environment, it follows that social factors determine the dynamics of change.

## SUPPLEMENTARY MATERIALS

All data and scripts necessary to replicate this study are archived at <https://doi.org/10.5281/zenodo.7622084>; this repository may also be downloaded from <https://github.com/evolving/ie-politeness> and a non-interactive version of the analysis is available at <https://evolving.github.io/ie-politeness/>.

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