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# Subgrouping: Trees vs. waves

*Alexandre François and Siva Kalyan*

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## 1 TREES, WAVES, AND THE COMPARATIVE METHOD

Languages commonly arise through the internal diversification of an earlier language.<sup>1</sup> The diversity of the modern Romance family, for example, can largely be explained as a result of the fragmentation of a relatively homogeneous variety of spoken Latin.

While we are fortunate, in the case of Latin, to have an attested ancestral language, for most other families the ancestor is merely hypothetical: it is reconstructed through systematic comparison of attested languages. This procedure, known as the Comparative Method (Weiss 2014, Hale 2014), was initially developed by the German Neogrammarians in the second half of the 19<sup>th</sup> century to reconstruct the ancestor of the Indo-European languages; it has since then proven to be of universal relevance.

The Comparative Method consists in identifying regular correspondences among a set of modern languages in their phonology, morphology, syntax and lexicon; these are then explained as the result of a shared linguistic history. Features that do not correspond across all attested languages are indicative of local innovations, revealing the different social bonds that once prevailed among ancient communities. The Comparative Method provides tools for detecting these local innovations, for identifying the descendant languages that reflect them, and for grouping these languages into “subgroups”. The task of subgrouping languages in a family is not only central to historical linguistics—it also builds bridges with the other social sciences by providing a window onto the history of past societies.

There are two models of subgrouping, which will be compared in this chapter: the Tree Model (or *Stammbaumtheorie*) and the Wave Model (or *Wellentheorie*). The Comparative Method tends to be associated exclusively with the Tree Model, an association that dates to August Schleicher’s introduction of the Tree Model in his 1853 article *Die ersten Spaltungen des indogermanischen Urvolkes* (see Bloomfield 1933:311, Campbell 2004:165). However, we will see that there is no intrinsic link between these two ideas, and that they should in fact be separated.

While the Comparative Method is unsurpassed in its ability to reconstruct language history, the Tree Model generally does a poor job of representing this history. Cladistic (tree-based) representations rest on the largely fictional scenario of languages emerging through the abrupt and total division of a language community into disjoint subcommunities. This fails to capture the much more common situation whereby linguistic families emerge through the slow fragmentation of a language into a network of dialects that remain in contact for an extended period of time (Bloomfield 1933:317, Saussure 2005 [1916]:273–278, Croft 2000: chapter 8, Garrett 2006, Heggarty *et al.* 2010)—the type of situation that Ross (1988, 1997) calls a ‘linkage’ (see section 3.3).

This chapter discusses the strengths and weaknesses of cladistic representations, and examines alternative ways of representing genealogies<sup>2</sup> of languages. We first summarise (in section 2) the traditional interpretation of trees in historical linguistics, and the assumptions they are built upon, before examining (in section 3) the underlying processes of language diversification, and whether the Tree Model is really suitable for representing them. We argue that, contrary to widespread belief, a rigorous application of the principles of the Comparative Method in situations of linkage disproves the Tree Model, and favours the Wave Model (§3.2) as a more accurate description of linguistic genealogies.

So far, the main weakness of the Wave Model has been the lack of an effective way of communicating its results. We address this in Sections 4–5 by presenting an approach that combines the rigour of the Comparative Method with the realism of the Wave Model: namely, *Historical Glottometry* (Kalyan and François 2018). This method identifies genealogical subgroups within a linkage, and assesses their relative strengths based on the distribution of innovations among modern languages. As we will illustrate with the Germanic family (after Agee 2021), glottometric results are easily visualised. Provided it follows a rigorous application of the Comparative Method, Historical Glottometry can help to unravel the genealogical structures of the world’s language families, by acknowledging the role played by linguistic convergence and diffusion in the historical processes of language diversification.

## 2 UNDERSTANDING THE TREE MODEL

### 2.1 Proto-languages and subgroups

Let us examine how language trees are classically understood.

Let there be five modern languages, labelled K, L, M, N, and O. These languages are considered genealogically related if they satisfy certain conditions (Campbell and Poser 2008:162ff), in particular the presence of cognates exhibiting regular sound correspondences in their morphology and basic vocabulary (Weiss 2014).

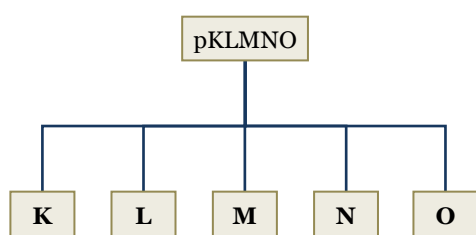


Figure 1 — A genealogical tree, unordered (rake-like)

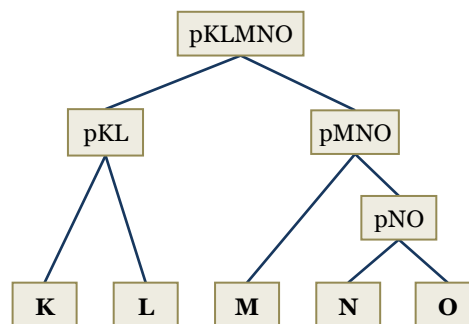


Figure 2 — A genealogical tree indicating internal subgrouping

To say that K, L, M, N, and O are genealogically related is to say that they share a common ancestor — a ‘proto-language’, here called Proto KLMNO. This is shown in Figure 1, a ‘rake-like’ or ‘fan-like’ representation — in the language of biologists, a ‘polytomy’. Such a minimalistic tree can be interpreted in two ways. This could be a case of ‘hard polytomy’, reflecting the historical facts themselves: a rake-like tree is, for example, the structure that obtains when an ancestral society broke up into several sub-communities within a short time frame, followed by rapid loss of social contact — as

Pawley (1999) explains about Austronesian languages. Alternatively, a rake-like structure may merely correspond to a ‘soft polytomy’, where the linguist simply avoids committing to a particular internal family structure, for instance due to a lack of data. It is typical for historical linguists to interpret every polytomy as a soft polytomy, under the assumption that further evidence will always resolve it into a tree with internal nodes, such as the one in Figure 2.

The tree in Figure 2 makes numerous claims about the structure of the KLMNO language family: for example, that languages K and L ‘subgroup’ together, by contrast with M, N and O; and that N and O form a subgroup of their own apart from M. N is thus said to belong to the NO subgroup, which in turn forms a ‘branch’ of the larger subgroup MNO, itself (recursively) a branch of the KLMNO family. Even though these subgroups could in principle be merely taxonomic constructs, it is common to give them a historical interpretation—one where each node in the tree corresponds to a language community that existed at some point in the history of the language family, and each subgroup is constituted by the descendants of this language community. Under this rather simplistic interpretation (as noted by Pulgram 1961), each split in the tree can be equated with the division of a unified language community into separate social groups.

Positing a subgroup that consists of M, N and O embodies a claim that these languages descend from an intermediate protolanguage (‘Proto MNO’) that was once spoken by a splinter group of the earlier ‘Proto KLMNO’-speaking community, and which developed separately from the community speaking Proto KL, the shared ancestor of modern languages K and L. Such a claim must be established by identifying linguistic innovations (whether phonological, grammatical, lexical, etc.) in the modern languages M, N and O, not found in other languages of the family. The idea is that, instead of positing the same change in three languages (M, N, O) independently, it is more parsimonious — following Occam’s razor — to propose that it took place in one language (Proto MNO) and was then inherited by the descendants of that language.

This parsimony-based principle was first articulated in historical linguistics by Brugmann (1884:231) — though it is often attributed to Leskien (1876:xiii). It states that every subgroup in a language family must be established in terms of *exclusively shared innovations* — what phylogeneticists call *synapomorphies* (Page and Holmes 2009). This idea is widely regarded as a cornerstone of the Comparative Method. Yet as we shall see, while its original motivation comes from the Tree Model, a thorough application of this principle leads us inexorably to the Wave Model instead.

## 2.2 Dealing with conflicting evidence

Each language in a tree can only be immediately contained in one subgroup: if M is a member of the MNO subgroup, then it cannot also be a member of a KLM subgroup. This follows from the very nature of the Tree Model, in which any two subgroups must be either disjoint or nested. Admittedly, such an assumption can make sense if the splits in the tree are meant to represent permanent physical separation: if the speaker communities of pKL and pMNO did indeed lose all contact with each other from the moment they separated, then it would be difficult to explain why some descendants of pMNO, but not others, could share innovations with pKL. And yet, studies of real language families often find precisely this type of situation.

In the context of Figure 2, it may be the case that some linguistic property is found to be shared by languages L and M, and only these two languages — despite the fact that they do not form a subgroup. There are a few ways to account for such data without abandoning the tree structure. For example, in some cases the shared property could be

reinterpreted as a *shared retention* (known as a *symplesiomorphy* in phylogenetics): namely, a property inherited from pKLMNO (as well as pKL and pMNO) but lost in all modern languages other than L and M. This shared retention would not indicate any particular event in the shared history of L and M (other than their shared descent from pKLMNO), and thus would not conflict with the subgrouping entailed by the tree.

Alternatively, it could be argued that the shared property, while indeed an innovation, happened independently in L and M: this is known as a *parallel innovation* — a *homoplasy* in phylogenetic terms.

A third possibility is that the shared property was innovated in one language and *borrowed* into the other, after they had fully separated. This process, described as ‘contact’, ‘horizontal transmission’ or ‘areal diffusion’, is responsible for much of language change (Lucas 2014), but is usually argued to be fundamentally different from the sort of ‘internal change’ that underlies the genealogical relations represented by a tree. Strictly speaking, contact-induced change can only happen among languages that already exist independent of one another; yet the study of genealogy pertains to how these languages arose, not what happened to them afterwards. Thus, in our example, a property borrowed from L to M (or from M to L) after their separation cannot be considered as evidence for a genealogical subgroup LM; rather, it would be considered irrelevant for the purposes of subgrouping.

But there is one final possibility for how one might account for a shared property whose distribution conflicts with a given tree. Rather than having been borrowed from one language to another, it may have diffused *within* the proto-language, after it had begun to break up into a network of dialects, but before these dialects had separated into distinct languages. Such INTERNAL DIFFUSION<sup>3</sup> can no longer be dismissed as ‘contact’, since it occurred within a single language community. Thus it is unquestionably part of language genealogy — yet it conflicts with the tree. This, then, is the real difficulty faced by the Tree Model; it provides the motivation for alternative models of language diversification, and for alternative methods for subgrouping.

### 3 THE WAVE MODEL

#### 3.1 Genealogy as the outcome of repeated diffusion

Let us take a step back, and re-examine the process of linguistic diversification in light of the sociolinguistic underpinnings of language change. A common assumption made when applying the Tree Model is that each linguistic innovation takes place in a ‘language’ or a ‘proto-language’, understood as a monolithic entity, and represented as a node on a tree diagram. Every innovation that the language undergoes supposedly affects the *whole* of the language community, and does so near-instantaneously (relative to the history of the language family). Such an assumption is not unique to historical linguistics, and is common in evolutionary biology as well (Baum and Smith 2013:79).

This view of languages as atomic units was in fact challenged in the late 19<sup>th</sup> century by dialectologists such as Gilliéron (1880) and Wenker (1881), who showed that a language may consist of a network of dialects that show great internal diversity. They found language properties distributed among these dialects in geographically coherent patterns, which they showed using *isoglosses*. Crucially, they found that these isoglosses rarely coincided neatly, but rather tended to intersect in complex ways (cf. Trudgill 1986, Chambers and Trudgill 1998, Fox 1995:129). These findings were later enriched by those of sociolinguists, who described the process by which innovations spread among individuals through social networks, whether involving physical or sociological

proximity (see Labov 1963, 1994–2001, 2007, Milroy and Milroy 1985, Milroy 1987, Eckert and Rickford 2001).

Taking a sociolinguistic approach to language change, we find that the proper unit of observation is neither the language nor the dialect, but rather the *idiolect*, i.e. the linguistic competence of an individual speaker at a certain point in time (cf. Hale 1998, 2014). Dialects and languages can then be understood as networks of *mutually intelligible idiolects*. Any change that is identified as having happened ‘once’ in a ‘language’ is really the culmination of a process of diffusion that took place across a network of idiolects, sometimes over multiple generations.

This language-internal diffusion of innovations gives rise to the very same genealogical relations that subgrouping studies seek to unravel: it occurs within a single language community, and its outcome is inherited by the descendants of that community. Yet it is not fundamentally different from the process of language contact: both forms of diffusion involve the progression of a new linguistic behaviour across a social network of individual speakers. The only distinction is that *contact* involves separate languages, whereas *language-internal diffusion* involves mutually intelligible idiolects that are part of a single, internally diverse language community.

An innovation diffusing through a dialect network may eventually become part of the mainstream usage of the entire language community, and thus become a feature of ‘the language’. When this happens, the change may be conveniently summarised by a formula of the type  $x > y$ ; it may even be understood, in retrospect, as though it were the product of a single event in the history of the language. However, the outcome of language-internal diffusion need not be so neat. Rather than targeting an entire language community, an innovation may settle down to just a cluster of dialects, with successive innovations targeting different segments of the network. In this case, the intricate patterns resulting from language-internal diffusion cannot be captured by a tree, and must be accounted for by a different model.

### 3.2 The Wave Model

The above reasoning provides the motivation for the ‘Wave Model’, or *Wellentheorie*, which Hugo Schuchardt and Johannes Schmidt proposed in the early 1870s (Schmidt 1872), as an alternative to August Schleicher’s Tree Model (*Stammbaumtheorie*).

These authors occasionally conceived their Wave Model as a challenge not only to the Tree Model, but to the Comparative Method as a whole (a view that has continued to be held by more recent critics of the Tree Model, e.g. Fox 1995:124, Dixon 1997, Aikhenvald and Dixon 2001, Bosson 2009): Schuchardt, for example, linked it with a general disbelief in the Neogrammarians’ views on the regularity of sound change (Schuchardt 1885). We believe that such a view is unnecessarily extreme, and throws the baby (the Comparative Method) out with the bathwater (the Tree Model). A synthesis should be possible, which preserves the principle of regularity and other useful tenets of the Comparative Method, yet replaces the simplistic tree representations with a wave-inspired approach.

Under the Wave Model, each instance of language change arises somewhere in a network, and from there diffuses to adjacent speaker groups. The propagation of the change can thus be compared to a ‘wave’ which expands away from its centre as the new feature is adopted across a broader territory. These waves are independent of each other, and are not necessarily nested. As Bloomfield (1933:317) put it, “[d]ifferent linguistic changes may spread, like waves, over a speech-area, and each change may be carried out over a part of the area that does not coincide with the part covered by an earlier change”.

Likewise, an innovation targeting a small cluster of dialects can be followed by a later one targeting a larger group.<sup>4</sup> Both of these patterns are incompatible with a tree.

Consider the (fictional) dialect network illustrated in Figure 3. We see eight close dialects labelled A to H, and six innovations numbered #1 to #6, such that innovation #1 arose in dialect D and spread to adjacent dialects until it covered the zone CDE; #2 encompassed AB; #3 spanned over CDEF; #4 over FG; #5 over EF, and #6 over EFGH. (We leave aside the fact that each of these innovations had to spread among individuals *within* each dialect community; we may treat each dialect as behaving in a unified manner.)

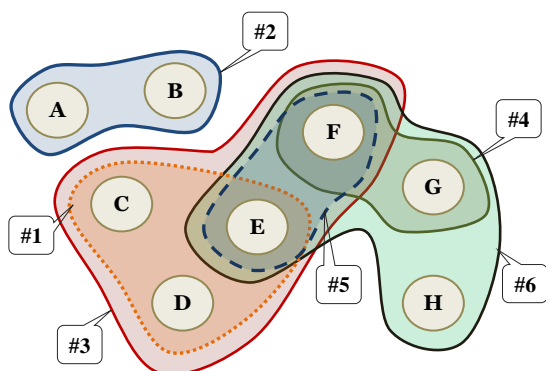


Figure 3 — *Intersecting isoglosses in a dialect continuum or a linkage*

The first innovation, which targeted the cluster C-D-E, was not radical enough to prevent mutual intelligibility with the other dialects: in the absence of a physical boundary between them, nothing then prevented the next innovation from targeting cluster E-F, then cluster F-G, etc. In this model, every innovation constitutes an instance of linguistic *convergence* — for the dialects that participate together in that innovation, e.g. F and G in #4 — as much as it is a case of linguistic *divergence* — for the dialects that become differentiated as a result of the change, e.g. E and F in #4 (cf. François 2011:231).

Over time, the layered innovations leave their footprint in each local dialect. Consider a pair of dialects, for example F and G. While the changes they share together (#4, #6) have increased their similarity in certain aspects of their systems, those which affected only one of them (either alone, or together with other neighbouring dialects — e.g. #3, #5) have increased their difference. If many more cross-cutting innovations (or ‘non-shared innovations’) accumulate over generations, then what started as mutually intelligible dialects F and G will become opaque to each other, and eventually become distinct languages. Unless later processes of dialect levelling (or *koineisation*) take place, each member of the network will inherit in its local system the innovations it has participated in, and these will be transmitted to its descendants. In this regard, all the innovations mentioned here, and represented in Figure 3, define the genealogical structure of the family.

As these dialects increase their differences and lose mutual intelligibility, the end result is an increase in the number of distinct languages. Yet crucially, whereas the Tree Model assigns linguistic diversification to social splits with loss of contact (§2.2), the Wave Model is compatible with scenarios where communities continue to interact. In fact, it treats linguistic contact — in the form of multiple, entangled events of diffusion across mutually intelligible dialects — as the very key to understanding patterns of language diversification (cf. François 2011). This is a radical shift in perspective.

An important implication of the Wave Model is that a given language can perfectly well belong to several partially overlapping subgroups. A GENEALOGICAL SUBGROUP is here defined as a group of languages whose ancestors participated together in the diffusion of one or more linguistic innovations, at a time when they were mutually intelligible. Crucially, nothing in this definition entails that subgroups should be nested, and indeed our claim is that they often are not. Thus in Figure 3, it is legitimate to say that E belongs simultaneously to the subgroups CDE, EF, CDEF, and EFGH — a situation which no family tree can represent (§2.3). In such a situation, the very principles of subgrouping will necessarily differ from those of the Tree Model.

### 3.3 From dialect continua to linkages

The issue of intersecting isoglosses has long been central to dialect geography (see Bloomfield 1933:321). It thus comes as no surprise that dialectologists tend to favour the Wave Model — or some model derived from it — over cladistic representations.

One could propose that the two models are complementary, in the sense that trees might be well-designed for representing the genealogical relations among separate LANGUAGES; whereas waves are only concerned with the relations between DIALECTS *within* the boundaries of each language. The two models would then both be useful, but at different scales of observation. We think that this view is mistaken, for one important reason: namely, that many language (sub)families — as we will see below — have in fact arisen from the diversification of earlier dialect continua. To the extent that local innovations are faithfully transmitted across generations, the resulting languages preserve the traces of earlier entangled isoglosses. If trees fail to represent genealogical relations between dialects, then they must also fail to capture the relations between the languages that are descended from them.

This point is forcefully made in the work of Malcolm Ross, who introduced the concept of a *linkage* (Ross 1988, 1997, 2001). Ross (1988:8) defines a linkage as “a group of communalects which have arisen by dialect differentiation” (where ‘communalect’ is a generic term which may refer to modern dialects or languages). When a dialect continuum — typically structured along the lines of Figure 3 above — evolves in such a way that its members lose mutual intelligibility, it becomes a linkage. A linkage can thus be defined as a cluster of separate languages that are all related and linked together by intersecting layers of innovations. It is a language family that cannot be faithfully represented by a tree.

While Ross initially developed this concept for the purpose of reconstructing the history of the Western Oceanic languages, it clearly has wider theoretical significance. Many language families or subfamilies have been shown to be linkages — whether the authors have used that term or not. The Oceanic languages of Fiji (Geraghty 1983) and Polynesia (Gray *et al.* 2010); the Kamta subgroup of Indo-Aryan (Toulmin 2009); the Karnic subgroup of Pama-Nyungan (Bowerman 2006); the northern Athabaskan languages (Krauss and Golla 1981); some parts of the Semitic family (Huehnergard and Rubin 2011); various branches of Sino-Tibetan (Hashimoto 1992, Chappell 2001, Pelkey 2015); the Sogeram language family of Papua New Guinea (Daniels *et al.* 2019); Western Romance (Penny 2000:9–74; Ernst *et al.* 2009), Germanic (Ramat 1998; Agee 2021), and even Indo-European as a whole (Bloomfield 1933:316, Anttila 1985:305): these are all examples, among many others throughout the world, of language families that have been shown to result from a long history of layered innovations with entangled patterns of distribution, akin to Figure 3 above; none of them could be accurately represented by a



tree. Section 4.3 below will propose a way to model such linkages, and examine the application of this model to the Germanic linkage.

### 3.4 Tree-like families as a special case of linkages

Based on empirical observation of the world's language families — as illustrated by the scholarly works cited above, and many others — it thus seems that genuinely 'tree-like' families are much rarer than is usually assumed. This is so true, that one may question the usefulness of the Tree Model as a suitable approach for representing language genealogy altogether.

One might propose to salvage the Tree Model as a useful approximation, at least for those (sub)families that are mostly compatible with it. This would go along with the conventional wisdom that the Tree Model and the Wave Model are complementary, and should both be preserved (Hock 1991:454, Rankin 2003:186, Labov 2007, etc.). However, this conclusion becomes superfluous once we observe that a tree-like structure is nothing more than a special case of a linkage — an exceptional case in which isoglosses just happen to be nested, and temporally ordered from broadest to narrowest. To see this, imagine that in the family descended from the dialect network shown in Figure 3 above, the members of the AB subgroup were found to share no innovation at all with the other members of the family: this is shown by the absence of any isogloss involving A, B or AB together with other dialects. Such an observation may reflect the fact that the speakers of A and B isolated themselves from the rest of their family, whether due to social attitudes or physical constraints — including migration with loss of contact. What we would then have represented is precisely the sort of neat social split that trees are designed to represent.

Would such cases of social split justify preserving the Tree Model? Not necessarily, for two reasons. First, even if the existence of a separate AB cluster could be represented visually by a 'branch' linking Proto ABCDEFGH to Proto AB, the entangled isoglosses among C, D, E, F, G and H would still be incompatible with a tree, and would need to be represented by waves anyway:<sup>5</sup> the wave diagram in Figure 3 is necessary and sufficient to display the splits in question, and a tree would add nothing more.

The second argument is of a more epistemological nature, and still favours the Wave Model even in situations of neat social split. Under the Tree Model, splits are assumed, *a priori*, to be the only force underlying the formation of subgroups. By contrast, under a wave-based approach, the identification of such splits is an empirical — and falsifiable — result of observation. In terms of historical reconstruction, this is an invaluable advantage of the latter method. In other words, waves are not only better designed than trees for tackling dialect continua and linkages; they even do better at detecting cases of neat split, which the cladistic model merely takes for granted.

### 3.5 Synthesis: Two competing models of language diversification

In sum, trees and waves constitute two competing attempts at representing the same thing, namely historical events of early language-internal 'horizontal' diffusion, apprehended through the traces they left in modern languages, via later 'vertical' transmission. Both approaches are equally concerned with diffusion (*shared innovations*) and with transmission (*shared inheritance*). They target the very same domain (*pace* Campbell and Poser 2008:399), and it is indeed *genealogical* relations that we claim are better represented by waves than by trees.

The Wave Model is agnostic as to whether subgroups should be expected to be nested or to intersect; therefore, it constitutes a more encompassing and flexible view of

language diversification than the cladistic approach. Conversely, the Tree Model entails a number of assumptions and simplifications which are not warranted by what we now know of the actual life of languages. In lieu of trees, historical linguists should use the Wave Model, or some approach derived from it, to achieve a more exact and realistic representation of the genealogical structure of the world's language families.

#### 4 A MODEL FOR CAPTURING INTERSECTING SUBGROUPS

What we need then is a method for identifying and representing genealogical subgroups when they intersect. Among several existing proposals for non-cladistic models (§4.1), this final section will focus on one possible way of formalising the Wave Model: Historical Glottometry.

##### 4.1 Alternative approaches to representing genealogy

One possible reason why trees have remained pervasive in historical linguistics, despite their long-recognised flaws, is a relatively trivial one: namely, that they offer a visually elegant and easy-to-read graphical representation. For the more realistic wave-based approach to ever be fully rehabilitated, then, it is necessary to design a model that readily lends itself to readability and straightforward interpretation, without compromising empirical accuracy.

In recent years, several phylogenetic studies have tried to tackle the flaws inherent in Schleicher's *Stammbaum* by using Bayesian methods to assess the degree of support for each subgroup in a tree (e.g. Dunn *et al.* 2008; Gray *et al.* 2010; Bowerman and Atkinson 2012; Bowerman 2018; Greenhill *et al.* 2020). These methods provide a welcome improvement, by moving us away from a simplistic reading of family trees, and providing a rigorous way of testing subgrouping hypotheses. Yet these are still cladistic approaches: while they can quantify the degree to which a linkage is '(non-)tree-like', they do not provide a convincing alternative representation of their own; in particular, they do not countenance the possibility that two overlapping subgroups may exist *simultaneously*, and not merely as probabilistic alternatives.<sup>6</sup>

There have also been proposals more clearly inspired by the Wave Model— e.g. Anttila's (1989:305) isogloss map of major Indo-European subgroups; Hock's (1991: 455) "truncated octopus-like tree"; Ross' (1997:223, 234) social-network diagrams of language change; Forster *et al.*'s (1998:185) "evolutionary network", etc. Each proposal contributes to the search for a representation of language genealogies that is free from the constraining assumptions of the Tree Model. However, they are mostly intuitive and programmatic, and have not been applied to detailed empirical data from specific language families.

An exception must be made for the network representations in Forster *et al.* (1998) mentioned above, as well as for NeighborNets, which have gained wide acceptance in recent decades (Bryant *et al.* 2005; Heggarty *et al.* 2010; Lehtinen *et al.* 2014; Gao 2020). These networks show intersecting groupings in the form of web-like 'reticulations', and may thus seem perfect for capturing linkage phenomena. However, these intersecting groupings are derived not from patterns of shared innovations, but from pairwise distances among the languages. Hence, these are not truly genealogical representations (François 2014:180), and cannot serve as a proper alternative to phylogenetic methods.

Another Wave Model-inspired approach to representing language diversity that is worthy of mention is *dialectometry* (Séguy 1973, Guarisma and Möhlig 1986, Goebel 2006, Nerbonne 2010). This family of methods uses multidimensional scaling and various clustering techniques, combined with innovative colour mappings, to visualise pairwise

distances among dialects on a choropleth map. Inspiring though it is, this approach, like NeighborNet, does not attempt to tackle language history *per se*: following accepted practice among dialectologists, its assessment of linguistic distance is based merely on the comparison of synchronic features, without distinguishing shared inheritance from shared innovations.

#### 4.2 Crossing the Comparative Method with the Wave Model: Historical Glottometry

In the final part of this chapter, we present *Historical Glottometry*, a relatively new model that synthesises the theoretical principles discussed earlier. This method aims to combine the precision and realism of dialectological approaches (especially dialectometry, which inspired its name) with the powerful reasoning of the Comparative Method.

The objective of Historical Glottometry is to identify genealogical subgroups in a language family, and measure their relative strengths. Stronger subgroups can then be taken as indicators of stronger bonds among past societies — precisely the sort of insight that is the most valuable contribution of historical linguistics to other disciplines.

In line with the principles of the Comparative Method — in particular, Leskien’s principle (see §2.1) — the focus of attention in Historical Glottometry is not merely on synchronic properties of languages, but rather on those properties that are thought to reflect *shared innovations*. As we have shown, this is in no way incompatible with a wave-based or network-based approach: this is how, for example, Figure 3 above should be interpreted, with each isogloss corresponding to one or more shared innovations.<sup>7</sup>

The tools for distinguishing innovations from retentions are also those of the Comparative Method: in particular, they include the principle of regularity in sound change, and hypotheses on the directionality of change and on relative chronology. In this respect, the procedure is identical to the one used to identify innovations in a cladistic approach. Likewise, the Comparative Method has often proven capable of distinguishing which properties were diffused among dialects early in the history of a language family, and which were spread through later contact among separate languages (for example, by distinguishing regular and irregular sound changes: e.g. Biggs 1965 for Rotuman). It would be a mistake not to avail ourselves of such powerful tools.

Once shared innovations have been identified, we can proceed with subgrouping proper, i.e. observe which groups of languages have tended to ‘stick together’ over time. If a certain group of languages exhibits one or more shared innovations that can reasonably be attributed to language-internal diffusion, then that group of languages constitutes a (more or less well-supported) genealogical subgroup (§3.2).

Each subgroup has associated with it a number  $\varepsilon$  (*epsilon*) of ‘exclusively shared innovations’. This metric  $\varepsilon$  measures how often the subgroup is ‘attested’, i.e. how frequently its members have imitated each other’s speech (as opposed to the speech of non-members), as an effect of their historical social bonds;  $\varepsilon$  provides a first approximation to the strength of the subgroup. For example, in Figure 3 above, suppose that languages E and F shared 32 innovations, and F and G just 8: such a measure would show that community F had much stronger social bonds with E than it had with G.<sup>8</sup>

Historical Glottometry provides still more precise ways of measuring the relative strengths of subgroups — namely, *cohesiveness* and *subgroupiness*. These two metrics will be described in the next section, as we illustrate the glottometric method with data from a recent case study of the Germanic branch of Indo-European (Agee 2021).

## 5 USING HISTORICAL GLOTTOMETRY TO SUBGROUP EARLY GERMANIC LANGUAGES

Our initial publications presenting Historical Glottometry (e.g. François 2014, Kalyan and François 2018) have inspired several linguists to apply the method to the language families of their expertise (see §5.3). Among them, Agee (2021) used glottometry to propose a new subgrouping of early Germanic languages. In turn, we will borrow Agee’s approach and results, to illustrate how Historical Glottometry works.

### 5.1 The dataset

The early Germanic languages studied by Agee are Gothic (GO), Old Norse (ON), Old English (OE), Old Frisian (OF), Old Saxon (OS), Old Low Franconian (OLF) and Old High German (OHG) — all of which are historically well attested in writing. Subgrouping these should, by proxy, produce a subgrouping of the modern Germanic languages, since they all descend from these early languages (or from closely related varieties that no longer survive). For instance, Dutch is descended from OLF; Low German (Plattdüütsch) from OS; standard German from OHG; and so on.

Given that Germanic is one of the best understood branches of Indo-European, the main work of identifying shared innovations has already been done in accordance with the Comparative Method. Agee’s task thus consisted primarily of selecting and tabulating the innovations, before applying the formulas of Historical Glottometry.

Agee’s dataset (Agee 2021:349–354; see Agee 2018 for a fuller presentation) consists of 162 innovations that are each found in two or more languages. His list, which draws heavily on Ringe (2006) and Ringe and Taylor (2014), includes cases of regular sound change [RSC], irregular (that is, lexically-specific) sound change [ISC], morphological change [Mrph], and lexical replacement [Lex]. Semantic, syntactic and pragmatic change (which feature in other glottometric studies such as Kalyan and François 2018) were excluded. Table 1 shows a random sample of 12 innovations from Agee’s dataset.

Table 1 – A sample of 12 innovations attested among the early Germanic languages

id	type	innovation	GO	ON	OE	OF	OS	OLF	OHG
B1.18	RSC	*-jj-, *-ww- > -ddj-/-ggj-, -ggw-	1	1	0	0	0	0	0
(2021)	RSC	syncope *-ai- > ∅	0	1	1	0	0	0	0
D2.2.2	Mrph	epenthetic *w in hiatus (*āa > *āwa)	0	0	1	1	0	0	0
D1.1.4	RSC	*-lþ- > *-ld- (e.g. *gulþīn ‘golden’)	0	0	1	1	1	0	0
D1.1.8	ISC	1pl pronoun *wiz: *-z > ∅	0	0	1	1	1	1	0
C3.8	ISC	*þar ‘there’, *hwar ‘where’: *a > *ā	0	0	1	1	1	1	1
C3.13	Lex	‘wash’: innov. *waskan	0	0	1	1	1	1	1
D1.3.3	Mrph	*sīn: reflexive → 3sg poss ‘his’	0	0	0	1	1	1	1
C2.13	Lex	‘name’ *namō neut. → masc.	1	1	0	0	1	1	1
F3.17	Mrph	‘be’: 1sg, 2sg → forms in b-	0	0	0	0	1	1	1
F3.3	Mrph	‘be’: new infinitive *sīn	0	0	0	0	0	1	1
F2.22	Mrph	merger 1sg, 3sg endings → 3sg	0	0	0	0	1	0	1

For each innovation (row), the table gives the corresponding ID in Agee (2018:63–237); notes what type of change it represents; and describes the change briefly. Most importantly, it specifies which of the early Germanic languages reflect each innovation (using ‘1’ if a language reflects it, and ‘0’ if it does not). Unusually, this dataset does not

have any blanks, such as missing data or inconclusive cases — a situation which Glottometry can also deal with (Daniels *et al.* 2019).

Even before we proceed to calculations, we can already note that Table 1 is typical of a linkage. This is evident from its chain-like distribution of ‘1’, where almost every language shows conflicting affiliations, and potential subgroups constantly overlap.

## 5.2 Applying Historical Glottometry

In Historical Glottometry, a genealogical subgroup is defined (see §3.2) as any set of languages that have undergone at least one innovation together, at a time when they were still mutually intelligible. In this respect, any historical isogloss potentially defines a subgroup. However, allowing subgroups to be based on such minimal evidence runs the risk that the subgrouping may be unduly influenced by the accidental inclusion of parallel innovations or late borrowings in the data.

To avoid this situation, Historical Glottometry proposes a method for weighing the amount of evidence that supports each subgroup, so as to reconstruct the most significant patterns in the genealogical history of a language family.

### 5.2.1 COHESIVENESS

The simplest way of measuring the strength of a subgroup is to count the number of innovations that define it: these correspond to the ‘exclusively shared innovations’ counted in the metric  $\varepsilon$  (§4.2). That said, we need to also bear in mind the intuition, clearly laid out by Pawley (2009:13), that “[t]he weight of [the evidence for a subgroup] depends on the number and quality of the innovations concerned *and on the number and quality of innovations that have conflicting distributions*” (our emphasis). Historical Glottometry thus proposes a metric called *cohesiveness*, which weighs the evidence supporting a subgroup against the evidence that contradicts it.

For any given subgroup  $G$ , let  $p$  denote the number of supporting innovations (i.e. innovations that cover the entire subgroup, whether exclusively or not), and let  $q$  denote the number of conflicting innovations (i.e. those that cross-cut  $G$ , by involving only some members of  $G$  together with some non-members). Then, the total amount of evidence that is relevant for assessing the cohesiveness of  $G$  is given by  $(p + q)$ . Now, if we call  $k_G$  the cohesiveness value of  $G$ , we have:<sup>9</sup>

$$k_G = \frac{\text{number of supporting innovations}}{\text{total number of relevant innovations}} = \frac{p}{(p + q)}$$

Given any set of languages, cohesiveness measures how closely it approximates the subgroups found in a tree (such as the tree in Figure 2). In this idealised situation, subgroups are never contradicted by cross-cutting innovations, and their cohesiveness value is necessarily 100%. But this value is hardly ever found in real-life linkages, where innovations constantly intersect.

In the Germanic dataset used by Agee (2021), there are 129 innovations shared by Old English and Old Frisian — including  $\varepsilon = 11$  that they share exclusively. Conversely, there are five “non-shared” innovations (i.e. ones that affected only one of the two languages, together with at least one other language); two of these are shown in Table 1 (the syncope of \*-ai- shared by ON and OE, and the new 3sg possessive \**sīn*, shared by OF and other languages, but not OE). In other words, the cohesion of the language pair *Old English–Old Frisian* is confirmed  $p = 129$  times, but “betrayed”  $q = 5$  times. The cohesiveness of this subgroup is thus  $k_{OE-OF} = 129/(129 + 5) = 0.963$ : this means

that whenever either language underwent a shared innovation with at least one other language, this innovation encompassed both languages 96.3% of the time.

This cohesiveness value can be compared with that of the pair *Old Norse–Old English*, which forms a subgroup defined by a single exclusively shared innovation ( $\varepsilon = 1$ ). For this subgroup,  $p = 27$  and  $q = 109$ , so that  $k_{ON-OE} = 27/(27 + 109) = 0.199$ . That is, among all the changes that affected either ON or OE, only 19.9% affected both. In other words, OE–OF is almost a perfect subgroup, whereas ON–OE (being contradicted way more often than supported) is a very poor one. In terms of social history, this means that speakers of Old English (or their ancestors) had much closer ties with speakers of Old Frisian than with those of Old Norse.

### 5.2.2 SUBGROUPINESS

In sum, the degree of support for a genealogical subgroup can be measured in two ways. In absolute terms, the number of *exclusively shared innovations* ( $\varepsilon$ ) measures how many times the subgroup is attested; in relative terms, the rate of *cohesiveness* ( $k$ ) measures how close it is to a perfect subgroup.

These two measures are independent of one another. A subgroup for which both  $k$  and  $\varepsilon$  are high is clearly well-supported: this is the case, for example, with the pair *OE–OF*, for which  $k = 96.3\%$  and  $\varepsilon = 11$ . By contrast, the subgroup *ON–OF–OS–OLF–OHG* (which Agee calls ‘Continental Northwest Germanic’) has both low cohesiveness ( $k = 16.5\%$ ) and low attestation ( $\varepsilon = 1$ ): it is thus poorly supported. But certain subgroups are low on only one of these dimensions, and thus merit an intermediate level of support. For example, the pair *OLF–OHG* (‘Teuto-Franconian’) has high cohesiveness ( $k = 90.6\%$ ), but is only attested  $\varepsilon = 5$  times in Agee’s database.

An ideal index of subgroup strength would combine both metrics. Thus, Historical Glottometry proposes to define *subgroupiness*, denoted by the Greek letter sigma ( $\zeta$ ), as  $\zeta = \varepsilon \times k$ . Table 2 lists the nine Germanic subgroups with best support — that is, those for which  $\zeta$  was calculated to be higher than a conventional threshold  $\theta = 1$  (cf. Agee 2021:343).<sup>10</sup>

Table 2 — Attestation ( $\varepsilon$ ), cohesiveness ( $k$ ), and subgroupiness ( $\zeta$ ) of the best-supported subgroups of early Germanic (threshold  $\theta = 1$ ).

SUBGROUP NAME	LANGUAGES	$\varepsilon$	$k$	SUBGROUPINESS ( $\zeta = \varepsilon \times k$ )
West Germanic	{OE-OF-OS-OLF-OHG}	66	0.897	<b>59.20</b>
NW Germanic	{ON-OE-OF-OS-OLF-OHG}	21	0.913	<b>19.17</b>
Ingvaemonic	{OE-OF-OS}	20	0.814	<b>16.28</b>
[unnamed]	{OS-OLF-OHG}	16	0.774	<b>12.38</b>
Anglo-Frisian	{OE-OF}	11	0.963	<b>10.59</b>
Teuto-Franconian	{OLF-OHG}	5	0.910	<b>4.55</b>
Ingvaemonic–OLF	{OE-OF-OS-OLF}	6	0.715	<b>4.29</b>
Teuto-Saxon	{OS-OHG}	5	0.755	<b>3.78</b>
N NW Germanic	{ON-OE-OF-OS}	5	0.211	<b>1.06</b>

### 5.2.3 A GLOTTOMETRIC DIAGRAM

Agee (2021:347) displays all 15 of the subgroups attested in his data using a type of figure that Kalyan and François (2018) refer to as a *glottometric diagram*. We recreate this

diagram in Figure 4, showing only the subgroups listed in Table 2 (those for which  $\zeta > 1$ ). In a glottometric diagram, each isogloss is drawn with a line whose thickness is proportional to the *subgroupiness* ( $\zeta$ ) of the corresponding subgroup. Additionally, the brightness of each line's colour may be made proportional to the *cohesiveness* ( $k$ ) of the corresponding subgroup (though this convention is optional, and is not recommended if the diagram is to be displayed in grayscale).

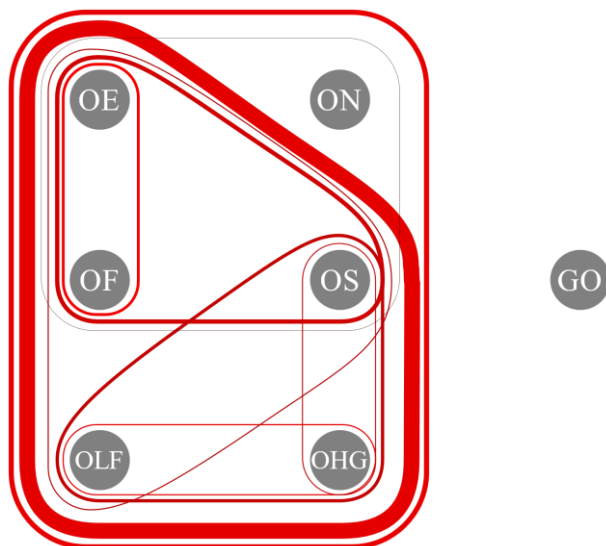


Figure 4. A glottometric diagram of the early Germanic languages (based on Table 2, and the data in Agee 2021). [Abbr.: GO Gothic, ON Old Norse, OE Old English, OF Old Frisian, OS Old Saxon, OLF Old Low Franconian, OHG Old High German.]

This result is cogently analysed by Agee (2021:335–347); here we simply mention a few highlights. First of all, the subgroupiness values, as well as the diagram derived from them, confirm the idea that the early Germanic languages form a *linkage* in which isoglosses, and hence subgroups, constantly intersect. For example, Old Saxon (OS) is a member of the “Ingvaemonic” subgroup (OE–OF–OS,  $\zeta = 16.28$ ); but also, simultaneously, of another subgroup OS–OLF–OHG ( $\zeta = 12.38$ ). In addition, the latter subgroup is a perfect example of a dialect chain — as shown by the strength of both OLF–OHG ( $\zeta = 4.55$ ), and OS–OHG ( $\zeta = 3.78$ ).

It is worthy of notice that the glottometric approach can *also* detect and represent those situations which are ‘tree-like’ (see §3.4). Agee (2021:344) thus notes that “the divergence of East Germanic from Northwest Germanic may have been a relatively clean split” — as evidenced by the high level of cohesiveness of Northwest Germanic (91%). (An example of a conflicting innovation is Holtzmann’s Law: see the first row of Table 1.) And yet, these pockets of treelikeness are evidently a rarity in what is fundamentally a non-tree-like language network.

Somewhat expectedly, the groupings of languages appear to correlate closely with their (historical) spatial distribution. That said, Historical Glottometry can also detect discrepancies between geography and genealogy (François 2017:71–73). For example, even though Old Norse and Old Frisian were probably neighbours, they have very few exclusively shared innovations. Likewise, Old Frisian shares much more with Old English than with Old Low Franconian (the ancestor of Dutch), even though it was once adjacent to both. Such results illustrate the utility of the glottometric method for reconstructing former social interactions.

### 5.3 Prospects

Glottometric diagrams offer a viable alternative to family trees for representing genealogical relations among languages. They are built on the analysis of shared innovations that is the pillar of the Comparative Method; yet they also incorporate the key insight of the Wave Model, namely that genealogical subgroups regularly intersect.

The glottometric analysis summarised in this section is just one among several that have been carried out in recent years: notably, on the Oceanic languages of northern Vanuatu (François 2014, 2017); the Numic subgroup of Uto-Aztecan (Rannap 2017); the Enlhet–Enenlhet languages of Paraguay (van Gysel 2017); the Sogeram subgroup of the Madang languages in Papua New Guinea (Daniels *et al.* 2019); the Boni subgroup of Cushitic, in Kenya and Somalia (Elias 2019); and the Arabic dialects of Egypt and Sudan (Leddy-Cecere 2021). Beyond the application to specific language families, several publications have also addressed theoretical issues raised by Historical Glottometry: e.g. on the question of intermediate protolanguages (François 2017:75–6), on the method for reconstructing chronology (Kalyan and François 2019), and on the methodology of glottometric calculations and visualisation (Daniels *et al.* 2019); see also the various contributions in Kalyan *et al.* (2019).

Considering how many of the world’s language families are known or believed to be linkages, there remains a great need for glottometric studies. In 2022, we released an online tool called the “Historical Glottometry online analyser”.<sup>11</sup> If the user uploads a table of innovations such as Table 2, the analyser returns a table showing the most significant subgroups (i.e. those whose subgroupiness  $\zeta$  exceeds a chosen threshold  $\theta$ ), along with the  $\varepsilon$  and  $k$  values of each subgroup. For every dataset, the analyser also provides a formulation of the main results in plain English. Finally, if the user uploads a set of geographic coordinates, the tool will also produce a preliminary glottometric map.

We hope this online analyser encourages linguists to adopt Historical Glottometry among their methodological approaches, as they endeavour to achieve a realistic representation of a family’s linguistic history.

## 6 CONCLUSION

Thanks to the Comparative Method, the linguist can reconstruct historical innovations in a given language family, and track their distribution among its members. The next stage is the task of *subgrouping*: that is, of grouping together the languages that have several innovations in common. The idea is that these shared innovations reflect periods of social interactions between the ancestors of modern communities, at a time when they still spoke mutually intelligible dialects in an earlier continuum.

Subgrouping can be done following either the Tree Model or the Wave Model. We compared the two approaches, and argued that the Wave Model provides a more accurate picture of the processes of language diversification. Indeed, except in scenarios of language isolation, or swift migration and dispersal, the diffusion of innovations across mutually intelligible idiolects typically yields a pattern of overlapping isoglosses. The resulting language family, a ‘linkage’, cannot be represented by a tree, but only by a diagram in which subgroups intersect.

This form of language diversification — probably the most common in the world — requires an approach ultimately inspired by Schmidt’s *Wellentheorie* and its overlapping waves. Among various such approaches that have been proposed, Historical Glottometry aims at detecting the genealogical structure of language families in a fine-grained, reliable and testable manner, by combining the strengths of the Comparative Method with a diffusionist, non-cladistic model of language diversification.



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## NOTES

- <sup>1</sup> While this chapter originated as François (2014), it has changed sufficiently to be considered an entirely new publication. We would like to thank Malcolm Ross for his feedback on an earlier version of François (2014). This work relates to the axis “Typology and dynamics of linguistic systems” within the Paris-based program *Empirical Foundations of Linguistics* (LabEx EFL, ANR).
- <sup>2</sup> We follow here the proposal by Haspelmath (2004:222) to use the term ‘genealogical’ for what have been traditionally labelled ‘genetic’ relations, to avoid confusion with biological genetic relations. For a discussion of what is meant by *genealogy* in historical linguistics, see §3.1.
- <sup>3</sup> We use the term *diffusion* here in its usual sense of propagation through a social network of individuals (as in Labov 2007). This is distinct from the process of *lexical diffusion*, which describes the way certain forms of sound change propagate across the lexicon (Labov 1994:421).
- <sup>4</sup> For empirical illustrations of this point, see for example Geraghty (1983) for Fijian communalects, Garrett (2006) for ancient Greek dialects, and François (2011:201) for northern Vanuatu.
- <sup>5</sup> A similar argument could be made in response to Jacques and List (2019), who argue that the patterns of intersecting isoglosses found in linkages can be accounted for in terms of ‘incomplete lineage sorting’ (Galtier and Daubin 2008), i.e. by positing sociolinguistic variation in the proto-language that gets ‘ironed out’ differently in each descendant language. While this provides a way of somehow salvaging the Tree Model, ultimately it just shifts the problem of conflicting isoglosses from the family to the proto-language – without providing any additional insight into the exact processes of internal diversification. In any case, the Wave Model would be needed in order to unravel the precise history of dialectal variation in that proto-language (see Kalyan and François 2019).
- <sup>6</sup> Another problem is that some of this work is not based on the Comparative Method. For example, in Dunn *et al* (2008), subgroups are identified on the basis of word order features, rather than the reconstruction of linguistic forms and the identification of shared innovations.
- <sup>7</sup> Unlike in dialectology, isoglosses in Historical Glottometry are always drawn as closed curves surrounding those communities that exhibit the innovative variant of a feature (as in Bloomfield 1933:316, following Schrader 1883:99).
- <sup>8</sup> This sort of reasoning is reminiscent of Schmidt’s (1872:18) argument that Balto-Slavic is closer to Germanic than to Indo-Iranian, on the grounds that “[t]he Balto-Slavic lexicon... contains four times as many Indo-Iranian elements [i.e. cognates] as does Germanic (61 : 15) and ten times as many Germanic elements as does Indo-Iranian (143 : 15)” (our translation).
- <sup>9</sup> This formula is an adaptation of Goebel’s (2006:412) ‘Relative Identity Value’ (RIV), and is also known as the ‘Jaccard coefficient’. It appears as ‘formula W’ in Kroeber and Chrétien (1937:99) and as the ‘coefficient of similarity’  $r_n$  in Ellegård (1959:142).
- <sup>10</sup> The motivation for this threshold is that any subgroup that is attested just once—i.e. with  $\varepsilon = 1$ —will necessarily have  $\zeta \leq 1$ , since  $0 < k \leq 1$ . Thus, any subgroup that has  $\zeta > 1$  is *necessarily* attested more than once, and is hence unlikely to be due to an error in the data.
- <sup>11</sup> The Historical Glottometry online analyser can be accessed at <https://tiny.cc/HGOA>.
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