Automated languages phylogeny from Levenshtein distance

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Abstract.
Languages evolve in time according to a process in which reproduction, mutation and extinction are all possible. This is very similar to haploid evolution for asexual organisms or for mtDNA of complex ones. Exploiting this similarity it is possible, in principle, to verify hypotheses concerning their relationship. The key point is the definition of the distance among pairs of languages in analogy with the genetic distance among pairs of organisms. Assuming that vocabulary is the analogue of DNA, distances can be evaluated from lexical differences.

This concept seems to have its roots in the work of the French explorer Dumont D’Urville. He collected comparative words lists of various languages during his voyages aboard the Astrolabe from 1826 to 1829 and, in his work about the geographical division of the Pacific, he proposed a method to measure the degree of relation among languages. The method used by modern glottochronology, developed by Morris Swadesh in the 1950s [20], measures distances from the percentage of shared cognates, which are words with a common historical origin. The weak point of this method is that subjective judgment plays a relevant role. In fact, even if cognacy decisions are made by trained and experienced linguists, the task of counting the number of cognate words in a list is far from being trivial and results may vary for different studies. Furthermore, these decisions may imply an enormous working time.

Recently, we proposed a new automated method which has some advantages: the first is that it avoids subjectivity, the second is that results can be replicated by other scholars assuming that the database is the same, the third is that no specific linguistic knowledge is requested, and the last, but surely not the least, is that it allows for rapid comparison of a very large number of languages. The distance between two languages is defined by considering a renormalized Levenshtein (or edit) distance among words with the same meaning and averaging on the words contained in a list of 200 features. The renormalization, which takes into account the words length, plays a crucial role, and no sensible results can be found without it. Assuming a constant rate of mutation, these lexical distances are logarithmically proportional, in average, to the genealogical ones. Then, phylogenetic trees can be reconstructed from the matrix which contains the genealogical distances between all pairs of languages in a family. We applied our method to the Indo-European and to the Austronesian groups considering, in both cases, fifty different languages. From the two matrices, we obtained two genealogical trees using the Unweighted Pair Group Method Average (UPGMA) [19]. The trees are similar to those found by previous research [6, 7] with some important differences concerning the position of few languages and subgroups. Indeed, we think that these differences carry some fresh information about the structure of the tree and about the phylogenetic relations inside the families.
1. Introduction

Glottochronology tries to estimate the time at which languages diverged with the implicit assumption that vocabularies change at a constant average rate. The idea is to count the number of words that have been replaced in a language considering a list, initially proposed by M. Swadesh [20], which contains terms which are common to all culture and which concern the basic activities of humans. The choice is motivated by the fact that the vocabulary learned during childhood changes very slowly over time.

The use of Swadesh lists in glottochronology is popular since half a century. Glottochronologists use the percentage of shared cognates in order to compute the distance between pairs of languages. These lexical distances are assumed to be, on average, logarithmically proportional to divergence time. In fact, changes in vocabulary accumulate year after year and two languages initially similar become more and more different. A recent example of the use of Swadesh lists and cognates to construct language trees are the studies of Gray and Atkinson [6] and Gray and Jordan [7].

Cognates are words inferred to have a common historical origin, their identification is often a matter of sensibility and personal knowledge. In fact, the task of counting the number of cognate words in the list is far from trivial because cognates do not necessarily look similar. Therefore, subjectivity plays a relevant role. Furthermore, results are often biased since it is easier for European or American scholars to find out those cognates belonging to western languages. For instance, the Spanish word leche and the Greek word gala are cognates. In fact, leche comes from the Latin lac with genitive form lactis, while the genitive form of gala is galactos. Also the English wheel and Hindi cakra are cognates. These two identifications are possible because of our historical records, hardly they would have been possible for languages, let’s say, of Central Africa or Australia.

The idea of measuring relationships among languages using vocabulary, seems to have its roots in the work of the French explorer Dumont D’Urville. He collected comparative words lists of various languages during his voyages aboard the Astrolabe from 1826 to 1829 and, in his work about the geographical division of the Pacific [4], he introduced the concept of lexical cognates and proposed a method to measure the degree of relation among languages. He used a core vocabulary of 115 base terms which, impressively, contains all but three of the terms in Swadesh’s 100-item list. Then, he assigned a distance from 0 to 1 to any pair of words with the same meaning and finally he was able to resolve the relationship for any pair of languages. His conclusion is famous: La langue est partout la même.

In our work we used an automated method which avoids any subjectivity so that our results can be replicated by other scholars assumed that the database used is the same. For any language we wrote down a list of the same 200 words according to the original choice of Swadesh [20], then we compared words with same meaning belonging to different languages only considering orthographical differences. This may appear reductive since words may look similar by chance, while cognate words may have a completely different orthography, but we will try to convince the reader that indeed this
is a simpler, more objective and more efficient choice with respect to the traditional glottochronological approach.

To be precise, we defined the distance of two languages (section two) by considering a renormalized edit distance among words with the same meaning and we averaged on the two hundred words contained in the lists. [21]. The renormalization, which takes into account the word’s length, plays a crucial role, and no sensible results would have been found without it. Then, we transformed these distances, by a simple rule, in separation times (section three) and we applied this to the Indo-European and the Austronesian groups considering, in both cases, fifty different languages. From the two matrices, we obtained (section four) two genealogical trees using the Unweighted Pair Group Method Average (UPGMA) [19]. The trees are similar to those found by [6] and [7] with some important differences concerning the position of few languages and subgroups. Indeed we think that these differences carry some new information about the structure of the tree and about the position of some languages for which we separately analyzed the structure of distances with respect to all the others (section five).

2. Definition of lexical distance

We start by our definition of lexical distance between two words, which is a variant of the Levenshtein (or edit) distance. The Levenshtein distance is simply the minimum number of insertions, deletions, or substitutions of a single character needed to transform one word into the other. Our definition is taken as the edit distance divided by the number of characters of the longer of the two compared words.

More precisely, given two words \( \alpha_i \) and \( \beta_j \) their distance \( D(\alpha_i, \beta_j) \) is given by

\[
D(\alpha_i, \beta_j) = \frac{D_l(\alpha_i, \beta_j)}{L(\alpha_i, \beta_j)}
\]

where \( D_l(\alpha_i, \beta_j) \) is the Levenshtein distance between the two words and \( L(\alpha_i, \beta_j) \) is the number of characters of the longer of the two words \( \alpha_i \) and \( \beta_j \). Therefore, the distance can take any value between 0 and 1. Obviously \( D(\alpha_i, \alpha_i) = 0 \).

The reason why we renormalize can be understood from the following example. Consider the case in which a single substitution transforms one word into the other with the same length. If they are short, let’s say 2 characters, they are very different. On the contrary, if they are long, let’s say 8 characters, it is reasonable to say they are very similar. Without renormalization, their distance would be the same and equal 1, regardless of their length. Instead, introducing the normalization factor, in the first case the distance is \( \frac{1}{2} \), whereas in the second, it is much smaller and equal to \( \frac{1}{8} \).

We use distance between pairs of words, as defined above, to construct the lexical distances of languages. For any pair of languages, the first step is to compute the distance between words corresponding to the same feature in the Swadesh list. The lexical distance between each pair of languages is defined as the average of the distance between all words. As a result we have a number between 0 and 1 which we claim to be the lexical distance between two languages.
Assume that the number of languages is \( N \) and the list of words for any language contains \( M = 200 \) items. Any language in the group is labeled a Greek letter (say \( \alpha \)) and any word of that language by \( \alpha_i \) with \( 1 \leq i \leq M \). Then, two words \( \alpha_i \) and \( \beta_j \) in the languages \( \alpha \) and \( \beta \) have the same meaning (they correspond to the same feature) if \( i = j \).

The above defined distance between two languages is written symbolically as

\[
D(\alpha, \beta) = \frac{1}{M} \sum_i D(\alpha_i, \beta_i)
\]

where the sum goes from 1 to \( M \). Notice that only pairs of words with the same meaning are used in this definition. It can be seen that \( D(\alpha, \beta) \) is always in the interval \([0,1]\) and obviously \( D(\alpha, \alpha) = 0 \).

The database used here \([21]\) to construct the phylogenetic tree is composed by \( N = 50 \) languages of the Indo-European group and \( N = 50 \) languages of the Austronesian group. The main source for the database for the Indo-European group is the file prepared by Dyen et al. in \([5]\) which contains the Swadesh list of 200 words for 96 languages. Many words are missing in \([5]\) but for our choice of 50 languages we have filled most of the gaps and corrected some errors by finding the words on Swadesh lists and on dictionaries freely available on the web. For the Austronesian group we used as the main source the lists contained in the huge database in \([8]\). The lists in \([8]\) contain more than 200 words which do not coincide completely with the words in the original Swadesh list \([20]\). For our choice of 50 Austronesian languages we have retained only the words which are in \([5]\) and are also in the original Swadesh list. The resulting list has many gaps due to missing words in \([8]\) and because of the incomplete overlap of \([8]\) with the original Swadesh list. Also in this case we have filled some of the gaps by finding the words on Swadesh lists available on the web and, in one case (Malagasy), by direct knowledge of the language.

For some of the languages in our lists \([21]\) there are still few missing words. When a language has one or more missing words, these are simply not considered in the average that gives the lexical distance between two languages. This implies that for some pairs of languages, the number of compared words is not 200, but smaller. There is no bias in this procedure, the only effect is that the statistic is slightly reduced. Indeed, the definition \([2]\) is modified, by replacing \( M = 200 \) with the number of word pairs with same meaning existing in both lists and the sum goes over all these pairs.

In the database only the English alphabet is used (26 characters plus space); those languages written in a different alphabet (i.e. Greek etc.) were already transliterated into the English one in \([5]\). Furthermore, in \([8]\) many additional characters are used which we have eliminated so that also in this case we reduce to the English alphabet plus space. Our database is available at \([21]\).

The result of the analysis described above are two \( 50 \times 50 \) upper triangular matrices whose entries are the 1225 non-trivial lexical distances \( D(\alpha, \beta) \) between all pairs in a group. Indeed, our method for computing distances is a very simple operation, that
Automated languages phylogeny from Levenshtein distance

does not need any specific linguistic knowledge and requires a minimum of computing time.

3. Time distance between languages

A phylogenetic tree can already be built from one of these matrices, but this would only give the topology of the tree, whereas the absolute time scale would be missing. In order to have this quantitative information, some hypotheses on the time evolution of lexical distances are necessary. We assume that the lexical distance among words, on one side tends to grow due to random mutations and on the other side may decrease since different words may become more similar by accident or, more likely, by language borrowings.

Therefore, the distance $D$ between two given languages can be thought to evolve according to the simple differential equation

$$
\dot{D} = a (1 - D) - bD
$$

where $\dot{D}$ is the time derivative of $D$. The positive parameter $a$ is related to the increasing of $D$ due to random permutations, deletions or substitutions of characters (random mutations) while the positive parameter $b$ considers the possibility that two words become more similar by a “lucky” random mutation or by words borrowing from one language to the other or both from a third one. Since $a$ and $b$ are constant, it is implicitly assumed that mutations and borrowings occur at a constant rate.

Note that with this choice, word substitution is statistically equivalent to the substitution of all characters in the word itself. The first reason for this approximation is reducing the number of parameters to be used in the model. The second, and more important, is that it is very hard to establish if a word has changed because many characters have been replaced or if the whole word has been replaced. This would be possible only by historical knowledge of the languages and it would imply again the use of cognates and a subjective analysis of the problem, something that we want to avoid with our model. In fact, the main point for the model is to use the fastest and simplest algorithm to compare languages. More complicated models could be introduced with more parameters and even with time-dependent parameters. But at the present stage we prefer to keep the model as simple as possible.

At time $T = 0$ two languages begin to separate and the lexical distance $D$ is zero. With this initial condition the above equation can be solved and the solution can be inverted. The result is a relation which gives the separation time $T$ (time distance) between two languages in terms of their lexical distance $D$

$$
T = -\epsilon \ln(1 - \gamma D)
$$

The values for the parameters $\epsilon = 1/(a+b)$ and $\gamma = (a+b)/a$ can be fixed experimentally by considering two pairs of languages whose separation time (time distance) is known. We have chosen a distance of 1600 years between Italian and French and a distance of 1100 years between Icelandic and Norwegian. The resulting values of the parameters
are $\epsilon = 1750$ and $\gamma = 1.09$, which correspond to the values $a \approx 5 \times 10^{-4}$ and $b \approx 6 \times 10^{-5}$. This means that similar words may become more different at a rate that is about ten times the rate at which different words may become more similar. It should be noticed that (4) closely resembles the fundamental formula of glottochronology. We use this choice of the parameters both for the Indo-European and Austronesian groups.

A time distance $T$ is then computed for all pairs of languages in the database, obtaining two $50 \times 50$ upper triangular matrices with 1225 non-trivial entries. These matrices preserve the topology of the lexical distance matrices but they contain all the information concerning absolute time scales.

In order to check the validity of the parameters used in the model we verified that the time distances between other pairs of languages estimated from the model were in the range of the time distance known from historical studies. In particular, we obtained from the model a time distance of about 2000 years for Italian and Romanian.

4. Trees

Phylogenetic trees in Fig. 1 and in Fig. 2 are constructed from the matrix using the Unweighted Pair Group Method Average (UPGMA) [19]. This algorithm works as follows. It first identifies the two languages with shortest time distance and then it treats this pair as a new single object whose distance from the other languages is the average of the distance of its two components. Subsequently, among the new group of objects it identifies the pair with the shortest distance, and so on. At the end, one is left with only two objects (languages clusters) which represent the two main branches at the root of the tree.

To check the stability of the main results (separation in subgroups) obtained from the phylogenetic trees constructed using the UPGMA algorithm, we computed many trees in which given numbers of languages were removed randomly. The computation of these trees shows a certain stability in the main features of the trees, namely all the distances between subgroups are stable if few languages of each subgroup are removed.

We use UPGMA for its coherence with the trees associated with the coalescence process of Kingman type [10]. In fact, the process of languages separation and extinction closely resembles the population dynamics associated with haploid reproduction which holds for simple organisms or for the mitochondrial DNA of complex ones, as humans. This dynamics, introduced by Kingman, has been extensively studied and described, see for example [16, 18]. It should be considered that in the model of Kingman, time distances have the objective meaning of measuring time from separation while in our realistic case time distances are reconstructed from lexical distances. In this reconstruction we assume that lexical mutations and borrowings happen at a constant rate. This is true only on average, since there is an inherent randomness in this process [14] which is not taken into account by the deterministic differential equation (3). Furthermore, parameters $a$ and $b$ may vary from a pair of languages to another and also they may vary in time according to historical conditions.
We would like to compare now our results with those published in [6] and in [7].

The tree in Fig. 1 is similar to the one in [6] but there are some important differences. First of all, the first separation concerns Armenian, which is an isolated branch close to the root, while the other branch contains all the remaining Indo-European languages. Then, the second separation is that of Greek, and only after there is a separation between the European branch and the Indoiranian one. This is the main difference with the tree in [6], since therein the separation at the root gives origin to two branches, one with Indoiranian languages plus Armenian and Greek, the other with European languages. The position of Albanian is also different: in our case it is linked to European languages while in [6] it goes with Indoiranian ones. Finally, the Romani language is correctly located together with Indian languages but it is not as close to Singhalese as reported in [6]. We will come back to this last point in the next section.

In spite of these differences, our tree seems to confirm the same conclusions reported in [6] about the Anatolian origin of the Indo-European languages. In fact, in our research, the first separation concerns the languages geographically closer to Anatolia, that is to say Armenian and Greek.

Also the tree in Fig. 2 is similar to the one in [7] but differences here are more important. The first separation concerns Formosan (Atayal group) languages which are in the first main branch, while all the other Formosan languages (Paiwan group) are in the second main branch together with all other languages of the group. In this second main branch the first separation concerns the Oceanian languages, the second separation the Malagasy, the third all the remaining Formosan languages (Paiwan), the fourth the Philippino languages, and, finally, the fifth, the Indonesian/Sulawesi languages with two subgroups: Sulawesi and Indonesian.

The fact that the first separation concerns Formosan languages of the Atayal group could be coherent with the idea that the Austronesian group originated in Formosa. Nevertheless, the second group of Formosan languages (Paiwan) is clustered differently and closer to the Philippino and Indonesian languages. This result, if confirmed, would suggest two different waves of migration from Formosa. An alternative, and more likely, explanation could be an Austronesian homeland outside Taiwan [2].

Finally, the Malagasy language is not grouped as close to Kalimantan languages as often claimed in the literature. Even the language closest to it, Maanyan, is in that group. This fact suggests a multiple origin which we will further investigate in the next section.

5. Malagasy and Romani

In this section we discuss the position of Malagasy and Romani with respect to the other branches of their group and with respect to their closest languages. Then, we compare our results and conclusions with previous ones in the two papers [6], [7].

In our tree in Fig. 2 the Malagasy language is not in a cluster together with
Kalimantan languages but it forms an early branch by itself. Indeed, it seems from Fig. 2 that separation of Malagasy from Indonesian, Sulawesi, Formosan (Paiwan) and Philippino branches occurred earlier. In order to investigate further this result, we plotted, in Fig. 3 the average distance of Malagasy with respect to languages of various groups. It turns out that the time separation of Malagasy from Indonesian, Sulawesi, Formosan (Paiwan) and Philippino groups is almost the same and it is of about 3500 years, on the contrary, the separation from Oceanic and Formosan (Atayal) groups is more ancient. This plot confirms the picture of the tree in Fig. 2.

Nevertheless, it turns out that the language closest to Malagasy is Maanyan, which is spoken in Kalimantan. The fact that Malagasy is related to the Indonesian and Philippines languages, and more closely with the Southeast Barito group of languages spoken in Kalimantan is well known.

The time separation of Malagasy from Maanyan is of only 2650 years, much more recent than the 3500 years of average separation from the other languages of the four closest groups. Even more surprising, the second closest language is Maranao which is spoken in Philippines with a separation of 3000 years while the third closest is Buginese spoken in south Sulawesi with a separation of 3100 years. The fact that Malagasy, as expected, is very close to Maanyan, but the next closest languages are not in Kalimantan could suggest a multiple origin of the language. In fact, there are many similar loanwords in Malagasy and Malay, and there are also a number of similar loanwords in Malagasy and Javanese. The Malay and Javanese loanwords belong to all sorts of semantic domains but Malay loanwords are particularly well represented in the domain of maritime life and navigation.

Archaeologists place the arrival of Austronesian settlers in Madagascar with their outrigger canoes in the centuries between 200 and 500 A.D.. Nevertheless, Malagasy mythology portrays a people, called the Vazimba, as the original inhabitants and indeed, there are some indications, that these first colonizers were part of a previous Austronesian expansion. There are also indication of successive arrivals of Austronesian immigrants during the following centuries. This may explain why many manifestations of Malagasy culture cannot be linked up with the culture of the Dayaks of the Southeast Barito area. For example, Malagasy use outrigger canoes, whereas Southeast Barito Dayaks never do. The Malagasy migration to East Africa presupposes navigational capacities typical of many Indonesian peoples which Dayaks do not have. Some of the Malagasy musical instruments are very similar to musical instruments in Sulawesi, and some of the Malagasy cultivations (wet rice) cannot be found among Barito river inhabitants. On the contrary, some funeral rites as the famadihana (second burial) are similar to those of Dayaks.

But the main problem is that it is unlikely that Maanyan speaker Dayaks fulfilled the spectacular migrations from Kalimantan to Madagascar, since they are forest dwellers with river navigation skills only. A possible explanation is that they were brought there as slaves by Malay seafarers, which also took slaves from other parts of Southeast Asia. If the Southeast Barito speakers formed the majority in the initial
group, their language could have constituted the core element of what later became Malagasy. In this way Malagasy absorbed words of the Austronesian languages of the other slaves and of the Malay seafarers. In this scenario, Malay and Javanese were spoken by the dominant class (Merina society is up to now divided in three classes whose individuals appear different in aspect). Later the language of dominators was superseded but it left an important contribution to the Malagasy lexicon. This multiple origin could explain why Malagasy, which is so similar to Maanyan, is scattered in an isolated position in Fig. 2.

Let us discuss the case of Romani, the language of Roma and Sinti, which is less controversial. In our tree in Fig. 1 it is correctly located together with Indian languages but it is not as close to Singhalese as reported in [6]. Also in this case we plotted, in Fig. 4, the average distance of Romani with respect to languages of various groups. It turns out that the closest group, as expected, is the Indian one, with a time separation of about 3300 years. But if we consider the closest three languages we find Nepali (2000 years), Bengali (2000 years) and Khaskura (2950 years). Nepali and Kaskura are similar and they are spoken in Nepal and northern India (the second is the language of Gurkhas), while Bengali is spoken in Northeast India and Bangladesh. We remark that these distances are not significantly different from average distance of 3300 years to the whole Indian group and almost identical to distances of other languages spoken in Northern India. This implies a geographical origin in Northern India for Roma’s and Sinti’s, according to the beliefs of the majority of researchers. On the contrary, we find Romani quite far from Singhalese which in Fig. 1 separated 3950 years ago, a time distance which is comparable to the distance Romani/Italian (4150 years). Our results are different from those found in [6] where a close relationship Romani/Singhalese is detected.

Finally, many scholars have pointed out some similarities with Greek (and to a less extent with Iranian languages and Armenian) which is usually explained by a prolonged stay in Anatolia after the departure from Northern India. Indeed, in Fig. 4 one may appreciate that, beside the Indian group, the closest language is Greek followed by the Iranian group.

6. Discussion and conclusions

Automated language classification is very important for the understanding of language phylogeny. In particular, it is very useful for those languages for which finding cognacy relations is a difficult task. It also permits to classify a huge number of languages in a very short time by using computer programs.

The automated method described here was later used and developed by another large group of scholars [1, 9]. They placed the method at the core of an ambitious project, the ASJP (The Automated Similarity Judgment Program) whose aim, in the words of its proponents, is The ASJP project aims at achieving a computerized lexicostatistical analysis of ideally all the world’s languages. The two main purposes
are to provide a classification of all languages by a single, consistent and objective (if perhaps not ideal) method and to perform various statistical analyses regarding the historical and areal behavior of lexical items. In their work, they used a refinement of our definition of distance, which implies a second renormalization which eventually accounts for accidental similarities in vocabularies.

Recently [13], we have completed our research by a careful study of the words stability problem. This study allows us to find the optimal length of the lists of words to be used for the phylogeny reconstruction of a group of languages. The method is also automatic and gives lists of stable words which depend upon the language group, according to its peculiar cultural traits.

More recently, together with other scholars [2], we have used lists of automatically computed distances for a deeper analysis of relationships among languages. The point is that a tree is only an approximation, which obviously skips more complex phenomena as horizontal transfer. Our method, which takes a network point of view, correctly finds out language clusters but also gives a lot of new information. It seems, for example, that it allows for some more accurate understanding of some important topics, as migration patterns and homeland locations of families of languages.

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References

Automated languages phylogeny from Levenshtein distance


[21] The database, modified by the Authors, is available at the following web address: http://univaq.it/~serva/languages/languages.html. Readers are welcome to modify, correct and add words to the database.
Automated languages phylogeny from Levenshtein distance

Figure 1. Indo-European phylogenetic tree constructed from the matrix of distances using the UPGMA.
Automated languages phylogeny from Levenshtein distance

Figure 2. Austronesian phylogenetic tree constructed from the matrix of distances using the UPGMA.
Figure 3. Time distance between Malagasy and all the other subgroups in the Austronesian group.
Figure 4. Time distance between Romani and all the other subgroups in the Indo-European group