

Automated languages phylogeny from Levenshtein distance

(Filogenia automatizada de línguas a partir da distância de Levenshtein)

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Abstract

Línguas evoluem com o tempo em um processo em que reprodução, mutação e extinção são todos possíveis, de forma semelhante ao que acontece com os organismos vivos. Usando esta similaridade é possível, em princípio, construir árvores genealógicas que mostrem o grau de parentesco entre línguas.

O método usado pela glotocronologia moderna, desenvolvido por Swadesh na década de 1950, mede distâncias entre línguas a partir do percentual de palavras com origem histórica comum em uma lista. O ponto fraco desse método é o grau de subjetividade presente no julgamento da distância.

Recentemente propusemos um método automatizado que evita a subjetividade, cujos resultados podem ser replicados por estudos que usem a mesma base de dados e que não necessita nenhum conhecimento linguístico específico por parte do pesquisador. Além do mais, o método permite uma comparação rápida de um grande número de línguas.

Aplicamos nosso método aos grupos Indoeuropeu e Austronésio considerando, em cada caso, cinquenta línguas diferentes. As árvores genealógicas resultantes são semelhantes às de estudos anteriores, mas com algumas diferenças importantes na posição de poucas línguas e subgrupos. Acreditamos que essas diferenças carregam informações novas sobre a estrutura da árvore e sobre as relações filogenéticas dentro das famílias.

Languages evolve over time in a process in which reproduction, mutation and extinction are all possible, similar to what happens to living organisms. Using this similarity it is possible, in principle, to build family trees which show the degree of relatedness between languages.

The method used by modern glottochronology, developed by Swadesh in the 1950s, measures distances from the percentage of words with a common historical origin. The weak point of this method is that subjective judgment plays a relevant role.

Recently we proposed an automated method that avoids the subjectivity, whose results can be replicated by studies that use the same database and that doesn't require a specific linguistic knowledge. Moreover, the method allows a quick comparison of a large number of languages.

We applied our method to the Indo-European and Austronesian families, considering in both cases, fifty different languages. The resulting trees are similar to those of previous studies, but with some important differences in the position of few languages and subgroups. We believe that these differences carry new information on the structure of the tree and on the phylogenetic relationships within families.

1 Introduction

Glottochronology tries to estimate the time at which languages diverged with the implicit assumption that vocabularies change at a constant rate. The idea, initially proposed by M. Swadesh [20], is to restrict the comparison to a list of terms which are common to all cultures and which concern the basic activities of humans. The choice is motivated by the fact that these terms are learned during childhood and they change 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 distances between pairs of languages. Divergence times are assumed to be, on average, logarithmically proportional to these *lexical* distances. A recent example of the use of Swadesh lists and cognates to construct language trees are the studies of Gray and Atkinson [5] and Gray and Jordan [6].

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 [3], he 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 determine the degree of kinship for any pair of languages.

In our work we used an automated method which avoids 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 between two languages (section two) by computing a normalized Levenshtein distance among words with the same meaning and by averaging on the two hundred terms contained in the lists [22]. The normalization, which takes into account the word's length, plays a crucial role, and no sensible results would have been found without it. We applied this strategy to the Indo-European and the Austronesian families considering, in both cases, fifty different languages and obtaining two matrices of distances with 1225 non trivial entries.

These distances can be transformed, by a simple logarithmic rule, in separation times (section three) and two genealogical trees can be generated (section four) using the Unweighted Pair Group Method Average (UPGMA) [19]. The trees are similar to those found by [5] and [6] 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 as Malagasy and Romani.

2 Definition of lexical distance

We start by our definition of lexical distance between two words, which is a variant of the Levenshtein 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 Levenshtein distance divided by the number of characters of the longer of the two.

More precisely, given two words α_i and β_j (the Greek letter indicates the language while the Latin subscript indicates the meaning) their distance $d(\alpha_i, \beta_j)$ is given by

$$d(\alpha_i, \beta_j) = \frac{d_l(\alpha_i, \beta_j)}{l(\alpha_i, \beta_j)} \quad (1)$$

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. Therefore, the distance can take any value between 0 and 1 and, 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 another 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 $\frac{1}{8}$.

For any language, the first step is to write down a list of the words corresponding to the Swadesh's choice of meanings. Then, the lexical distance between a pair of languages is defined as the average of the distance between all pair of words corresponding to the same meaning. Assume that the number of languages is N and the list of words for any language contains $M = 200$ items. Any language in the family is labeled a Greek letter (say α) and any word of that language by α_i with $1 \leq i \leq M$. Then, two words α_i and β_j in the languages α and β have the same meaning if $i = j$.

The above defined distance between two languages is written symbolically as

$$D(\alpha, \beta) = \frac{1}{M} \sum_{i=1}^M d(\alpha_i, \beta_i) \quad (2)$$

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 [22] to construct the phylogenetic tree is composed by $N = 50$ languages of the Indo-European family and $N = 50$ languages of the Austronesian one. The main source for the Indo-European database is the file prepared by Dyen et al. in [4] which contains the Swadesh list of 200 words for 96 languages. Many words are missing in [4] but for our choice of 50 languages we have filled most of the gaps and corrected some errors by finding the words on dictionaries freely available on the web. For the Austronesian family we used as the main source the lists contained in the huge database [7]. The lists in [7] contain more than 200 words but the meanings do not coincide completely with those of the original Swadesh list [20]. For our 50 Austronesian languages we have retained only those words corresponding to the meanings which are also in the original Swadesh list. There are many gaps due to this incomplete overlap and because of many missing words in [7]. Also in this case we have filled some of the gaps by finding the words on the web and, in the case of Malagasy, by direct knowledge of the language.

For some of the languages in our lists [22] 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 on 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 [4]. Furthermore, in [7] 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 [22].

The result of the analysis described above are two 50×50 upper triangular matrices whose entries are the 1225 non-trivial lexical distances $D(\alpha, \beta)$ between all pairs in a family. Indeed, our method for computing distances is a very simple operation, that does not need any specific linguistic knowledge and it 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

$$\dot{D} = a(1 - D) - bD \quad (3)$$

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 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. Only historical records would give this information but this would imply again a subjective analysis that we want to avoid within our model.

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 $T(\alpha, \beta)$ between two languages α and β in terms of their lexical distance $D(\alpha, \beta)$

$$T(\alpha, \beta) = -\epsilon \ln(1 - \gamma D(\alpha, \beta)) \quad (4)$$

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 $a \cong 5 * 10^{-4}$ and $b \cong 6 * 10^{-5}$. 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 families.

A time distance $T(\alpha, \beta)$ is then computed for all pairs of languages in the database, obtaining two 50×50 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.

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]. We use UPGMA for its coherence with the coalescence process of Kingman type [8]. 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. This dynamics, introduced by Kingman, has been extensively studied and described, see for example [14, 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 the 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 [12] 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.

To check the stability of the phylogenetic trees we computed many trees in which some languages were removed randomly. The computation of these trees shows a strong stability in the main features of the trees, namely, all the large branches remain the same if some of their leaves are removed.

The Indo-European tree in Fig. 1 is similar to the one in [5] but there are some important differences. First of all, the first separation concerns Armenian, which is a 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 at variance with the tree in [5], 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 [5] it goes with Indoiranian ones.

Finally, in Fig. 1 the Romani language is correctly located together with the Indian languages but it is not as close to Singhalese as reported in [5]. Romani is the language of Roma and Sinti, it turns out that the closest three languages are Nepali, Bengali and Khaskura. Nepali and Kaskura are spoken in Nepal and northern India (the second is the language of Gurkhas), while Bengali is spoken in Northeast India and Bangladesh. This implies a geographical origin in Northern India for Roma's and Sinti's, according to the beliefs of the majority of researchers. Our results are different from those found in [5] where a close relationship Romani/Singhalese is detected.

Also the tree in Fig. 2 is similar to the one in [6] but differences here are more important. The first separation concerns the Atayal Formosan languages in a branch, while the Paiwan Formosan languages are in the other branch together with all the Malayo-Polynesian 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 [1].

Finally, the Malagasy language is isolated even if the closest language is Maanyan, which belongs to the south-east Barito group of languages spoken in Kalimantan [2]. Surprising, the second closest language is Maranao which is spoken in Philippines while the third closest is Buginese spoken in south Sulawesi. The fact that Malagasy, as expected, is very close to Maanyan, but other close languages are not in Kalimantan could suggest a multiple origin. It should be mentioned that Malagasy has many loanwords from Malay, particularly in the domain of maritime life and navigation.

The main problem is that it is unlikely that Maanyan Dayaks undertook 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 south-east 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 (and African) languages of the other slaves and of the Malay seafarers.

5 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 team of scholars that 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 "...achieving a computerized lexicostatistical analysis of ideally all the world's languages" [21].

In [11], 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 family of languages. The method is also automatic and gives lists of stable words which depend upon the language family, according to its specific cultural traits.

More recently, together with other scholars [1], we have used lists of automatically computed distances for a deeper analysis of the relationships among languages. The point is that a tree is only an approximation, which skips complex phenomena as horizontal transfer. Our method, which gives a geometric representation, correctly finds out language clusters but also gives a lot of new information. It allows, for example, a more accurate understanding of some important topics, as migration patterns and homeland locations of the families of languages.

Finally our method was able to resolve some of the mysteries concerning the settlement of Madagascar [16, 17].

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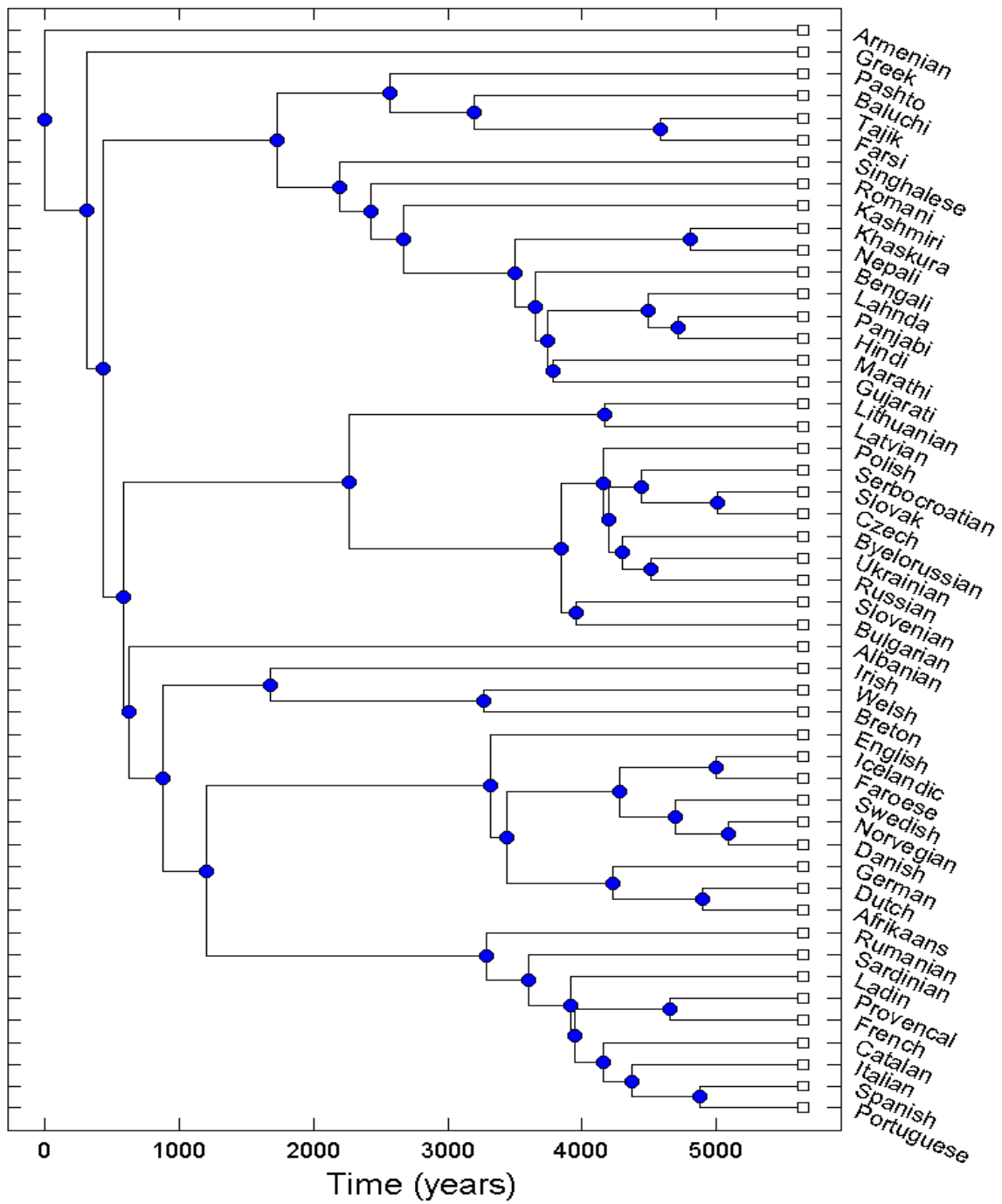


Figure 1: Indo-European phylogenetic tree constructed from the matrix of distances using UPGMA.

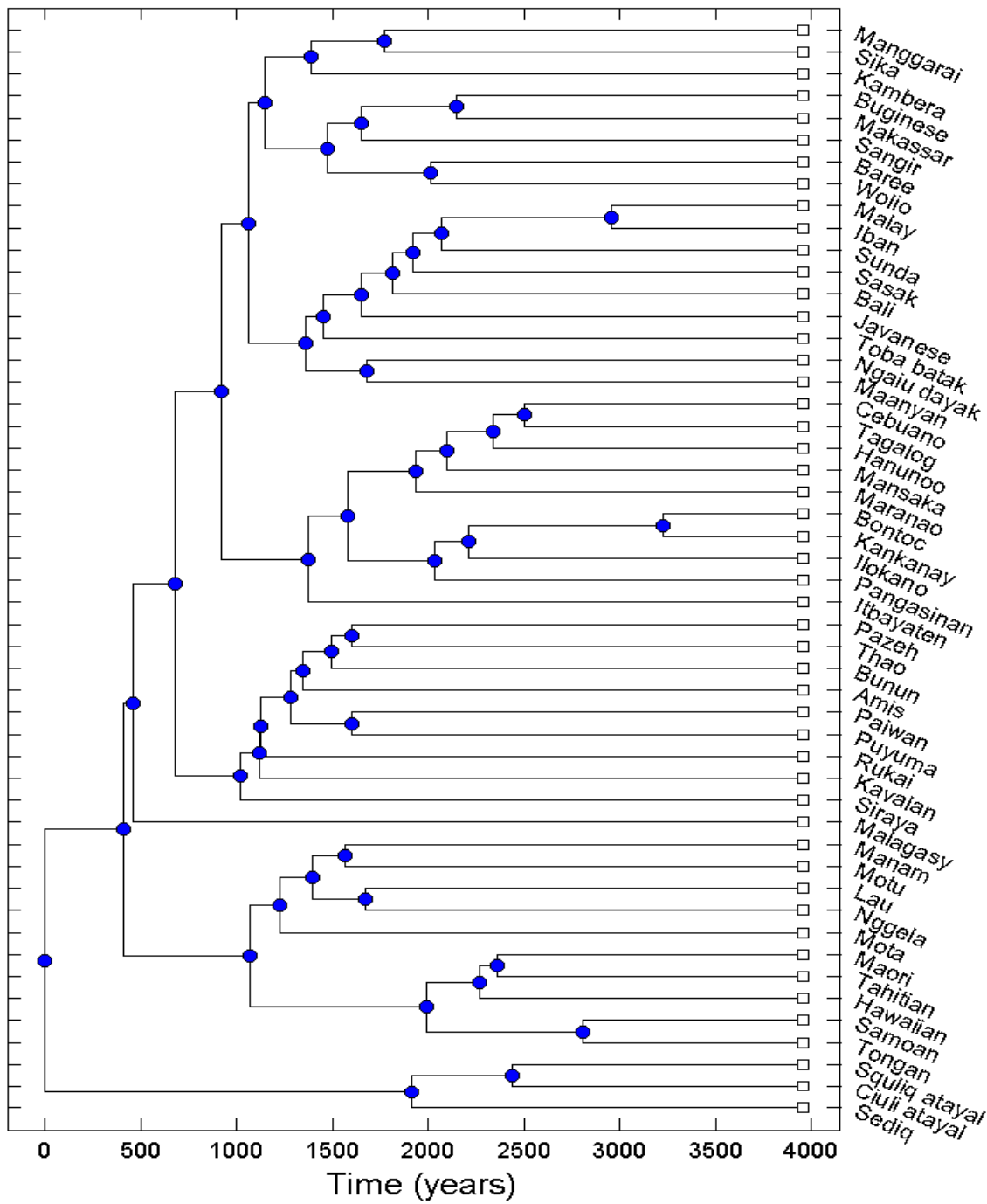


Figure 2: Austronesian phylogenetic tree constructed from the matrix of distances using UPGMA.