

LANGUAGE, TIME AND HUMAN HISTORIES

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1. Evidence for human histories

Any discussion of language and time within historical linguistics must begin with a consideration of the direction of time. The most obvious direction, in the sense that most work in historical linguistics at present follows this course, is from the past towards the present: this is the study of language change, and involves tracing the developments that have transformed an earlier stage of a language into a later one. In this paper, however, I shall be concentrating on the opposite direction, and on the idea that, using certain methods, we can reverse time, and find out whether particular languages which are now separate systems, were once a single language. In other words, I shall be discussing language families. But those languages in the past, like languages today, also had speakers, so it follows that human histories, rather than simply linguistic histories, are necessarily involved.

However, it is impossible to find out about those human histories through linguistic work alone: we have to take an interdisciplinary approach. One such approach, which is certainly in the scientific news at the moment, is the 'new synthesis'. Its proponents argue that we can bring together evidence from linguistics, genetics and archaeology, assess whether meaningful correlations exist between these disciplines and then use this cumulative evidence to provide clues to earlier human histories. The idea of constructing trees for linguistic and genetic groupings and measuring the degree of similarity between them is, of course, not a new one: we might trace the start of work on mappings between linguistics and genetics to the publication of the well-known Cavalli-Sforza et al. (1988) parallel linguistic - genetic tree. As is well known, there has been a good deal of criticism of this tree, both because of lack of independence of the populations sampled (some genetic populations, like Na-Dene, are defined on the basis of the language spoken in the community, which rather begs the question), and because it includes very long range comparisons – many historical linguists would consider constructs like Amer-

ind, Nostratic and Eurasiatic essentially unfounded (McMahon & McMahon 1995). However, it would naturally be unreasonable to reject any prospect of meaningful matches because of problems in a single early application, and hopes are currently high for the ‘new synthesis’ (Sykes 1999, Cavalli-Sforza 2000).

Nonetheless, it should be noted that much recent work in this area has involved correlations between archaeology and genetics: Renfrew & Boyle (2000) coin the term ‘archaeogenetics’ for exactly this bilateral disciplinary match. There remain some doubts over the feasibility of including linguistic evidence, in large part because of the generally non-quantitative approaches favoured by historical and comparative linguists, and the consequent difficulties of establishing repeatable, demonstrably correct results, let alone parallels with other disciplines. However, after a gap following Embleton (1986), there is now something of a resurgence in interest in quantitative methods among historical linguists (Kessler 2001, Ringe, Warnow & Taylor 2002, McMahon & McMahon 2003). Most recently, Forster & Toth (2003) have applied phylogenetic methods to data from a range of Celtic languages, generating lively discussion in the scientific press. Linguists might be somewhat concerned by Forster & Toth’s use of their methods to date language splits, in view of the general discrediting of glottochronology within historical linguistics (see Renfrew, McMahon & Trask 2000); nonetheless, it would be fair to say that there is a great deal of interest in the possibilities of methods of this kind. As quantitative methods develop further, one of the main barriers to integrating linguistics into the ‘new synthesis’ seems set to disappear. It is therefore timely to consider some general issues relating to correlations specifically between linguistics and genetics, and this is the topic of the rest of this paper.

2. Correlations between linguistics and genetics

2.1 Caveats and cautions

We should begin by defining, at least in a very general way, just what we mean by correlations between genetics and linguistics. Most importantly, of course, there is no claim of determinism between genetics and linguistics (which at its most problematic and simplistic would mean that the genes an individual carries determine the language she speaks). For one thing, work on correlations is operating at the population level, with calculations based on, ideally, many individuals, so that we are taking a higher-level look at characteristics of groups, based on averages and probabilities, not absolute values for individuals. We are working, then, with population genetics, or evolution-

ary biology, rather than molecular genetics. It is worth reminding ourselves also that populations are abstractions, like speech communities, with which linguists may be more familiar. It would clearly be unrealistic to expect, in a sociolinguistic survey, that each member of a speech community will use a particular variant 33% of the time, or that all middle-class women will use that same variant in precisely 95% of their formal speech (even assuming that we are confident we can define relativistic constructs like ‘middle-class’ or ‘formal’ in such a definite and non-overlapping way). As linguists, however, we are able to interpret data of this kind in a meaningful way, as having reality for the speech community, even if not in precise terms for every individual belonging to it. Individual speakers are not robbed of their identity or their uniqueness by being grouped together, in studies of a particular kind, into broader categories; and for different purposes, we can study the individual or the group.

Exactly the same is true of genetic studies of populations. Individuals are important; but there are some studies for which we need to take a broader view, and categorise people into groups according to the average of their genetic characteristics. It may seem unlikely, looking at cosmopolitan, modern, urban European populations, for instance, that we can ever reach any meaningful conclusion on their genetic characteristics, since each individual will have his or her own highly specific history; but averaging over a sufficiently large number of individuals can indeed reveal particular frequent, key attributes for the group, alongside individual markers which signal a history outside that population as unusual and marginal. Put in linguistic terms, we might doubt, listening to several speakers from the same area, that we can subsume their distinct and individual accents under a single system; but grouping together a whole range of such speakers may well reveal shared characteristics. I have a noticeably Scots accent; closer inspection reveals that I have acquired a marginal contrast of /æ/ versus /a/ over 15 years of living in England, though typically Scots lack this distinction and have a single, undifferentiated low mid /a/ vowel as I once did. This does not remove the general impression of Scottishness when I speak; and it does not contradict the observation that most Scots lack the *Sam – psalm* opposition. Both observations are valid, and relevant for different purposes. It is also important to note that contemporary urban populations, with their history of input from widely divergent genetic (and linguistic) sources, are by no means the norm either diachronically or diatopically: smaller, closer-knit communities with greater continuity represent a more usual basis for human histories.

This has three implications for work of the sort discussed below. First, it is important that we should collect both linguistic and genetic data from ‘older’, more isolated populations before admixture levels out many of the signals in which we are interested. Second, those of us who are urban speakers and rejoice in our mixed and exotic heritage have to accept that we are relatively unusual in global terms, and therefore that our own experiences and expectations do not amount to a necessary rejection of the methods discussed below. Equally, however, we cannot simply ignore all those mixed populations that do exist, and of course admixture at some level occurs even in the smallest and most traditional of groups (see R. McMahon, forthcoming): hence, we must as a matter of urgency investigate means of recognising and, where necessary, removing admixture. This will be a recurring theme in the discussion below, and as we shall see, differences in practice here between geneticists and historical linguists represent a significant threat to progress in the ‘new synthesis.’

These preliminaries are important in breaking down possible misperceptions of the meaning of genetic / linguistic correlations. Turning to a broad definition of those correlations, we mean simply that, all else being equal, when the languages spoken by two populations are closely related, we might expect genes present in the two populations to be similar; and conversely, when the languages are only distantly related (or unrelated), the genetic profiles of the two populations should also show considerable differentiation. We can then hope to use these affinities between linguistics and genetics to help us cast light on the histories of particular populations.

2.2 Evidence for correlations

A range of recent studies in the genetics literature discuss evidence for correlations between genetics and linguistics at the population level. Looking ahead, we shall see that there are interesting parallelisms, but that correlations seem less significant in some cases than others. As I shall show, a very influential factor here, which has not so far been taken into account, is the different attitudes of linguists and geneticists to admixture between systems¹.

Considerations of space mean it is possible to discuss only one study, Rosser et al. (2000), though a series of other papers, including Gray & Jordan

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(2000), Poloni et al. (1997) and Sokal (1988) point to essentially the same conclusions. Rosser et al. studied 11 separate Y-chromosome polymorphisms on 3,616 chromosomes drawn from 47 European populations, and their main suggestion is that the primary determinant of both the linguistic and the genetic variation seems to be geography. In other words, variation in both linguistic and genetic terms relies on the degree of physical distance between populations. Where the populations compared are on different continents, so that there is considerable physical distance between them, we would expect, and indeed find, a good deal of linguistic and genetic distance too. Exceptional cases of large linguistic and genetic differences between geographically close populations are often associated with clearly identifiable local barriers, such as mountain ranges or stretches of water: for instance, as Rosser et al. (2000) note, the Georgian and Ossetic populations are geographically close, but are genetically and linguistically distinct, and separated by the Caucasus mountains.

These findings allow two alternative accounts of our linguistics – genetics correlations. If geography is the real explanatory factor, then the apparent correlation between languages and genes is revealed as secondary. On the other hand, it might be that the indubitable effect of geography is not the main, or the only factor, but is masking a true correlation between genetics and linguistics which reflects shared population history. One way to reduce the confounding effect of a third common variable is to use a statistical technique known as autocorrelation analysis to ‘remove’ the effect of the third variable. For a partial correlation of genes and language with geography held constant, this amounts to asking what the correlation for language and genes would be for all those populations with the same geographic distance from each other. This then isolates the relevant component of total variation, revealing the extent to which a knowledge of the genetic relationships between populations can be used to infer the relationship between their languages and vice versa.

Rosser et al. (2000) were extremely careful in their treatment of geography, since they considered both local barriers and distance. Their conclusion was that, within continents, geography is by far the greatest explanatory force for genetic distances, eclipsing the contribution of language as an independent barrier to gene flow. However, even in their work, significant correlations between linguistic and genetic characteristics of populations were found where samples include populations on different continents or otherwise separated by major physical barriers: although Rosser et al. included only European populations in their main analysis, they did also consider two African

populations, and here the linguistic – genetic correlations did become significant.

It is self-evident that the likelihood of contact and interbreeding is much lower for populations on different land masses or separated by a major physical boundary than for adjacent or physically close populations. Indeed, before the development of relatively recent technological innovations, simple distance even within continents would have correlated very strongly indeed with the likelihood of contact between members of different populations. Genes in populations do naturally change and diverge; but the further apart two populations are geographically, the greater the divergence is likely to be, because in geographically close populations, interbreeding and consequent admixture will cause genetic convergence, running counter to the effects of normal divergence. It follows that we should expect to find considerably less genetic distance between geographically close populations which are not separated by any significant physical barrier – and if there is anything in the claims of correlation between genetics and linguistics, we should expect that relatively small genetic distance to be paralleled by less linguistic distance. Of course, these distinctions are all more difficult to observe in studies sampling only modern, mobile groups, since technological innovation has led to a greater likelihood of interbreeding between even the most distant populations.

These expectations are supported by our knowledge that contact between two populations does not only have the genetic effect caused by interbreeding. Contact is also possible at a linguistic level, and has its own consequences there (Thomason 2001). Depending on the intensity of contact, and on other imponderables like language attitudes, prestige, and so on, these effects may range from the occasional, nativised lexical item, to wholesale structural borrowing, convergence, pidginisation and creolisation, language mixing, and the like. And just as interbreeding was less likely, at least until relatively recently, for geographically distant populations, so language contact might be expected to be less intense, the further apart two speech communities are.

If neither genetic nor linguistic mixing takes place to any great extent between populations on different continents, or with a major physical boundary separating them, then one can well understand why the correlation between the two types of evidence seems relatively strong for populations under these circumstances. However, where populations are geographically close, with no intervening physical barrier, one would equally expect increased similarity at the genetic level to be mirrored in increased linguistic similarity; and here we have a paradox, because within a continental mass, the correla-

tions are less significant. In other words, where populations are geographically adjacent, one would expect recent history, and its consequences in terms of admixture, to blur to an equivalent degree any more distant historical relationships in both genetics and linguistics. What seems to happen, however, is that some of these geographically close populations remain more distant linguistically than would be anticipated given the probability of recent contact: here, the expected correlation with genetics is disturbed.

There are two approaches to interpreting this apparent paradox. Either contact between populations does not have any linguistic consequences, or only very minor ones. Or, contact-induced change is going on all right in both linguistics and genetics, but linguists and geneticists handle admixture in very different ways. It does not even seem worth testing the hypothesis that language contact does not happen – putting it at its most cartoonishly simple, there are simply many more opportunities for conversation than for interbreeding, especially where the latter must end up in the production of viable offspring if the genetic profile of a population is to be affected by admixture. As for the second hypothesis, there has certainly been a long-standing tendency in comparative linguistics to marginalize or exclude contact-induced changes, either by saying its effects are insignificant, or by removing loans from the data.

However, both these strategies are problematic. So many cases of far-reaching contact-induced changes have now been reported that it is no longer tenable to claim that we are dealing with only minor effects (Thomason 2001, Bakker 1997, 2000, Bakker & Mous 1994, Matras 2000). On the other hand, removing borrowings from the data, even with data we know and understand very well, is not always a successful strategy: in a conventional 200-word Swadesh-type basic vocabulary list for Indo-European, Embleton (1986) found 12 borrowings from French into English (including *river*, *flower*); 16 from North Germanic into English (including *die*, *skin* and *wing*); and 15 from Dutch into Frisian.

These observations lead us to two conclusions. First, it has certainly been true in the past that if historical linguists can exclude borrowings, they will – and they will certainly prioritise data which seem less amenable to external influence; hence the construction of basic vocabulary lists. The important point is that this is exactly what geneticists do not do. The tendency in population genetics has been to recognise and accept migration, and its genetic consequences, and there is a significant history of attempts to provide measures of interpopulation exchange, and indeed models of how this might happen, and the extent of its effects, under particular circumstances.

Given this discrepancy in practice between linguistics and genetics, it seems worth investigating the possibility that the actions of linguists in denying, downplaying or attempting to screen out the effects of borrowing may make the correlation between linguistic and genetic variation for geographically close populations seem nonsignificant. The exclusion of borrowings will automatically prioritise data indicating common ancestry for the linguistic systems concerned, while the genetic systems for the same populations will also include more recent innovations due to contact and admixture. This would create an obvious mismatch between those systems, which would then appear less comparable in geographically adjacent populations, disrupting the overall correlation between linguistics and genetics. In other words, the discrepancy does not indicate that the linguistic and genetic histories are different: it arises because half the linguistic history is being analysed out. That is, our linguistic methodologies attempt to exclude contact-induced changes, and this conspires against the recognition of parallels between linguistics and genetics.

However, there is a further linguistic question here. If historical linguists have sought to exclude loans from their data, and if they have succeeded in doing so, then there should be no discrepancy between their practice and that of geneticists, who also factor out and measure the contribution of admixture. If borrowings are creating these apparent mismatches between linguistics and genetics, the only possible interpretation is that these are borrowings which historical linguists have missed. The only way of demonstrating this is to develop other methods of finding those loans. In what follows, I shall discuss the development of quantitative methods to track down undiagnosed loans in comparative linguistic data.

3. *Finding borrowings*

In our project we start from the assumption that borrowings are not always easy to find, and that some are likely to slip through the net of even the most careful comparative work. As Embleton's (1986) figures above indicate, simply working with basic vocabulary does not automatically safeguard against loans, because even basic vocabulary can be borrowed. We also use techniques already established in biology, because often biologists have already confronted, if not entirely solved, the problems we find in historical linguistics. Although we are also developing alternative methods for language comparison, for instance using phonetics (Heggarty 2000), we have also considered conventional meaning lists to assess whether computational approaches can help us get more out of traditional data.

We follow Embleton (1986) in using lists with 200 items, and are working with a substantial database, Dyen, Kruskal & Black (1992), with lists and cognacy judgements for 95 Indo-European languages and dialects. We used their distance matrices to draw family trees, but with resources from biology, where computer programs typically find the best, or most parsimonious tree from the whole range of possible trees, providing an accepted means of testing which tree is the best, and of evaluating what that means. We used Felsenstein's (2001) PHYLIP package, a suite of programs developed to draw and select biological trees². The method and results are discussed in greater detail in McMahon and McMahon (2003), where examples are provided, showing that the conventional subfamilies within Indo-European are routinely found by these methods.

However, the important results for present purposes relate to the assumption that meaning lists, being based on basic vocabulary, should have had all the borrowings filtered out. We tested this using Lohr's (1999) measures of the relative reconstructability and retentiveness of meanings. Lohr reached her conclusions by considering reconstructions of four protolanguages - Proto-Indo-European, Proto-Afroasiatic, Proto-Austronesian and Proto-Sino-Tibetan, to see which meanings could be reconstructed for all these protolanguages, and were therefore less likely to be culture-specific: this measure informed Lohr's measure of reconstructability. Lohr also calculated how often a different form is documented with that same meaning, or the number of replacements for that meaning, in a range of periods and languages within Indo-European, thus developing a measure of retentiveness.

Lohr's intention in providing these measures was to refine conventional basic vocabulary lists as far as possible, focusing only on the most highly reconstructable and highly retentive meanings. Our procedure was rather different, since we chose to work with two opposing sublists. We tested two extreme samples from the Dyen, Kruskal & Black (1992) database – a class of highly conservative meanings, listed in (1), and a class of much more changeable ones, listed in (2).

(1) Highly reconstructable, highly retentive sublist

four, name, three, two, foot, give, long, salt, sun, other, sleep, to come, day, to eat, not, thin, five, mother, ear, I, new, night, one, to spit, star, to stand, thou, tongue, tooth, wind

² For reasons of space no trees are included here.

(2) Low reconstructability, low retentiveness sublist

grass, mouth, stone, heavy, year, bird, near, smooth, wing, man, neck, tail, to walk, back, to flow, left (hand), to pull, to push, river, rope, straight, to think, to throw

If all these meanings were contributing equally to the analysis, we should find that trees generated from the highly conservative sublist in (1) should match those produced from the much less conservative sublist in (2), but this is not the case, as we showed in McMahon & McMahon (2003). For example, when only the low reconstructability : low retentiveness meanings are used, Frisian appears as a sister of a group containing Afrikaans, Flemish and Dutch; and English appears (along with an English-based creole) as a relatively distant sister of the whole Germanic group (as is also the case for the full 200-meaning list). However, when the high reconstructability : high retentiveness sublist is used, Frisian is related to West Germanic only at a deeper level; whereas English migrates into West Germanic, with close affinities to both German, and the Flemish – Afrikaans – Dutch cluster. Our interpretation of these different trees is that they indicate a ‘signature’ of borrowing, and this seems to be backed up by the direction in which the borrowing languages move. Frisian has borrowed heavily from Dutch, which it gravitates towards when we look at the less stable meanings; and for English, although the trees themselves are less informative, we know that there is considerable early borrowing from Norse. English does not move into the North Germanic group altogether; but this is quite possibly because of the additional, extensive borrowing from Romance, which is effectively pulling English towards the margins of Germanic altogether.

Crucially, however, if these shifts and differing trees are the result of loans in one subset of data but not the other, that must mean undiagnosed loans, since we know that normal practice among comparative linguists is to exclude known borrowings from meaning lists. How, then, can we confirm the existence of undiagnosed loans? We have gone back to the Dyen, Kruskal & Black (1992) data and checked their coding for the forms that Embleton (1986) lists as loans in her Germanic data. First, of the meanings which Embleton lists as involving borrowing within Germanic, at least 6 (‘wing’, ‘left (hand)’, ‘to pull’, ‘to push’, ‘river’ and ‘to throw’) occur in our set of 23 least conservative meanings, and none at all in the 30 highly retentive, highly reconstructible list. Secondly, and potentially much more importantly, Dyen, Kruskal & Black have wrongly coded a small number of loans as actually

being cognates. Their normal practice is to assign unique states to loans, indicating some development beyond the normal processes of descent and change; but in these few cases they have failed to provide this special marker, hence treating these meanings as cases of common inheritance. For example, they have coded ‘left (hand)’ as cognate for Frisian and Dutch, though it is in fact a borrowing from the latter into the former; and likewise, ‘wing’ is not recognised as a loan from Danish into English – and both these meanings are in the less conservative sublist in (2) above. It would appear, then, that these rather small numbers, in the list of least conservative meanings, cause the shifts we have observed between trees calculated on those meanings, and on the alternative, much more conservative sublist.

Of course, if this is the case within Germanic, which is a well understood group within a very well characterised family, it follows that we can scarcely be confident that we have excluded loans in other cases where the data are less well known. The method I am promoting here seems to offer the possibility of using different sublists to identify cases of borrowing. We may in future be able to show exactly which meanings are being affected, by removing individual meanings to check the effect on the relative position of the languages in question. We might not even be tied to Swadesh-type basic vocabulary any more, if we can divide any list into sublists with different degrees of retentiveness. This is an interesting prospect, but it does raise another, final concern. The problem here is that the usual method of displaying linguistic relatedness involves family tree diagrams, and these are not compatible with contact-induced development. This might not be seen as problematic if we are confident that we can remove all evidence of borrowing from the data: but if, as I am advocating here, we are interested in contact and see it as contributing to linguistic history, albeit not in the sense of common ancestry and divergent development, how do we then display our results?

In our project, we are currently exploring another biological program, this time Network (Bandelt et al. 1995): again, biology and linguistics share a problem here, in that there can be considerable genetic flow into a population from other populations. This network model produces a multi-dimensional matrix to show complex relationships within a population – but perhaps the most interesting aspect of network analysis is that, although the program is designed to draw networks, cases where there has been no borrowing will automatically be represented by the most likely tree. So the program involved draws a tree when the relationships are clear and tree-like, and a more complex network when the connections are more complex and show more interaction.

There is space here only to provide two preliminary examples. Figure 1 shows the output of Network for Romance and Germanic, for the most conservative sublist in (1) above; Figure 2 involves the same languages, but the least conservative sublist in (2).

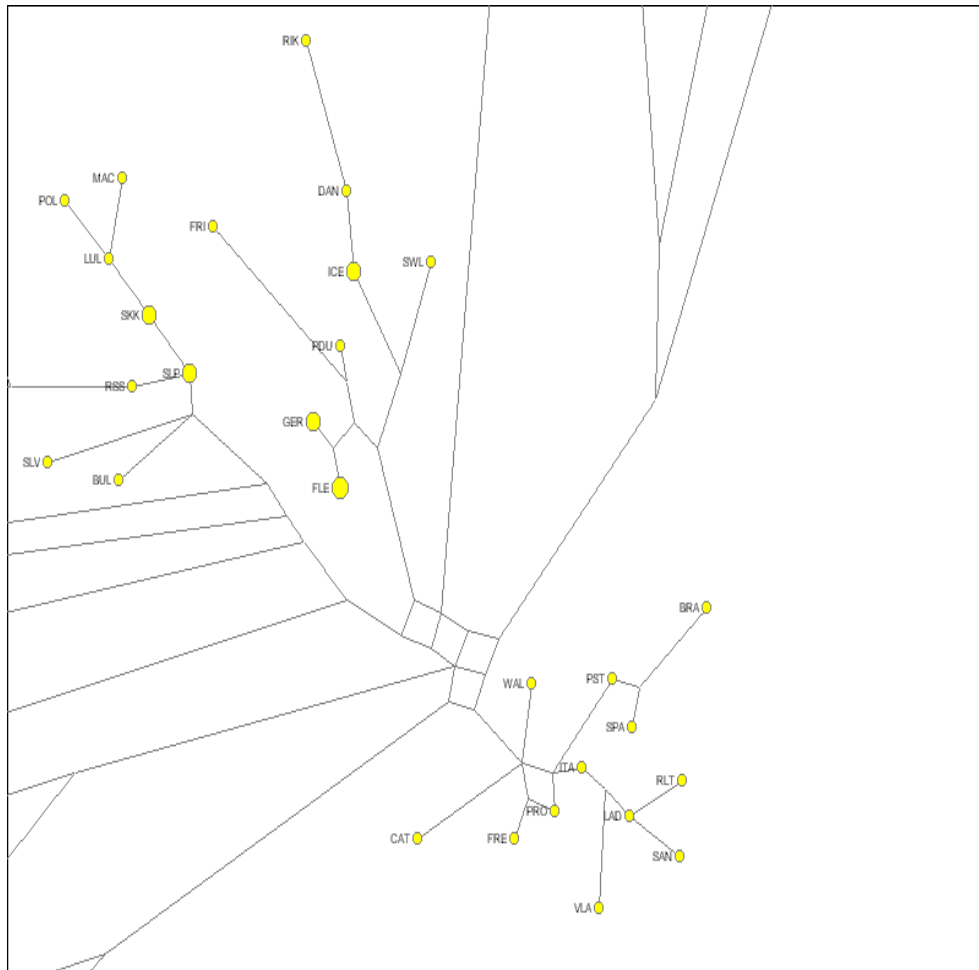


Figure 1. Network for Romance and Germanic, most conservative sublist

LANGUAGE, TIME, AND HUMAN HISTORIES

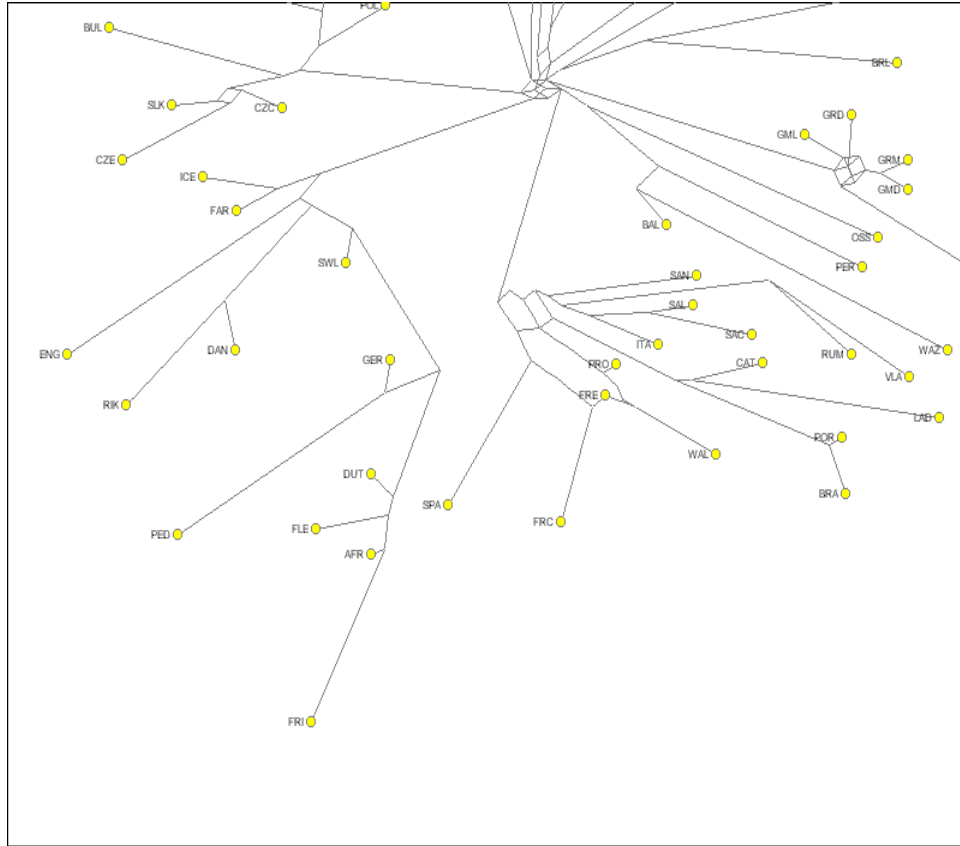


Figure 2. Network for Romance and Germanic, least conservative sublist

It is clear that the program is essentially drawing trees for both the sets of data shown in Figures 1 and 2. However, whereas the highly conservative list produces a very tree-like result for Romance in Figure 1, there are many more reticulations in the least conservative sublist in Figure 2 – a reticulation being simply a case where the program draws a box rather than a line, because it cannot work out the order of events unambiguously. Reasonable linguistic interpretations of that lack of clarity might be borrowing or a dialect continuum relationship.

Turning to Germanic, initially the two different diagrams do not appear to reflect the interborrowings we tracked down in the least conservative sublist. There are no reticulations in either Figure 1 or Figure 2 for Germanic. On the other hand, Network shows a particularly clear and sensitive reaction to the undiagnosed loans identified earlier. Specifically, in the most conservative

tree in Figure 1, English is contained in a cluster with German, and is squarely within West Germanic, while in the least conservative tree in Figure 2, English has shifted altogether into North Germanic (and it is also worth noting that Frisian, in the same least conservative tree, is clustered with Dutch / Flemish / Afrikaans). Although we are seeing trees rather than networks in these cases, then, they are trees with shifting subgroups depending on the presence of loans in the data. The next step is to optimise the settings for Network so that the program experiences greater difficulty in drawing trees where borrowings are present, forcing reticulations in these cases. Already, however, the program notes several difficulties it has experienced in reducing the multidimensional network from the least conservative list into a tree at all, and these problem points include all our cases of loans within Germanic.

In this brief paper, I have only been able to indicate the current outline of our research, and provide some pointers to ongoing work. One advantage of this research so far is the demonstration that there is potential even in very simple and unsophisticated data like word-lists, which can be divided into more and less conservative sublists and combined with computational techniques to provide information on both family relationships and contact. Both common ancestry and borrowing are important to our full understanding of the histories of languages, and new, quantitative methods offer the possibility of analysing both these different contributions, and crucially, of distinguishing them. This allows a clearer and more meaningful comparison to be made between linguistics and genetics, provided that we ensure all the linguistic and genetic data are considered, rather than making methodological decisions (like excluding loans) in one discipline which might jeopardise interdisciplinary comparisons. We may then approach with optimism the prospect of using a synthesis of evidence types to cast some light on human histories – that is, histories of languages, and of their speakers.

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LANGUAGE, TIME, AND HUMAN HISTORIES

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APRIL MCMAHON

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