Stochastic approach to worldwide language classification: the signals and the noise towards long-range exploration

Beaufils Vincent¹, Tomin Johannes²,

¹ Independent researcher, Vienna, Austria

² Independent researcher, Vienna, Austria

Abstract

The exploration of distant language relationships reaching back to the Neolithic age remains very demanding and is often perceived as controversial. Over the last two decades, significant advances in computational linguistics offer alternatives to the methods in use so far to classify languages, but less quantitative research has been devoted to long-range language relationships. Classical methods reach their limits at a level where the signals they infer are more likely to be due to chance than to relatedness. We created a distance-based method without dependency on human relatedness judgments to set up an automated language classification inference system. We used a backward selection method to optimize the key elements of the system towards existing reference classifications: a word list, sound change rules and other parameters. We arbitrated choices in study design and features, which are beneficial for longer-range inference, if necessary at the cost of the short-range performance. The scope of the project is global: the system processes 1962 languages from all families, the limit for inclusion of more languages being the availability of the material needed by our system. After exploring the methodology, we show that it leads to a reliable language classification, matching the reference listings to a high proportion. We then apply a series of statistical models to target middle- and long-range relationships and explore connections outside the well-established classifications. By shedding light on relationships between top-level language families in the context of chance interference, our results deliver a strong support for two major long-range hypotheses: Eurasiatic (connecting Indo-European, Uralic, Turkic, Mongolic and Tungusic) and Austric (connecting Austronesian, Tai-Kadai, Austroasiatic and Hmong-Mien). Further support is given to parts of the Nostratic macrofamily, to a dozen other long-range hypotheses and to internal classifications of established language families.

Introduction

Retracing the origin of our languages and building their family trees gives a fascinating glance at the past, far beyond recorded history. Throughout the 19th and 20th centuries, classical methods in comparative linguistics like the reconstruction of proto-languages have delivered a very high level of consensus about the classification of languages in top-level families (TLF) and their subfamilies, but many aspects of these classifications remain unknown and the number of TLF or primary language families is high. The term “primary language family” does not necessarily imply that no earlier relationship exists between the established ones. Ideally, with further progress in the fields, the number of primary language families will become smaller overtime. When it

comes to infer connections deeper in time, the classical methods reach their limits: the available data is too eroded for these methods to fully apply. For this reason, in the research of long-range relationships between languages, proto-language reconstruction is not the main activity. The search for relatedness signals is widely extended to related meanings and roots with semantic proximity for various concepts, which seem to share similarities. Authors like Aharon Dolgopolsky, V.M. Illych-Svitych, Josef H. Greenberg, Allan R. Bomhard to name but a few have compiled big lists of such evidence, which lead to hypotheses for macrofamilies linking established top-level families, including reconstructed roots for very old proto-languages. The most discussed hypotheses – Eurasiatic and Nostratic – have gathered abundant publications and today, it is less the recognition of their existence which is at stake but more their exact composition. The Moscow School of Comparative Linguistics and its Global Lexicostatistical Database [1] are the leading reference in long-range research. A major point of criticism of long-range hypotheses is that their evidence can be due to chance: the researchers gather clues for hypotheses by extending the possible list of cognates to synonyms and more or less clearly semantically related concepts. By doing so, they increase the exposure to chance.

An alternative can be seen in quantitative approaches. First large-scale quantitative methods around the work of Mauricio Swadesh from the 1950s onwards are known under the terms “lexicostatistics” and “glottochronology”. They have been regarded mostly as controversial by mainstream historical linguists and the revival of quantitative methods in the 2000s cannot be seen as their continuity. The possibilities new technologies bring along have offered historical linguists not only methods for automatic word comparisons [2] but also a wider set of mathematical techniques, including Bayesian inference and machine learning, most of the time adapted from biology and genetics [3]. These techniques have proven to be reliable for short- and medium-range classifications, with a first global Automated Classification of the World’s Languages (Brown, C. H., E. W. Holman, S. Wichmann, and V. Velupillai) [4] in 2008. Further research in the past 10 years have made considerable steps forward, with Gerhard Jäger’s Global-scale phylogenetic linguistic inference from lexical resources [5] as a key example of a successful computer-assisted language classification in 2018. The ERC-funded research project ”CALC” (Computer-Assisted Language Comparison) aims at ”reconciling classical and computational approaches in historical linguistics” and pushes forward a productive use of computational approaches. Attempts to use mathematical and computer techniques for long-range exploration are increasing, however they do not lead to converging results yet. We have mentioned that long-range research needs to adapt to fading signals in classical approaches. The same applies to long-range research in computational historical linguistics and this aspect is the main focus of our research.

Our key idea is that the use of a quantitative approaches to explore long-range language relationships should address chance as big statistical noise in an environment with very few signals. We are not looking for signals that support specific hypotheses: we create a system which delivers a huge number of results along with the probability that these results and better ones are due to chance. In this context, the system infers possible candidates for long-range hypotheses and we check if such hypotheses already exist in the last step. Clusters of results linking more than just pairs of top-level families are statistically particularly convincing. Designing a system, dedicated to long-range exploration cannot be done without first proving it also works well on shorter-range classifications. For this reason, a big part of the research is devoted to the conception and calibration of the system towards an ideal performance on the classifications which are not contested among scholars. This represents the first step in the project. With a clear focus on the ability to detect longer-range signals and powerful features to challenge results with chance, we have managed to shed light on a

number of long-range hypotheses from a probabilistic perspective: Nostratic, Austric as the bigger ones, as well as support for smaller macrofamilies in the Americas and Caucasus. Support is also given to the Mande - Niger-Congo and West Bomberai - Timor-Alor-Pantar - Trans-New Guinea connections. It is important to point out that our focus is on probabilistic issues. The distinction between relatedness and potential early language contacts is a separate issue, which leaves uncertainty over final judgement about macrofamilies of languages.

Materials and methods

I. Word encoding

To handle comparisons, we encode the lexical items to make them computer-readable. We use the ASJP database [8] as source of lexical items for all languages. The encoding rules have to be adapted to the material available for a wide range of languages. In well-studied language, a high degree of precision of the pronunciation is available. In other languages, only approximations are at our disposal. A central requirement is to use the same rules all over the system. For this reason, we choose a level of precision for the word encoding, which is adapted to the material we have at our disposal from various sources, using the same accuracy degree.

System based on consonants

We make the choice to keep only consonants – and exclude vowels. This choice is a key point in the design of this research. The higher stability of consonants [6] is a good condition to retrace medium- and long-range relationships. In some cases, vowels resist longer to change than consonants do, but on a global scale, our experience hints at greater value of vowels for short-range comparisons – their value decreasing with the researched time depth. In few cases, most notably in the classification within the Polynesian subfamily of Austronesian, which has been very conservative in its vowel systems [7], the lack of vowel assessment leads to a misclassification within the subfamilies. These biases certainly affect – to various extends – our results in other language groups as well. This weakness is the manageable downside in the search for a simple and universal system. As a second reason to keep vowels out is that their inventory is smaller than the consonants’ inventory. The ASJP Database [8] uses 33 consonant symbols versus only 7 vowels symbols, so using vowels brings a bigger exposure to chance than using consonants. The third reason is the lack of their availability in some sources, especially for ancient languages.

Grouping consonants into classes

There are dozens of consonants in use in world languages – with languages reported to use up to 122 consonants [9]. However, for most languages, modern and ancient, only a sound approximation is available in the sources. It is neither possible to codify the available material in 1962 languages according to the very detailed IPA classification nor does it make sense: slight nuances determine the difference between numerous consonants. At the other end of modelling possibilities are Dolgopolsky’s ten fundamental sound classes, which deliver few false positive observations in cognate search, but miss potential for finding enough cognates [10]. Matching consonant classes in further quantitative research [11] also tends to use bigger classes. To balance between the extremes, we group the consonants into 27 classes. Consonants share the same class when they differ only slightly from each other, underlying similar change rules towards other classes. Our consonant classification system is summarized in Fig 1.

Fig 1. The consonant classification used in our research.

Consonant class	ASJP equivalent	IPA code of included sounds
-B-	b	B, β, b
-C-	c	ts, dz
-CH-	C, T	tʃ, tʃʰ, ʧ, ʧʰ
-D-	d	d, dʰ, ɖ, ɖʰ
-F-	f	f
-G-	g	g, ɣ, ʒ
-H-	h	h, ɦ
-J-	y	j
-K-	k, q	k, q
-KH-	X, x	χ, ɣ, ʁ, x, ɣ
-L-	l, L	l, ɭ, ɮ, ʎ
-M-	m	m
-N-	n, N, ɳ	n, ɳ, ɳ
-NN-	*	
-NG-	ŋ	ŋ
-P-	p	p, ɸ
-R-	r	r, ɾ, ʀ, ɽ
-S-	s	s
-SH-	ʃ	ʃ
-T-	t	t
-TH-	θ	θ, ð
-V-	v	v
-W-	w	w
-Z-	z	z
-ZH-	ʒ, j	ʒ, dʒ
-7-	ʒ	ʒ
-0-	0	θ, ɬ, ɬʰ, ɬʰ, ɬʰ

Some of the classes are particularly challenging in the word encoding: it is not always clear if a sound has to be classified as a consonant or as a vowel. This is particularly striking within the classes “-J-“, “-NN-“ and “-W-“. We apply clear rules to convert the source (the AJSP database [8] and ASJP sound classes [59]) to our format and there may remain room for discussion whether some sounds are correctly treated as consonant or not. However, for our methodology, the most important is to make sure that a given rule applies without exception to all datasets, without subjective human intervention. The system may codify some vowels as consonants. If it does so, it does this in a regular way, allowing these sounds to be treated according to the very same clear rules throughout the system.

II. Pairwise comparisons

Comparison of words across different languages is a critical task for quantifying language similarity. A common way to perform word comparison is based on the methods for sequence alignments. Sequence alignments intend to discover similarities or differences between sequences algorithmically. There have been developed different systematic pairwise alignment approaches in computer science dated back to 1970s (e.g Needleman-Wunsch, Smith-Waterman), which calculate sequence similarity first by computing the optimal alignment for two sequences and second by deriving a distance score using underlying scoring matrix for sound correspondences. We implemented our own systematic rule-based approach to determine word similarity, which is specifically adapted to the short sequences due to the fact that we compare only consonants, assessing full and partial matches. This approach of processing a pairwise comparison consists of three steps at following levels:

1. Syllable to syllable level (sound matching rules):

Each syllable of the first word is compared with the syllables in the second word. Inferring syllables automatically is a task, which leads to imperfections. What the system needs is not necessarily to distinguish syllables in a strict linguistic sense but to define which the smallest unit it compares within the words is. For convenience, we call the smallest units to be processed a syllable, even if they are not always syllables *stricto sensu*.

The sound change model we use for matching rules in syllable to syllable comparisons consists of points from 0, which corresponds to no resemblance to 100 for the same consonant on both sides of the syllable to syllable comparison.

To quantify differences between sets of data, a clear and stable model has to be established. Sound change quantification is the way we choose to measure erosion. Sound change is very complex and often specific to the various language families. The search for universal aspects of sound change applying in all languages necessarily leads to approximations. However, to process our comparisons, we need a set of rules, which delivers relatedness signals across all language families. We infer the rules best suited for a global classification with an iterative process we also use for the choice of lexical items, as described in §IV. We do not try to integrate as many items as possible, but want to find relevant ones with a fair degree of stability and universality. For this reason, we use only the part of sound change, which the system identifies as relevant in most language families. We need to choose the strongest signals, with the lowest possible chance interference. To do so, we apply an approach of word alignment according to our chosen rules arranging the consonants to identify regions of similarity that may be a consequence of evolutionary relationships between the words.

Our starting point of the search for a suitable sound correspondence model is the IPA [12] chart.

Fig 2. IPA chart for pulmonic consonants.

THE INTERNATIONAL PHONETIC ALPHABET (revised to 2015)

CONSONANTS (PULMONIC) © 2015 IPA

	Bilabial	Labiodental	Dental	Alveolar	Postalveolar	Retroflex	Palatal	Velar	Uvular	Pharyngeal	Glottal
Plosive	p b			t d		ʈ ɖ	c ɟ	k ɡ	q ɢ		ʔ
Nasal	m	ɱ		n		ɳ	ɲ	ŋ	ɴ		
Trill	ʙ			r					ʀ		
Tap or Flap		ⱱ		ɾ		ɽ					
Fricative	ɸ β	f v	θ ð	s z	ʃ ʒ	ʂ ʐ	ç ʝ	x ɣ	χ ʁ	ħ ʕ	h ɦ
Lateral fricative				ɬ ɮ							
Approximant		ʋ		ɹ		ɻ	j	ɰ			
Lateral approximant				l		ɭ	ʎ	ʟ			

Symbols to the right in a cell are voiced, to the left are voiceless. Shaded areas denote articulations judged impossible.

As described in §I ‘Word encoding’, we regroup similar consonants into classes. A match within the same class is the first, most obvious, sound correspondence rule: a same consonant or a same class at the same position on both sides of a pairwise comparison yields the maximum number of points (100). When the consonants in a same IPA cell are coded in our system in different classes (e.g. ‘t d’, ‘s z’, ‘ʃ ʒ’, ‘k ɡ’, ...) we apply a second set of sound correspondence rules with a own point level category. The third set of rules – with a further lower point level category -

is a supposed correspondence between plosives on the one side and fricatives on the other side (e.g. ‘p f’, ‘t s’, ‘t ø’, ‘s ø’, ‘d ð’, ‘p φ’, ‘b β’,...). Although these correspondences are often observed in vocabulary comparisons across languages, they may seem highly speculative for universal comparisons. For this reason, we test their impact in the iterative process described in §IV, inferring a list of “best rules”. We also test further rules observed in comparisons – these rules go beyond the described three categories and are compiled in a fourth one only if they appear to yield interesting results (more true positives than false positives). The outcome (S2 File) is a quite limited set of correspondences, which will seem familiar to anyone with a certain experience in vocabulary comparison across languages. There are hundreds of possible rules, which have a ‘local’ impact within and between the respective language families. Most of these rules are sorted out by the system because – on a global basis – they bring far less relatedness signals than statistical noise.

The decision, how many points each sound correspondence category yields in comparisons is arbitrary at the beginning. We have chosen ‘Category 1: 100, Category 2: 90, Category 3: 75 and Category 4: 50’ point model to start the analyses. This model was challenged in the iterative process described in §IV and the rounded values ‘100-95-85-75’ have been inferred by the system as the ones, which delivers the best results. The goal is to reward the identified relatedness signals on the one side, but to differentiate them according to the erosion level on the other side.

To summarize, we can represent our sound correspondence model in following four categories:

- Category 1: same sounds (e.g. ‘k - k’, ‘t - t’, ‘s - s’, ‘f - f’...) yield the maximum number of points in comparisons (100).
- Category 2: very similar sounds (same ‘cell’ in IPA table, e.g. ‘k - g’, ‘p - b’, ‘f - v’) yield 95 points.
- Category 3: algorithm-selected correspondences between plosives on the one side and fricatives on the other (e.g. ‘t - s’, ‘t - ø’, ‘s - ø’...) yield 85 points.
- Category 4: other correspondences, inferred through the iterative process described in §IV (e.g. ‘j - s’, ‘z - z’...) yield 75 points.

Each sound change rule we apply carries a specific potential of chance interference. The number of occurrences of each consonant group in the world languages is far from constant. An example in table 1 shows how a syllable with a consonant from the “-K-” class behaves in interaction with other sounds and how it accordingly exposes to chance.

Table 1. Example of sound correspondence rule used to process the comparison (class “-K-”)

Consonant class	Match with	Points given	Matching probability*
-K-	-K-	100	0.1005
-K-	-G-	95	0.0280
-K-	-KH-	85	0.0166
-K-	-H-	85	0.0309
-K-	-7-	85	0.0240
-K-	Other	0	0.7990

* The matching probability is the probability the rules apply according to the occurrence of the consonant class in the languages we use.

In a few cases, when languages undergo a high proportion of non-universal sound evolution patterns, the system tends to overestimate the distances from their respective core-families, because it skips a higher part of the relatedness signals. A good example is Armenian, which has developed a very specific sound change [14], not reflected in our model. This is a limit to the system, which affects the stability of the results: the case of Armenian is an obvious one, but this issue affects all languages to various degrees. This has an impact on the variance of the results.

The limited set of sound correspondence rules we infer cannot be compared with more elaborated sound correspondence rules inferred by comparatists. The purposes and the scope of their use as well as the methodologies of their inference are completely different.

2. *Word to word level (alignment analysis)*: At this level, the system has to determine which of the syllable-to-syllable matches are valid.

Due to the particularity of our system, which considers only consonants and has accordingly shorter alignments to analyze, we implement an own alignment analysis algorithm. This algorithm is much more basic than state-of-the-art methods [15] or frameworks like LingPy [16], but also gives us the flexibility to implement our own empirical rules considering partial match and filters and systematically calibrate the system towards the balance between relatedness signals and statistical noise (see §IV). Our primary goal is not the detection of cognates but the calculation of a distance value, without judgment whether this value means cognacy or not.

The system first iterates a comparison of all syllables from word 1 (word for a concept in language 1) with those of word 2 (word in language 2 for the same concept as in language 1), regardless of their respective positions within the words. All pairwise syllable comparisons are stored together with their respective positions. For example, the comparison of the second consonant in word 1 with the third in word 2 is stored as a variable 'W1C2W2C3' (Word 1 Consonant 2 vs. Word 2 Consonant 3) with the value of its match. The second step consists in counting the points for all acceptable combinations of syllable to syllable matches in the word to word context. Cross matches are not allowed (eg. 2nd consonant in word 1 matches 1st in word 2 and 1st consonant in word 1 matches 2nd in word 2) and too distant matches are not taken into account. The valid combinations the algorithm accepts are represented in Fig 3. All possible and accepted combinations are gathered in a list, from which the system selects the best match. Fig 3 represents how syllable to syllable matches in pairwise comparisons of words with each up to four syllables are validated. The visualisation contains four syllables on each side, but the same rules work well with any other number of syllables between one and four, on either side.

Fig 3. Alignment rules at word to word level: valid combinations of matches

Finally, we apply a series of filters to avoid statistical noise through very low signals. Basically, if a combination of only one match other than a match on the first consonant on both sides delivers the highest score, we set this score to 0 if one of the words on either side has 3 syllables or more. The last steps consists of a filter over the result regardless of the match position: the values from which the results are filtered are inferred in a special process described in part V.

The syllable to syllable points are averaged at word level, to obtain a value from 0 to 100 for each pair of word comparison.

3. *Language to language level:* the points obtained at word level are averaged to obtain a value from 0 to 100 for a comparison between two languages. This value is reversed to a distance value by subtracting it from 100. The result of a pairwise comparison between two languages is a distance between 0 (same language) and 100 (no single relatedness signal, not even by chance). Specific rules eliminate points obtained with too weak signals: this step is a first filter balancing signals and noise, with the aim to eliminate as much chance matches (false positives) without losing too much real signals (true positives). We refer to it as the ‘low signals filter’ further in our research. This filter plays a major role in the process and has to be calibrated to contribute to the best possible balance between relatedness signal strength and statistical noise.

The system does not calculate the proximity between languages by counting the number of cognate words in a sample, but by calculating the degree of similarity the words have. In this way, the results are continuous values and make a differentiation of the degree of erosion measurable. For example, the word “water”, codified [“W-T-R-“] gets more points when compared to German “Wasser” codified [“-V-S-R-”] than to Russian “voda” [“-V-D-“]. This system does not guarantee that the proximity between two words will always follow the actual proximity between languages – English “night” [“-N-T-“], which consonants better match Italian “notte” [“-N-T-”] than German “Nacht” [“-N-KH-T-“] is an example of results’ variance. The distance value at language level is 68 for English to Italian and 43 for English to German, which better reflects the degree of difference between these languages than it does with the comparison of the sole word “night”. Obviously, the variance gets lower when the number of words in the comparisons grows.

Distance values are relative to each other: Distances between languages can only be interpreted in the context of their respective distances to other languages. Browsing the

pairwise comparisons most of the time brings highly consistent results but also variations that lead to a surprising outcome. The causes are numerous and reflect important limits:

- The system assumes a constant rate of evolution, which does not correspond to the reality. Languages evolve at different speeds [13] in time and place.
- We compare languages in different states. Even if the lexical items in use are resistant to massive vocabulary loans, other aspects in the history of languages influence their evolution.
- Exposure to chance affects the distance values and hence influences the variance of the results.
- In short-range comparisons, the number of differences is small, giving each of the difference a very high weight, which heavily affects the variance of the short-range comparison results. If the aim is to be more accurate on short-range comparisons, more lexical items have to be used. We choose to focus on medium- and long-range classifications and our experimental research described in § III shows that more words do not necessarily lead to better medium- and long-range classifications: the choice of the best suitable lexical items is more important than the quantity we use.

III. Choice of the lexical basis

The Swadesh list, a standard list of basic vocabulary, is considered as the first reference for comparative linguistics based on lexical items. Since its first release with 215 words in 1950 [17] it has been a constant trend to reduce the number of words, concentrating on the most stable ones, with a final version of 100 words by Swadesh himself in 1972 [18]. Sergei Yakhontov has established a 35 subset [17] and more recently, the ASJP [8] project uses a 40 words list for its worldwide classification [4]. For this project, because it is our aim to quantify language relationships as far as possible in time, we have defined following criteria:

- the words should stand for concepts which were supposedly relevant to most human populations as early as 6000 to 8000 years BP,
- they have to be stable against borrowing - known borrowings have to be excluded,
- the resistance to semantic shift has to be high.

Our first goal is to find the word list, which is best adapted to classify languages. If a word list used in our system delivers a good phylogenetic classification of few but well documented languages, we can assume that it is adapted to generate reliable data for deeper analyses. The aim is not to use as many lexical items as possible, but to find the combination that delivers the best relatedness signals, with lowest possible exposure to chance. As a starting point, we use the 40 items wordlist from ASJP project [8], from which we infer a smaller but ideal items list using an iterative selection process described in § IV.

The basic vocabulary has to be resistant to influence from outside

The selected word list has a high resistance to borrowing. It resists to the influence of French in English and - to a big extent - of Arabic in Iranian and Turkic languages. Exceptions have to be identified – e.g. the influence of Indo-Aryan in Dravidian (three

words of the list), Arabic within the Afroasiatic family and towards other language families as well as Chinese on numerous Southeast Asian languages. We exclude loan words whenever we have the information available (in our source, ASJP, part of the known loans are documented as such and we exclude them), but we cannot rule out the possibility that unidentified borrowings from very ancient times can influence the results. The exclusion of loan words is a difficult trade off as there is no satisfactory possibility to remove them with a uniform knowledge over all language families. Sources for loan words are scarce and not always reliable.

Bias caused by different level of information about loan words across language families

Removing loanwords biases the uniformity of the results' quality in a direction that favors the performance of the classifications of languages for which loan words are well-documented in the sources. We chose to accept this bias in favor of the inclusion of all available information, even if this information is not equally available over all families. The quality of the data collected in the ASJP varies from language to language, with more or less concepts missing, no or many synonyms recorded and varying focus on loan words documentation. For many languages, the sources are based on the fieldwork of one or a few researchers (e.g. Amazonas, New Guinea) or even incomplete wordlists compiled decades or centuries ago.

Synonyms

Our source, the ASJP database [8], contains synonyms. The abundance of recorded synonyms varies strongly from language to language, which is not only due to the non-homogeneous availability in the respective languages, but also to the different approaches of the various authors who gathered the data. For some languages, the source contains up to 91 entries for our 33-words list. One approach, which we tested, is to always include synonyms and retain the match with the highest result in the word-to-word comparisons. This approach also delivers a bigger exposure to chance, which in turn strongly biases the results in form of statistical noise, especially with languages for which abundant synonyms were gathered. This also biases the calculation of confidence values of the results. To avoid this - and not reject the rich source of information these synonyms carry - we chose to keep the first entry from the records, but in some cases, which we documented in the supplementary material, we selected the entry which best matches the other languages within the same subfamily (WALS genus). This in turn was done only if the change permutes an isolated form with one of the forms clearly repeatedly available in the family. This approach can influence the results in a way that favours longer-range classifications and have a negative impact on the short-range family detections. Since only one entry can be used, we chose to favour the entries which help to identify relatedness in long-range.

The ideal number of lexical items

Throughout our research, it became clearer and clearer that more words do not mean better classifications. As observed in other researches, very few words have a high degree of stability against borrowing, semantic shift and phonological erosion over a longer time frame [19]. In Fig 4, we see that the variance of the distance values in language to language comparisons decreases as the number of lexical items in use increases. But we also see that this benefit becomes weaker, especially when we have 30+ words in the comparison. Details on how we selected the word list and its ideal size is developed in § IV.

Fig 4. Impact of the number of observed words on the result’s variance (comparisons between unrelated languages)

Using strict meanings vs. related meanings

The search for long-range relatedness of languages applied by various authors delivers an abundant evidence for connections between languages beyond the universally recognized macrofamilies [20] [21] [22] [23]. The longer the comparison time depth, the more indirectly signals come: relatedness in semantically shifted meanings deliver a significant part of the evidence. However, in these cases, the exposure to chance is bigger and more difficult to measure, opening the doors to critical judgments and discussions. For this reason, serious research is still rejected by a part of the linguist community [24]. To avoid this trap, even in the small list of lexical items we use in our project, we choose to let aside obvious evidence visible in semantic shift: for example in the concept of “dying” (‘to die’, ‘death’), the stem “-M-R-T-”/“-M-R-”/“-M-T-” is present in languages across several macrofamilies. In Germanic languages however, this stem has shifted to the ‘active’ concept of death (“Murder”). In our system, we compare the words only from their strict meanings: automatic rules support no exception. Using this kind of evidence would mean that we include partially subjective expert judgment to our otherwise unmodified objective sources. It would also make statistical assessment of the results impossible.

All words have been converted to the format of this project (consonant classes see §I) and codified using the same criteria, excluding vowels. The conversion rules are clearly visible in the R script available in the online Supporting Information S3 File.

The sources and the choice of the languages to compare

We choose to apply our system on all language families reflected in the source we use: the ASJP [8] database. Many ASJP doculects share the same ISO 639-3 code (e.g. numerous Pashto, Wakhi, Romani, Shina and Hindko doculects). As we are using only consonants, the low degree of differentiation between very similar doculects makes our system very sensitive to smallest differences, including imprecisions in sources and codification. For this reason, we choose to limit the number of languages by using only one doculect, the one with the most documented concepts and synonyms (if several doculects have an equal highest number of concepts), for each ISO 639-3 code.

In all available sources - and so in the ASJP database in use here - the sources for many languages are incomplete and make only a part of the word list available. Fig 4 makes clear that when using only few words, the variance of the distance values is much too high: the point level reached by chance increases when the number of available words for the comparison decreases. Different word availabilities in the samples bring different levels of exposure to chance, which biases the results in the phylogeny. For this reason, we choose to limit our dataset to languages, for which at least 30 words out of the 33 we use in our source (the AJSP database [8]) are available - with a few exceptions for languages which have a key position in classifications (e.g. Hittite, Gothic, Maori - 1,67 % of our sample) and for which we set the limit down to 26 words. This is crucial to limit biases in the clustering process.

IV. Search for the best set of words and sound change rules

As elaborated in §II and §III, the comparison algorithm uses four fundamental variable inputs:

- A lexical item list of basic vocabulary.
- A sound correspondence model.
- A point system within the sound correspondence model.
- A low signals filter in the algorithm itself (trying to act as squelch in radio transmissions).

These lists, models and numeric values are all variable. By varying the setup of items in the word list and/or sound correspondence model, as well as by trying different point assignment values and low signal filters, we produce different phylogenies, which each partially matches differently the reference classification. We do not change the input data itself, but the parameters according to which the input data is analyzed. Changing word lists and observing which words contribute to produce better results is a common practice in most lexicostatistical research. This can also apply to the other aspects - sound change rules and parameters used in the algorithm. However, this brings us to one fundamental issue. We get better results by varying parameters, but is this not the result of chance? We make multiple iterations, so we increase the chance to find the result we are looking for. Reflecting the observation “*If you torture the data long enough, it will confess* [25]”, we can wonder if the data ‘confesses’ what the reality is or if it ‘confesses’ what we want it to confess? To avoid doubts about this issue, we choose to use a systematic method, which allows not only to infer the parameters, which generate the best possible classification from the available data, but also to make sure the good results are not simple overfitting: the best possible representation in a given context but not suited as a general model.

There are several millions possible combinations which can be applied combining the four available criteria ‘Word list’, ‘sound correspondence list’, ‘point system and ‘low signals filter’. If we consider alone the possibility to select 15 words out of a prefixed corpus of 40 words, the number of possible word combinations is $\binom{40}{15}=40,225,345,056$. To find the best combination, we apply a heuristic optimization process, modelling a cost function, which we use to minimize an error. The system applies multiple word and sound correspondence lists to iterate a series of classifications for languages for which

the classification is known and universally accepted. We take a subset of the classification by Glottolog [26] as our reference and use it as our ‘response variable’. In a further series of iterations, we apply the same system changing the values of the point system and low signals filters. We compute phylogenies changing the lists and parameters until we reduce the error between the computerized classification and the reference classification to a minimum. We combine the search for the best word list with the search for the best sound correspondence rules and ideal parameters for the point system and low signals filter.

In this process, the system gradually excludes the items with a similarity detection power that is weaker than their exposure to chance. Whenever an item has a negative impact on the results, we can assume that it is not stable enough and/or its exposure to chance is stronger than the signals it yields towards relatedness detection. This process leads to a limited final set of words and sound change rules, as well as to an optimal point system. The minimization of the number of items is the result of the error reduction process towards a complex reference classification, which leaves very little room to chance.

Overfitting

As mentioned before, a possible limit of this approach is that computer-based algorithms are strong in modelling predictor variables towards complex classifications, but the possibility to handle thousands of ‘try and error’ iterations also may deliver a model, which generalizes well in the context we train it, but fails to do so in a new context. For this reason, we have split our data into two sets: a training set, which contains a part of the Indo-European, Uralic, Mongolic, Afroasiatic and North Caucasian languages and a second set, which contains all other languages. We carried out the optimization iterations with the languages from the training set, which represented 63.5 % of the languages in our data at the time of the experiment. The remaining languages – for which classifications are also known and widely accepted – gave us an opportunity to test our results and to see if the system also performs well for languages it has not been optimized for. The outcome was positive, although the error rates of the two categories of languages cannot be strictly compared, since their respective classifications are not equally challenging. This process has been carried out in an early stage of the project, when less than 800 languages were included in the data. Adding new languages and language families afterwards was an opportunity to confirm the system’s performance in new contexts, outside the original training and testing data sets.

Final selection

The iterative process delivers optimal values for the four variable criteria of the system:

1. The best word list (Table 2).
2. The optimal set of sound correspondence items (S2 File, col. 1-2).
3. An ideal point system for 2) (S2 File, col. 3).
4. The low signal filter delivering the best values - balance between reducing exposure to chance and allowing distant relatedness signals (online Supporting Information S1 File).

Best word list

During the selection process, we identified 7 words from the ASJP 40 items list [8], which we found to have a negative impact on the reference language classification. The most negative items are “to come”, “liver”, “path” and “person” which negative impact was obvious in an early stage. In a second stage, the items “fish”, “mountain”, and “stone” were the most challenging to spot as less useful and/or negative in their impact. If we consider this list, we can find an explanation for most items: “liver” is certainly not a word suited for medium- and long-range classification, as it implies some kind of stable knowledge of anatomy at an equal level in various parts of the world. The concepts “to come”, “path”, “person”, “mountain”, and “stone” appear to be challenging in the data collection: there are often several available roots due to nuances in their meanings and it is difficult to decide which one to choose. This may explain their low contribution to classifications.

Table 2. Best word list

blood	drink	hand	leaf	nose	sun	water
bone	ear	hear	louse	one	tongue	we
breast	eye	horn	name	see	tooth	you (thou)
die	fire	I	new	skin	tree	
dog	full	knee	night	star	two	

* In an early stage of the research we identified the concepts ”four”, ”three”, ”wind” and ”who?” as very contributive. Unfortunately, they are not available for most languages in the source we use, so we have to drop them for this research.

V. Statistical Methods

Our system relies on similarity signals, which are gathered from pairwise comparisons of words. When these signals are positive, this can be due to the fact that the languages are related or it can be the result of statistical noise. For example, if we take the word “to die”, which is broadly covered with the consonant class chain “-M-T-“ or “-M-R-T-“ in Indo-European languages and look for similarities outside that family, we find matches in a series of top-level families, including such for which no hypothesis exist linking them to Indo-European, like Cariban and Pama-Nyungan languages. The probability to get “-M-T-“ on both sides of a comparison if the words always have two syllables is $0.074 * 0,08 = 0.006$ (see online Supporting Information S2 File). It means we expect to obtain such a match by chance every 167 comparison. This probability grows for partial matches (different word lengths, sound correspondences, etc.) These matches alone in Cariban and Pama-Nyungan are not a clue for relatedness. Therefore we require objective and systematic methods to measure whether observed results are significant or occur as a result of random noise.

Applying methods of descriptive and inferential statistics allowed us to make objective generalizations about pairwise comparisons for language-to-language and for middle- and long-range relationships without a manual interference. In particular, statistical inference is primarily concerned with measuring the quality of statistical parameter estimates and its variability that we obtained running the experiments. We also set up a hypothesis testing framework for the different language relationships where we consider two competing hypotheses. The null hypothesis (H_0) that represents the perspective that two languages or language families are not related and the alternative hypothesis (H_A) claiming that two languages or language families are related. We

established a hypothesis testing framework selecting H_0 and H_A before seeing the actual data and so avoiding to introduce a bias into our procedure. Our aim is to accept or to reject the null hypothesis using our data.

However hypothesis tests are not without faults and still one can lead to wrong decisions by wrongly accepting the alternative hypothesis when actually the null hypothesis is true (*Type I Error*) or fail to reject the null hypothesis when the alternative hypothesis is true (*Type II Error*). We are able to quantify the strength of the evidence against the null hypothesis by calculating the probability (p-value) of observed data or more extreme value given the null hypothesis is true. Formally the p-value is a conditional probability.

First we describe a key part of the statistical framework that will be encountered repeatedly through this paper. Since we do not know the theoretical type of the distribution that best describes unrelated languages, we construct an empirical distribution for unrelated languages by generating random languages from our data set. In this way we will be able to assess statistically whether two languages or languages families are significantly similar or not. This empirical distribution will be representing our null hypothesis H_0 or in other words, it represents the null distribution. Moreover a simulated data set of randomized languages will also enable us to visually assess the stability of derived phylogenetic tree in later stage.

Null Distribution from generating randomized languages

To simulate null distribution we first generate random words. For this purpose we first estimated several empirical probability distributions. Each lexical item is treated separately: the respective lengths are typically shorter or longer in almost all world languages and the consonant classes of a word have different probabilities to appear. Therefore, we used a probability distribution for consonant class occurrence (Fig 5) and word length (for example approx.. 48% of all words in our data have two consonants.)

Fig 5. Probability distribution of consonant classes

Also, we considered the fact that some consonants are more likely to occur at a particular position in a word where some other consonants are less likely to do so.

The last issue to take into account is how often the respective words are available in our source (the AJSP database [8]). We need to replicate the lack of availability of certain words in a certain proportion in the random data we generate.

To make sure the generated random words are good representatives of the statistical noise observed in the data, we carry out statistical tests of the distributions of the comparison results between random languages against the distributions of comparisons between languages we know as unrelated. Our goal is to generate random languages, which behave the same way as real languages. This approach has the potential bias that we may not consider enough features to generate the random words. Therefore, it is *stricto sensu* an approximation of random languages. This method is interesting to gain understanding about how pairwise results have to be considered in the context of chance. However, using it involves processing each single pairwise comparison with a big number of random languages, which would increase the processing time of the distance matrix for all languages from 5 days to several weeks or months. Moreover, as a basis for bootstrapping, this method is not more challenging (in fact even slightly less challenging than the next ones).

Null Distribution from non-related languages

In an alternative approach, we gather the distance values of pairwise comparisons between languages from different top-level families, for which no hypothesis is available that they may be remotely related (e.g. Indo-European to Quechuan, Austronesian to Atlantic-Congo, etc.). We can use these values as pseudo randomized pairwise distance values. We can also use their empirical distributions to infer random pairwise distance values in unlimited quantities. These two related approaches also have their pitfalls: the choice of the families we use for comparisons has to be very conservative: if we compare two families, which are reported as not related in reference classifications, there is a risk that we use comparisons between families that are actually related, but this relatedness is not considered so far as proven. For this reason, we take care not to select comparisons between families, for which some hypothesis about a potential genetic relationship exists – even if this hypothesis is broadly rejected (Uralic to IE, Turkic, Mongolic, comparisons between American top-level families...) A further source of bias is – of course – the potential presence of undetected loan words across unrelated families. Using comparisons between languages families which are geographically remote contributes to reduce this bias.

Null Distribution from random sample

Another approach to generate a null distribution when performing a hypothesis test involves taking a random sample from the data set without making any prior assumptions of the data. This approach is particularly simple to implement and when sampling the data set with replacement we even can generate a sampling distribution for any statistic of our choice e.g mean and standard error of the distribution. This is the method we use throughout our research.

Language to Language

In order to evaluate the statistical significance of similarity between two languages we estimate an *empirical p – value* based on a bootstrap simulation that samples the null distribution with replacement. Having the observed distance score $\tilde{s}$ between two languages $L1$ and $L2$ calculated as :

$$\tilde{s} = 100 - \frac{1}{n} \sum_{i=1}^n d(L1W_i, L2W_i)$$

where $n = \min(|L1|, |L2|)$ and d being a distance function between $words_i$ of $L1$ and $L2$ respectively. Moreover we generated a vector $s = (s_1, s_2, \dots, s_N)$ where s_i contains simulated bootstrap statistics from our null distribution. Bootstrapping is a resampling technique that randomly samples data with replacement creating many simulated data. This allows to perform hypothesis testing for statistical parameters. The nature of how our distance values are determined and the fact that they are physically bounded between 0 and 100, unrelated languages having higher scores than related ones, has an impact on the shape of the distribution. In Fig. 6 we can clearly observe that the null distribution will be left skewed having related languages concentrating in the tail at the left of the distribution. For this reasons we are considering a one-sided statistical test:

- $H_0 : \tilde{s} = \hat{s}$, $L1$ and $L2$ are not related
- $H_A : \tilde{s} \neq \hat{s}$, $L1$ and $L2$ are related

In order to calculate the p-value we count the number of statistics s_i that are greater than or equal to the $\tilde{s}$ value and divide by the number of the experiment size:

$$p - value = 1 - \frac{\sum(\tilde{s} \leq s)}{N}$$

In a simplified view, setting the significance level $\alpha = 0.05$ we reject the null hypotheses when $p - value < \alpha$. Since we conduct multiple statistical tests for all the language pairs we make $S = (1962 \times 1962)/2 = 1924722$ comparisons. When performing a large number of statistical tests, some will return $p - values < \alpha$ purely by chance, and may wrongly accept the alternative hypothesis causing a *Type I error*. To overcome this, applying a conservative Bonferroni correction can be a more appropriate approach: we correct the p-value by the number of tests being conducted, having a new rejection policy $p - value < \frac{\alpha}{S}$. However, in the context of results with high variances, the p-value is a help for the interpretation and certainly not a tool to firmly accept or reject an hypothesis.

Fig 6. Distribution of pairwise comparisons: IE languages vs. randomized languages

Language Subfamily to Subfamily - middle-range

To assess statistical significance between language subfamilies ($SF1, SF2$) we want to test the null hypothesis that distribution of distances between all the paired languages within $SF1$ and $SF2$ have the same observed mean μ_x as the mean μ of the null distribution, however not necessarily the same distribution. In order to conduct this two-sample bootstrap test, we shift both distribution to have the same mean, since we are simulating the hypothesis that their means are, in fact, equal $\mu = \tilde{\mu}$. We then draw bootstrap samples out of the shifted arrays and compute the difference in means.

- $H_0 : \mu_x - \mu = 0$, $SF1$ and $SF2$ are not related
- $H_A : \mu_x < \mu$, $SF1$ and $SF2$ are related

This constitutes a bootstrap replicate, and we generate many of them. The p -value is the fraction of replicates with a difference in means greater than or equal to what was observed.

Language family to language family - long-range

With the statistical framework for language to language comparisons, we generate p-values for all pairwise comparisons between languages. However, our long-range exploration is based on the analysis of relationships between top-level language families. We need a method to interpret the series of p-values generated by the comparisons between the languages of the researched families and statistically aggregate all the p-values to make valid comparisons between top-level families. A meta-analysis of the significance values of our pairwise comparisons can be attempted using established methods to combine p-values, most of which are designed for independent experiments. In our situation, comparing the pairwise distances and their p-values for all languages from two top-level families (TLF), we have a series of comparisons which are not completely independent from each other: each TLF consists per definition of related languages. This forms a bias, which is stronger when the TLFs are more homogeneous. To reduce the problem, we do not compare all pairwise languages between the TLFs, but select only one per respective subfamily (on the basis of the WALS genus list) and always take the subfamily to subfamily comparison with the lowest distance into account. This correction helps to reduce the unnecessary inclusion of highly dependent experiments but does not resolve the dependency issue completely. A recent research by Daniel J. Wilson [27] derives a statistical technique for addressing multiple comparisons problems by combining multiple tests. It generates a harmonic mean and takes the dependency of tests into account in a meta analysis of p-values:

$$\tilde{p} = \frac{\sum_{i=1}^L w_i}{\sum_{i=1}^L w_i / p_i}$$

, where $w_1, \dots, w_L$ are weights with $\sum_{i=1}^L w_i = 1$. This approach also improves on the power of Bonferroni correction by performing combined tests. The use of weights is optional and makes sense only if information representing these weights is available in the data.

VI. Clustering - phylogenetic analysis

One major mathematical tool to explain evolutionary relationship between languages was actually developed in computational biology and it is called phylogenetic inference,

using a tree based data structure. In historical linguistics, the use of phylogenetic trees has expanded in the past decades [28].

There are two main groups of methods to examine phylogenetic relationships between languages:

- Phenetic methods: trees are examined by considering distance based similarities of languages, therefore require distance matrices as an input. The resulting tree is called dendrogram and it shows the hierarchical relationship between languages. It also allocates languages into clusters of highest similarity based on distances.
- Cladistic methods: trees are examined by considering various possible combinations of the tree and are based on parsimony or maximum likelihood methods. Cladistics methods do not take into account distances between languages, but rather compare characteristics of languages with each other. A characteristic of a language could be presence/absence of cognates in words. The resulting tree is called a cladogram. Cladogram show relations among languages, however it does not show how ancestors are related to descendants, even though it is possible to infer evolutionary trees from a cladogram.

Maximum likelihood methods are being considered state of the art today. They are computationally very intensive, since this method evaluates all possible trees, and calculates the likelihood for each tree using a probabilistic model. The tree with the maximum likelihood is the most probable tree.

In this research we produce a distance matrix between all possible pairs of languages. To obtain meaningful insights, we have to identify clusters of languages out of this data. A wide choice of computer programs to process phylogenies from distance matrices is available. We use the APE-Package [29] of R [30], which not only generates phylogenies, but also brings flexibility in analyzing the results, combining the power of a standard functionality with the ability to write own scripts for further, tailor-made analyses.

Choosing the right algorithm

The phylogenetic tools for distance based methods offer different algorithms, each of which has strengths and weaknesses. We choose to use an improved version of the neighbor joining method, BIONJ [31]. This algorithm performs better in our tests than other available distance-based algorithm: UPGMA, NJ and FastME.

When examining a phylogenetic tree it is necessary to assess the quality of the tree. We use two methods to quantify the quality of phylogenetic tree: by adding an outgroup to the tree and by bootstrapping the tree to quantify its stability. Outgroup method basically involves adding a set of randomized languages or languages being not related with other languages at all. Bootstrapping [32] [33] is a resampling technique that repeatedly samples data and performs inference about a sample from resampled data to derive statistical parameters. We analyze how well targeted references or long-range hypotheses are represented not only in the original NJS tree, but also in 100 resampled versions of it (we explain this technique in next paragraph "Results validation"). The median value of the inferred scores reflect a node support by at least 50% of the resampled trees. In practice, most of the scores are supported by far more than 50% of the trees since the result convergence is most of the time higher, with a large proportion at 100%. These values can be displayed in a table only, not in a consensus tree.

Results validation – Bootstrapping the distance matrix with random pairwise distances

In a phylogenetic tree, we need to identify the stability of the inferred nodes and branches. Nodes and branches which vary when we make small changes to the

algorithm or when we add or subtract datasets are unstable. In what is to our knowledge a own approach, we use the randomized values method (third method, "Null Distribution from random sample") and insert as many random pairwise distances to our matrices as they contain real language distance values. The insertion of different random values happens directly into 100 versions of the main distance matrix. This way, we generate 100 resampled versions of the tree (Fig 7).

Fig 7. Adding random values to a distance matrix

This approach enables us to infer bootstrap values from 0 to 100. This figure reflects the number of partially randomized trees (out of 100) which support a given node. Nodes which withstand all the changes in the matrices get a bootstrap value of 100. Nodes which get modified in 40 cases get a value of 60, etc. How the nodes get challenged is visible if we edit a tree inferred from a bootstrapped matrix: branches with random languages as taxa mix up with real languages and form new nodes - ideally at a higher level than the nodes which make up our correct classifications. An example is represented in Fig 8.

The bootstrap values we infer are not confidence values. They are only a stability indicator in the context in which we use them. We can interpret the value for a node only when we consider it relatively to the values of the other nodes in the same tree.

To better understand how our outgroup or random values affect the trees, we represent a part of the phylogeny where random languages are included (Fig 8). The effect is the same with random pairwise values injected into the matrix or with random languages computed together with real ones before we construct the distance matrix.

This approach enables us to infer the bootstrap values of the nodes of the original NJS tree. They tell us for each node how often it is found in the same state in the 100 resampled trees. However, observing the resampled trees, we see that they often display connections (via nodes) which are not visible in the original tree. Adding random languages values to produce resampled trees has a "cleaning" effect, clustering instable signals with the random signals. To measure the value inferred by this "cleaning effect" - and thus infer bootstrap values for the nodes which are visible only in bootstrapped

trees, we match each resampled tree with a reference and/or researched classification and get the opportunity to extract either the best values or - to reflect stability - the median values for the frequency the given node is supported in the 100 trees. This is the "Maximum Likelihood alternative" for our non sequence-data based system explain above. We show in Part II of this paper how this effect helps to improve our results and to support the search for longer-range relationships between language families.

Fig 8. Example from a raw tree: challenging Altaic connections with randomized languages

Languages for which fewer words are available

As explained in "Materials & Methods/Choice of the lexical basis", languages for which fewer words are at our disposal, especially the ones with very few known items like Phrygian, Mycenaean, Oscan, Hurrian, Safaitic, etc. bias the classification in the phylogeny: with their very few lexical items, they do not have the same exposure to chance as languages with a complete set of meanings available. We have the possibility to include such languages (some of which are not available in the ASJP database but in

other sources) in our data set, and to compare them with all other languages, even with randomized ones and to infer distances with corresponding p-values. This is done outside the phylogenetic analyses.

Results

I. Pairwise results and their interpretation

We have explained how we generate basis data for language classifications based on the consonants of a set of basic vocabulary items. To interpret the results, we have to take some time to understand them in their raw state and consider what this data is – and what it is not.

The distance values computed in single comparisons are certainly interesting for a wider audience, as people like to express any phenomenon with figures. Quantifying observations - even abstract ones - is popular. However, reducing complex phenomena to a single figure leads to approximations. With our system, each pairwise comparison of languages leads to a single value. We should neither overestimate nor underestimate it and avoid the possible confusion, which consists in considering this figure as the genetic distance value between two compared languages. The figure we infer is a distance value based on up to 33 lexical items with a certain algorithm. Of course, we have designed the choice of the items and the methods behind the distance calculations to make this data correlate as much as possible with a hypothetical genetic distance, but as with anything in nature we observe in the context of a correlation, there is a variance. If we consider a straight line between English and languages from a same subfamily, the values should all be the same – but they are not. This is due to the variance of the results.

A characteristic of a distance value in its statistical context is that it does not state whether two languages are related or not. It delivers a distance value and its p-value (in our context: the probability that the observed distance and a smaller one are due to chance). There is no judgment about relatedness. In many cases, related languages share a large distance with a very high p-value (false negatives) and unrelated languages have a relatively small distance with a very low p-value (false positives).

The distance values correlate with what we perceive as language relatedness. The question is not, whether a single result is right or wrong but how well and with which variance it correlates with language relatedness. A way to illustrate this is to consider all pairwise comparisons of English with other languages (Fig 9). If we consider these results, we see a picture, which is quite consistent with the reality we know. The nearest neighbors of English are the Germanic languages, followed by the Slavic, Roman, and other Indo-European languages. The first unrelated and random languages (red in the table) appear from distance values of about 75 and from there, they mix more and more with the most distant IE languages. From a certain value (82), no IE language appears in the list. The variance of the results is clearly visible: languages of a same language subfamily have values which are near to each other but which are not equal. When we consider the low amount of material in use, the approximations that are part of the methodology and the presence of statistical noise in quantified models based on few lexical items, we realize that the presence of a certain variance in the results is not avoidable. This variance ‘contains’ everything the system does not explain: non constant evolution rates, undetected loan words, not modeled complex process of evolution and of course, approximations and mistakes in gathering sources and encoding words. The more we know and take into account in our data, the lower the variance.

Pairwise results for use in other contexts

Using distances between languages is useful for research in numerous non-linguistic fields of science (e.g. psychology, sociology,...). Language proximity can correlate with various phenomena. There is no absolute value for language distance and any attempt to establish some - like in our system - is an approximation. However, even approximations can turn out to be useful. We publish a form for queries of all pairwise distances in the online Supporting Information S1 Appendix, which can be used in other research. The raw data is the one we use in our research. We infer also a more stable result, which averages the subfamily-wise values in pairwise comparisons to reduce the variance in medium- and long-range comparisons: for example all pairwise searches between any Germanic and any Slavic language deliver the same distance, which is the average distance between all Slavic and Germanic languages. Comparisons of languages within the same subfamily deliver the same different results as in our system. Flat files for both result sets are available in S2 Appendix.

Fig 9. Pairwise distances of English to other languages - visualization of the loose boundaries between signals and noise

English to	Dist.	English to	Dist.	English to	Dist.	English to	Dist.
E GERMANIC SCOTS	21	E NURSTANIEASTERN_KATVIRI	77	E CELTIC MANX	81	NC BANTOID JITA	83
E GERMANIC SWEDISH	34	Ura MARIMEADOW_MARI	77	TK_KAM_TAI HAWYENG_ZHUANG	77	Teb TEBERAN_FOLOPA	83
E GERMANIC OLD_FRISIAN	34	E CELTIC CORNISH	77	Esu NUBIAN MEDOB_NUBIAN	77	An CELEBIC WAWONI_MENUI	83
E GERMANIC WEST_GERMANIC	35	E ST DIMALA DIMALA	77	Aua MUNDA AVESTA	77	Om PANONIAN_HIAFANO	83
E GERMANIC DUTCH	35	E IRANIAN SARKOLI	77	Alt TURKIC_TUVAN	77	ST_KUKI_CHN_NAGA_TANGKHUL	83
E GERMANIC OLD_ENGLISH	37	E IRANIAN PERSIAN	77	An CENTRAL_MALAYO_POLYNESIA	77	Arw NORTHERN_ARAWAKAN_BAR	83
E GERMANIC NORTHERN_LOW_SAXON	37	E ROMANCE JUDEO_ESPAGNOL	77	ST_TANLINJI	77	NC CROSS_RIVER OKOBO	83
E GERMANIC AFRIKAANS	37	E INDIC MALDIVAN	77	E INDIC PAMIA_NYUNGAN_THAYORE	77	Alt TURKIC UDEHE	83
E GERMANIC STELLINGWERFS	38	E TOCHARIAN_TOCHARIAN_B	77	ST DIGARON_IDU_MISHMI	77	UA NUMIC COMANCHE	83
E GERMANIC NORWEGIAN_BOKMAAL	39	Esu DAJU_NYALGULGULE	77	TK_KAM_TAI BLACK_TAI_2	77	15/1 Unrelated languages < >	
E GERMANIC NORTH_FRISIAN_AMRUM	41	NC_KWA_AHLO	77	Alt TUNGUSIC MANCHU	77	Tup TUPI GUARANI_TAPIRAPE	95
E GERMANIC OLD_SAXON	42	E ARMENIAN_EASTERN_ARMENIAN	78	Ura SAAMI SKOLT_SAAMI	78	Dra NORTHERN_DRAVIDIAN_KURUX	95
E GERMANIC OLD_HIGH_GERMAN	42	AA LOWLAND_EAST_CUSHITIC DAASANA	78	An CELEBIC TOTOLI	78	Om KKHOO_KIYADI_GXANA	95
E GERMANIC FRISIAN_WESTERN	42	NC BANTOID_POIMO	78	Alt TURKIC BASHKIR	78	Om MIXTECAN MIXTECO_DE_YOSON	95
E GERMANIC STANDARD_GERMAN	43	An BILIC_TIRURAY	78	TK_KAM_TAI WANGMOU_BOUYEI	78	Com COMECRUDEAN COMECRUDEO	95
E GERMANIC YIDDISH_WESTERN	43	TK_KAM_TAI ZHUANG_NORTHERN	78	E INDIC SNTL_ROMANI	81	NC BANTOID_BAKURI	95
E GERMANIC ZEEUWS	44	E INDIC CHAKMA_UnnamedInSource	78	Alt TURKIC SAKHA	78	NC BANTOID_HEHE	95
E GERMANIC LIMBURGISH	46	Nah NAHALI_NHALI	78	NC BANTOID_DING	78	Aus PAMIA_NYUNGAN_YIR_YORON	95
E GERMANIC YIDDISH_EASTERN	46	An NORTHWEST_FORMOSAN_PAZEH	78	NC CROSS_RIVER_UDA	81	Om ZAPOTECAN_ZAPOTEC_LOXICH	95
E GERMANIC OLD_NORSE	46	E INDIC NAWAR_ZUTT	78	Tuc TUCANIAN_DREJON	78	Alg ALGONQUIAN_KICKAPOO	95
E GERMANIC LUXEMBOURGISH	48	E IRANIAN_AVESTAN	78	An CELEBIC KUMBAWANA	81	Om POPOLOCAN_POPOLOCA_SAN	95
E GERMANIC SAXON_UPPER	48	Aua MUNDA_ABRPARA_MAHALI	78	NC CROSS_RIVER_ANAANG	82	Pen TSMISHIANIC_COAST_TSMISHIA	95
E GERMANIC DANISH	49	Aua MUNDA_PAHARPUR_SANTALI	78	TK_HLAI_BAODING_HLAI	78	Aus DJERAGAN_KITJA	95
E GERMANIC FAROESE	49	Alt TURKIC_TOFA	78	An GREATER_CENTRAL_PHILIPPINE	82	Que QUECHUAN_QUICHUA_CANYAR	95
E GERMANIC CELANDIC	50	E INDIC HALBIHONG_TAI_LUE_2	78	E INDIC SAGE	82	Om MIXTECAN SANAPANANA_ENLHE	95
E GERMANIC PLAUTDIETSCHE	50	E CELTIC IRISH_GAELIC	78	NC NORTHERN_ATLANTIC_BALANTA	78	NC BANTOID_CHINGONI	95
E GERMANIC BERNESE_GERMAN	51	E BALTIC LITHUANIAN	78	MZ MIXE_ZOQUE_CHIAPAS_ZOQUE	82	An OCEANIC EMARE	95
E GERMANIC EASTERN_FRISIAN	52	E IRANIAN_NORTHERN_PASHTO	78	Son SONGHAY_ZARMA	78	Car CARIBAN_TIRYO	95
E GERMANIC SWABIAN	52	Aua MUNDA_ABRPARA_MAHALI	78	Aus PAMIA_MON	78	Om MIXTECAN HALMAHERAN_SAHU	95
E GERMANIC GOTHIC	56	An SOUTH_SULAWESI_BUGINESE	78	AA SOUTH_OMOTIC_BANNA	82	WP NORTHERN_HALMAHERAN_SAHU	95
E ROMANCE FRENCH	64	E IRANIAN_BALUCHI_WESTERN	78	E BALTIC_OLD_PRUSSIAN	82	Aus WEST_BARKLY_WAMBAYA	95
E ROMANCE PIEMONTESE_BARBANIA	65	NC BANTOID_DONG	78	Son SONGHAY_KOYRA_CHINI	78	Om POPOLOCAN_ICATEC	95
E ROMANCE CATALAN	66	Son SONGHAY_KOROBORO_SENNI	78	E INDIC MONIC	82	Om ZAPOTECAN SAN_PEDRO_QUJA	95
E SLAVIC RUSSIAN	66	Om PAMEAN_PAME_DE_JILAPAN_1958	79	E INDIC MARATHI	82	Krd TEGEM_TEGEM	95
E ROMANCE LIGURIAN_GENOESE	67	AA EAST_CHADIC_BIDIYA	79	Chi KUNA_KUNA_YALA_SAN_BLAS	82	Esu NARA_NARA	95
E ROMANCE LOMBARD_BERGAMO	67	Nda LEZGIC_BUDUKH	79	ST BOIC_MANAINGE	82	An OCEANIC NORTH_AMBRYM_FON	95
E ROMANCE ITALIAN_GROSSETO_TUSCA	67	AA SEMITIC SYRIAC_2	79	Aua BAHNIG_SITENG	82	Tup TUPI GUARANI_TUPARI	95
E ROMANCE BALEARC_CATALAN	68	AA BERBER_ZENAGA_2	79	TK_KAM_TAI LAMPANG_THAI	82	Om ZAPOTECAN QUIOQUITANI_QUE	95
E SLAVIC BELARUSIAN	68	E INDIC URDU	79	ST NUNGISH_RAWANG	82	An MALAYO_SUMBAWAN_INDONES	95
E ROMANCE ROMANIAN_RAVENATE	68	SaI TILLAMOOK_TILLAMOOK	79	Esu NILOTIC_SAMPUR	82	An MALAYO_SUMBAWAN_MALAY	95
E ROMANCE ITALIAN	68	E INDIC KASHMIRI	79	Dra NORTHERN_DRAVIDIAN_BRAHU	82	NC CROSS_RIVER_DONGO	95
E ROMANCE SICILIAN	68	E ROMANCE PORTUGUESE	79	AA SEMITIC_MODERN_MANDAIC	82	TNG ANGAN_MENYA_2	95
E ROMANCE GASCON	68	E INDIC BENGALI	79	TK_KAM_TAI WUMING_ZHUANG	82	Om ZAPOTECAN SANTA_INES_YAT	95
E ROMANCE VALENCIAN	69	Alt TUNGUSIC_XIBE	79	Aua PALAUNG_KHMUIC_MANG	82	Sep YELLOW_RIVER_NAMIA	95
E SLAVIC UKRAINIAN	69	NC SOUTHERN_ATLANTIC_EAST_LIMBA	79	Hua HUAVEAN_HUAVE_2	82	An ATAYALALAYAYAL	95
E ROMANCE SARDINIAN_CAMPIDANESE	70	E INDIC FINISH_ROMANI	79	Cam CAISA_KAISA	82	E ELEMAN_PROPER_OPAO	95
E INDIC DAMELI_2	70	NC BUAGO_BUAGO	79	NC CROSS_RIVER_EBUGHU	82	Tup TUPI GUARANI_PARAKANA	95
E ROMANCE ROMANIAN_MEGLENO	70	Alt TUNGUSIC_EVEN	79	NC CROSS_RIVER_TUMBUSO	82	Jab JABUTARIKAPU	95
E ROMANCE FRIULIAN	70	Aua MUNDA_HO	79	E BALTIC_CATVIAN	82	Tu TU_HNG_KS	95
E INDIC USHOLU	70	E INDIC TAIJIHONG_TAI_LUE_2	79	NC NORTHERN_ATLANTIC_NALU	82	Alg ALGONQUIAN_ZAPOTEC_MIXTEPE	95
E ROMANCE ROMANSH_VALLADER	70	E INDIC WELSH_ROMANI	79	NC SOUTHERN_ATLANTIC_BAGA_M	82	Alg ALGONQUIAN UNAMI_Unnamed	95
E ROMANCE NEAPOLITAN_CALABRESE	71	E ARMENIAN_WESTERN_ARMENIAN	79	Kad KADUGILI_KATCHA	82	KK KKHOO_KIYADI_KXOOE	95
E ROMANCE NONES_GARDENESE	71	An CELEBIC MORI_ATA5	79	Ura MORDVIN_ERZYA	82	Ele ELEMAN_PROPER_AHEAVE	95
E ANATOLIAN_HITTITE	71	NC NORTHERN_LIJON_YOGAD	79	Esu NUBIAN_NUBIAN_OF_DONGOLA	82	Om MIXTECAN MASA_SARWA_TATI	95
E SLAVIC BULGARIAN	71	TK_KAM_TAI KAM_ZHANGLU	80	Esu NILOTIC_DONGOTONO	82	Aus PAMIA_NYUNGAN_PINTURI	96
E ROMANCE ASTURIAN	71	ST NUNGISH_DRUNG	80	Esu NUBIAN_UNCUNWEE	82	TNG FINISTERRE_HUON_NUKNA	96
E CELTIC BRETON	71	Son SONGHAY_DENDI	80	Ura FINNIC_ESTONIAN	82	An OCEANIC_BUKAUA	96
E SLAVIC CZECH	71	E INDIC GUJARATI	80	ST MAHAKRANTI_PUMA	82	Om ZAPOTECAN ISTHMIUS_ZAPOTEC	96
E ROMANCE CORSICAN	71	Ura FINNIC_KARELIAN	80	An CELEBIC KODEOHA	82	Om SUBTABA_TLAPANECTLACO	96
E SLAVIC CROATIAN	72	Mat MATACOAN_WICHI_LHAMTES_GUISNA	80	AA SEMITIC_AKKADIAN	82	TNG CHIMBU_NARAK	96
E IRANIAN KURDISH_KURMANJI	72	Pen MWOK_MWOK_LAKE	80	Alt TURKIC_NOGAI	82	Tup TUPARI_TUPARI	96
E SLAVIC SLOVAK	72	E NURSTANIEASTERN_KATVIRI	80	NC AKPES_SHEKANI	82	NC HIGHLAND_EAST_CUSHITIC_HAE	96
E ROMANCE EMLIANO_REGGIANO	72	E INDIC LOVARA_ROMANI	80	TK_KAM_TAI TAI DAENG	82	Gum GUMUZ_DISOHA	96
E INDIC BROK_SKAD	72	E TOCHARIAN_TOCHARIAN_A	80	MZ MIXE_ZOQUE_SAYULA_POPOLU	82	An OCEANIC_NAMAKURA_BONGAB	96
E SLAVIC SERBOCROATIAN	72	ST KAREN_KAREN_GEBA	80	AA SEMITIC_DELLYS	82	An OCEANIC_SOUTH_EFATE_ERAKO	96
E IRANIAN TAJIK	72	TK_KAM_TAI DONGYU_LINGAO	80	An CELEBIC_DORONI	82	Sep KKA_JURU	96
E SLAVIC POLISH	72	Hm HMONG_MEN_DAPINGJIANG_MEN	80	Mab MABAN_KIBET	82	TNG ANGAN_AMPALE	96
E ROMANCE DALMATIAN	73	ST BURMESE_LOLO_XIANDAO	80	Ura UGRIC_MANSI	82	Sto SERRA_HILLS_POKO_RAWO	96
E IRANIAN SHUGHNI	73	Chq CHIQUITO_CHIQUITANO	80	An CELEBIC_TALOKI	82	NC KANJIGUITA	96
E SLAVIC SLOVENIAN	73	ST BOIC_TAIANG	80	ST BOIC_GARRO_DEURI	82	KK KKHOO_KIYADI_GWI	96
E IRANIAN EASTERN_FARSI	73	NC CROSS_RIVER_BIBIO_2	80	TK_KAM_TAI TAY	82	Om MIXTECAN_CUICATEC	96
E ROMANCE GALICIAN	73	ST KAREN_KAREN_SGAU	80	Aua KHASIAN_PNIAR_JOWAI	82	An MALAYO_SUMBAWAN_JAMBLM	96
E INDIC LAMANI	73	TK_KAM_TAI MENGJIAN_TAI	80	ST MAHAKRANTI_KHAMI	82	NC BANTOID_LINGALA	96
E IRANIAN BALUCHI_EASTERN	73	NC CROSS_RIVER_EFAI	80	TK_KAM_TAI TAL KHUEN	82	Aua PALAUNG_KHMUIC_BUMANG	96
E ROMANCE ROMANIAN	74	AA BIU_MANDARA_MAKARY_KOTOKO	80	An CELEBIC_TOLAKI_ASERA	82	Tup TUPI GUARANI_URUEWAWAU	96
E IRANIAN JUDEO_TAT_2	74	NC_KWA_ANMERE	80	Arw NORTHERN_ARAWAKAN_ISLA	82	Esu NILOTIC_NUER	97
E ROMANCE ARAGONESE	74	TK_KAM_TAI TAYANG_ALCHAM_2	80	NC IGBO_IGBO_ONITSHA	82	NC IGBO_IGBO_ONITSHA	97
E SLAVIC UPPER_SORBIAN	74	St SIOUTAN_DAKOTA	80	NC GUR_MAMARA_SENOUFO	82	Om SUBTABA_TLAPANECTEOCUIT	97
E ROMANCE LATIN	74	An MALAYO_SUMBAWAN_CHAM_WESTER	80	NC KRU_KLAO	82	Tup TUPI GUARANI_AMONDABA	97
E CELTIC OLD_IRISH	74	Mat MATACOAN_WICHI_LHAMTES_VEJOZ	80	Sio SIOUTAN_OSAGE	82	Mas MASO_GUAN SANAPANANA_ANGA	97
E INDIC SANSKRIT	74	An CELEBIC_WOTU	80	AA SEMITIC_ASSYRIAN_NEO_ARAM	82	Har HARAKIMIBET_AMARAKAERI	97
E SLAVIC OLD_CHURCH_SLAVONIC	74	E INDIC VAGRI_BOLI	80	NC CROSS_RIVER_ORO	82	AA WEST_CHADIC_BADE	97
E SLAVIC MACEDONIAN	74	ST MAHAKRANTI_CHEPANG	80	AA SOUTHERN_CUSHITIC_IRAQW	82	Sep RAM_AWTUWI	97
ST_TANLASHING	75	NC CROSS_RIVER_ENWANG	81	Aua KHASIAN_KHASI	82	Kun KUNZA_KUNZA	97
E INDIC PALI	75	E ALBANIAN_ALBANIAN_GHEG	81	NC CROSS_RIVER_ETEBI	82	AA HIGHLAND_EAST_CUSHITIC_SID	97
E INDIC HINDI	75	ST JINGHPRO_JINGPHO	81	Aua PALAUNG_KHMUIC_U	82	Om MIXTECAN_TRIGUI_COPALA	97
E ROMANCE SARDINIAN_LOGUDARESE	75	E INDIC PUNJABI_MAJHI	81	An OCEANIC_SOUTH_EFATE_ERAKO	82	NC CROSS_RIVER_ETEBI	97
E SLAVIC LOWER_SORBIAN	75	Teb TEBERAN_DARBI	81	An CELEBIC_PADOE	82	Tu TU_KAM_KA_KE	97
E IRANIAN TALYSH	75	AA SEMITIC_HARSUSI	81	An CELEBIC_TUKANG_BESI_NORTHE	82	NC PLATOID_NDUN	97
E ROMANCE SPANISH	75	Kom KOMAN_GVAMA	81	NC PLATOID_AKE	82	Kw KWAJIAN_KEREWU	97
E GREEK GREEK_ANCIENT	76	An SOUTH_HALMAHERA_WEST_NEW_GU	81	An OCEANIC_SOUTH_EFATE_ERAKO	82	TNG ANGAN_KAPAU	98
Alt MONGOLIC_MOGHOL	76	Alt TURKIC_UBZBEK	81	AA SEMITIC_HOBYOT	82	GA GREAT_ANDAMANESE_SOUTH	98
E GREEK GREEK	76	Hm HMONG_MEN_DAPING_MIEN	81	NC BANTOID_KILUBA	82	Tup TUPI GUARANI_PARINTINTIN	98
E CELTIC WELSH	76	Aua PALAUNG_KHMUIC_BIT	81	Alt TUNGUSIC_ULCHA	82	Nam NAMBIKURAN_SABANE	98
E INDIC SHINA_2	76	ST BOIC_EASTERN_BALTI	81	An CENTRAL_MALAYO_POLYNESIA	82	AA LOWLAND_EAST_CUSHITIC_GAI	98
E INDIC ORIYA	77	E INDIC NEPALI	81	Man WESTERN_MANDE_YALUNKA	82	TNG EASTERN_HIGHLANDS_YATE	98
E ROMANCE VLACH	77	MGe KARAJA_KARAJA	81	Krt KARTVELIAN_LAZ	82	TNG EASTERN_HIGHLANDS_AUYAN	98
Aus WEST_BARKLY_DJINGILI	77	Ura UGRIC_HUNGARIAN	81	Ura FINNIC_ESTONIAN_VORO	82	An OCEANIC_PIU	100

The non-averaged pairwise results come along with a p-value. In the interpretation of these p-values we have to be aware that we use more than 1.962 languages in the system. So finding a supposed distant relationship in the data, with a p-value lower than 0.01 is commonplace and not a proof for the discovery of an unknown relatedness. The p-value is a help in the interpretation, not a judgment validation. When computing multiple comparisons the odds of rare events increase, wrongly rejecting a null hypothesis.

II. Inferred classifications: results and benchmark

We deliver a worldwide classification we make available in the online Supporting Information S5 File. Fig 10 shows a subset with the Uralic languages as an example.

Fig 10. Example of an inferred classification: Uralic

Browsing the global phylogenetic tree can be somewhat difficult to get a global overview so we also present the results in the form of a benchmark with existing classifications.

Choosing and handling reference classification to benchmark the results

We choose WALS [34], Glottolog [26] and Etnologue [35] as expert based reference classifications and Gerhard Jäger [5]’s world tree as the – to our knowledge - best computer inferred global classification available so far. Reference classifications are evolving overtime. New knowledge and research output gets included constantly. As the authors of Glottolog themselves state “the classifications are subject to change as scholarship and interest in [those] languages increases” [36]. Measuring how reference classifications differ from each other is important to make transparent what a target performance for an automatic system can be: they do not agree completely with each other, so it is impossible to reach 100% agreement with each of them: “*Debate on language history is never free of disagreement among scholars*” [37]. An ideal automated classification will differ from the human based ones in a way, we cannot draw the difference which one is expert based and which one is computer based (similar agreement rate). We may need time to reach this level but measuring how near we are to it is a good orientation.

We use the Geiger [38] and Phangion [39] packages in R [30] to perform phylogenies and comparisons between/within phylogenies. Since we do not use all languages as available in all classifications, and the availability of languages differs in the different sources as well, we reduce all reference trees to the languages available in our data, common to all other sources. To make computing across several references possible, we choose to use the same language name codification as Gerhard Jäger [40]: “[WALS Family].[WALS genus].[ASJP doculect]”, using ISO 639-3 to link them.

Measuring and benchmarking performance

We infer three indicators to measure how well our tree matches the references:

- Score 1: a score representing the proportion of languages of a family or subfamily, which are member of the biggest cluster inferred for that family. For instance, if a

cluster with two thirds of the languages of a family is inferred by the tree, score 1 is 0.667 for that family. If all languages are in the inferred cluster, the score is 1. In practice, the result can split the family in several clusters. We choose to keep the value of the largest one to reflect the performance and make no difference whether the remaining languages are all gathered in a second cluster or scattered throughout the rest of the phylogeny. This value has the disadvantage that a good score for a small family (e.g. two members) has the same impact on the final result as the score of a large top-level family (TLF). So we use this score to infer Score 2, which we finally use in our assessment.

- Score 2: number of languages properly clustered in the biggest inferred cluster (Score 1 multiplied by the number of languages of the observed family). This value is derived from score 1 and eliminates the bias that big families are equally weighted as small ones in the assessment. Table 3 shows a subset of results for score 1 score 2 for a better understanding how these two scores are inferred.
- Score 3: the quartet agreement rate, derived from the quartet distance, which is defined as the number of subsets of four leaves that are not related by the same topology in the compared trees. These values, derived from the quartet divergence (Smith 2019a [41]) were calculated using the tqDist algorithm (Sand et al. 2014 [42]) implemented in the R package Quartet v1.1.0 (Smith 2019b [43]).

We have developed scripts, which allow to compare how classifications match each other and hence to measure the performance of a given classification against a reference. Table 3 shows a subset of results for score 1 and score 2. We implement the quartet agreement rate only for top-level families with at least 10 members, as the method delivers better results for the numerous smaller trees and bias the score wrongly positively.

Table 3. Example (subset) of benchmark of our results with Glottolog

Family	Size	Score 1	Score 2
Indo-European	135	1	135
Eastern Baltic	2	1	2
Slavic	14	1	14
East Slavic	3	0.667	2
South Slavic	6	0.5	3
Eastern South Slavic	3	0.667	2
Macedo-Bulgarian	2	1	2
Western South Slavic	3	1	3
Serbian-Croatian-Bosnian	2	1	2
West Slavic	5	0.6	3
Czech-Slovak	2	1	2
Sorbian	2	1	2
Insular Celtic	7	1	7
Brythonic	3	1	3
Southwestern Brythonic	2	1	2
Goidelic	4	1	4
Total	212	15.4	203
Percentage	100%	90.7%	96.7%

Table 4 gives an overview how Glottolog and Ethnologue match with each other and with the WALS classification, as well as how Jäger [5]’s NJS tree and our own NJS

results match with WALS, Glottolog and Ethnologue. These reference classifications have different granularities: the WALS classification delivers the top-level families, as well as a first level of subfamilies ("WALS Genus"). Glottolog and Ethnologue also have these levels of classification but also deeper ones. As mentioned above, these results we display are based exclusively on languages, which are common to all these classifications. The detail results are available in the online Supporting Information S4 File. The reference electronic version (Nexus) of the trees for WALS and Glottolog are taken from Jäger, G. [40]. The reference Nexus tree for Ethnologue is from Dediu, D. [44]

Table 4. Benchmark between classifications ('Score 2' clustered languages)

	WALS [34] TLF	WALS Genus	Glottolog [26]	Ethnologue [35]
Glottolog	93.1%	96.5%	100%	84.9%
Ethnologue	91.8%	95.2%	82.9%	100%
Jäger's NJS tree	82.8%	84.7%	61.8%	70.4%
Our NJS tree	78.0%	81.5%	59.3%	67.4%

Table 5. Benchmark between classifications (weighted agreement rates)

	WALS [34] TLF	Glottolog [26]	Ethnologue [35]
Glottolog [26]	0.993	1	0.868
Ethnologue [35]	0.869	0.868	1
Jäger [5]'s NJS tree	0.635	0.634	0.630
Our NJS tree	0.631	0.629	0.624

The high granularity of the Glottolog and Ethnologue classifications leaves room for discussions on some families. This explains the lower agreement rate between these two families, at least on their whole scope: their respective agreement rates on less granular WALS TLF and WALS Genus is much higher.

Results and time depth – limit of tree-like patterns reflected in performance

In our and Jäger's results, the performance of the computer-inferred classifications gets lower when the time range of the classifications gets shorter (Glottolog/Ethnologue, containing classifications within subfamilies, versus WALS containing only TLF and subfamily classifications). The biggest differences are found in the subfamilies. One of the reasons lies in the limitation of the tree-like patterns, which is a practical, but oversimplified mean of representing language evolution [45]. The biases the tree model carries is much higher in the short-range than in medium- and long-range classifications.

Our results performance represented on world maps

Our results' performance is not equal in all world areas: the performance is better in well documented language families, Eurasia delivering more stable results (Fig 11). This trend is visible more in details in the result table in the online Supporting Information S4 File. The fact that our system - but also other computer-based ones - best matches well documented families like Indo-European or Uralic shows that the major impact on results is data-quality. Data quality has a high impact on computer based classifications' performance.

Fig 11. Our results' performance (WALS genus contains all its members) on the world map

Visualizing and exploring results

The results in the form of one phylogenetic tree with 1962 languages, as inferred in our supporting information S5 File - is difficult to use in practice. The search for interesting findings is more accessible if we limit the representation to medium- and long-range results. As explained, our methodology is not designed for short-range classification and the variance of the results has its biggest impact here. The global tree contains all languages and inferred short-, medium- and long-range connections and is the reference when it comes to check the detail results. However targeting result exploration to medium- and long-range needs more proceedings. We address both in the next two sections.

III. Subfamilies: Exploring the internal classification of top-level language families

The inferred internal classifications of all top-level families with at least 3 subfamilies is available in the supporting information S6 File. In Fig 12 and 13, we display the internal classifications of the Indo-European and Afroasiatic top-level families.

Interpreting the results

Among scholars, the internal classification of subfamilies leads to much more agreement about the content of the clusters (which language belongs to which subfamily) than in how these subfamilies classify within the top-level family trees (the order in which they split). The reference classifications let the subfamilies connect directly to the root whenever the consensus among scholars about specific internal splits is low. Hypotheses about how subfamilies link with each other are numerous and there is no complete agreement even for well-documented families.

Fig 12. The internal classification and node stability of Indo-European as inferred by our system vs. conservative consensus

For Indo-European, the reference classifications [26] [35] record only two connected sub-groups: Baltic with Slavic and Indo-Aryan with Iranian, connecting these two and all other subfamilies directly to the root of Indo-European. We know that the Indo-European subfamilies did not split in separate directions at once. In which order the splits happened is subject to debate since almost 200 years [46]. This debate is of great relevance when it comes to linking linguistic data with findings from genetics and archeology. Analyzing our Indo-European tree of subfamilies (Fig 12), we get an quantitative answer to this question: Romance, Germanic, Celtic and Balto-Slavic form a cluster. As already widely accepted, Indo-Aryan, Iranian and Nuristani form a second cluster. These two clusters, form a next level group and Anatolian, Tocharian, Armenian, Albanian and Greek are outliers. Our data suggests that Anatolian and Tocharian separated first and the rest of the Indo-European family formed a common stock. The way Albanian, Armenian and Greek separated is not visible in our data but they did so before the next stock separated in two directions: Indo-Iranian and Italic-Germanic-Balto-Slavic and Celtic with the further splits leading to the subfamilies as we know them today. If we match these results with the raw tree with all languages (supporting information S5 File) the position of the IE Subfamilies with few elements (Anatolian, Tocharian, Greek, Armenian) slightly differs. Keeping the common, stable results across the two methods confirms the two big clusters "Iranian-Indo-Aryan-Nuristani" on the one side and "Celtic-Romance-Germanic-Balto-Slavic" on the other side.

The Afroasiatic tree is a similar challenge. Our system delivers results (Fig 13) which support existing views [47]. Dizoid and Omotic form a distant subgroup, with

strong bootstrap support. Chadic is positioned in a long-range subgroup together with Semitic and Berber. South Omotic, which is considered as a own top-level family by Glottolog is an outgroup in our tree and is not directly linked to North Omotic. The strong link between East-Chadic and Berber is certainly a misclassification in our tree.

Fig 13. The internal classification of Afroasiatic as inferred by our system

This analysis starts with the WALS Genus classification as constraint. This means that if some WALS subfamilies are regarded as disputed, a separate analysis with the diverging subfamily hypotheses should be carried out. The "strong" and "moderate" status of the nodes refer to the bootstrap support.

IV. Exploring long-range and disputed classifications

Exploring long-range language relationships out of the darkness of prehistoric times is a difficult path: the fascination it awakes should not overshadow the necessity to be very cautious when it comes to interpret signals inferred by various research. Reference classifications are very conservative when it comes to including new findings. It is their role to reflect results supported only by strong evidence and a wide consensus among the comparative linguists. In some cases, results diverge between the three references. The WALS classification includes top-level families, which are not supported by the other two references (Altaic, Hoka, Oregon Coast, Penutian). There is an abundance of hypotheses linking language families still pending recognition by reference classifications, even after decades of research. Some are regarded as highly speculative, other already have a broad support but still fail to meet the criteria needed for their inclusion. There are two main reasons for the doubts:

1. The lack of proof in form of regular sound correspondences and proto-languages reconstructions, which are the established methods to identify language families. With deeper time ranges, these methods become more difficult to apply, as the underlying data loses the signals with increasing erosion.

2. The identification of weaker but “visually” convincing signals makes out the bulk of supposed evidence for long-range connections. Such signals are controversial, because of the high probability that this evidence is simply due to chance.

Our system addresses the second issue and aims at using both signals and noise (chance resemblance) as the basis of the analysis, instead of focussing on the signals alone. We do so in two different ways: analysis of the phylogenies and meta analysis of p-values, which we explained in “Materials and methods” §V and §VI.

The signals and the noise in the phylogenies

Relatedness signals between macrofamilies are visible in the trees. However, the clues for long-range connections we get from raw trees have to be interpreted with great caution: in a rooted phylogeny, any top-level family necessarily links to some other – the branches *have* to find a place in the tree, even when the values linking them have to do with chance and not with relatedness. Using the bootstrapping technique explained earlier, we can track the stability of branches. If we consider only connections between top-level families, which the system infers in a block in our world tree (online Supporting Information S5 File) we find a very limited amount of stable TLF to TLF connections. We list them in table 6. Interestingly, all of them but one are part of existing long-range hypotheses, not yet accepted by the reference classifications.

Table 6. TLF pairs’ phylogenetic support (worldwide tree see online Supp. Inf. S5 File)

TLF 1	TLF 2	Hypothesis	Bootstrap value
Quechuan (Que)	Aymaran (Aym)	Quechumaran [48] [49]	100
Tacanan (Tac)	Panoan (Pan)	Pano-Tacanan [50]	100
Indo-European (IE.)	Altaic (Alt)	Eurasiatic [18]	100
Altaic (Alt)	Uralic (Ura)	Eurasiatic [18]	100
Austroasiatic (AuA)	Hmong-Mien (HM.)	Yangzian (Austic) [51]	100
Matacoan (Mat)	Guaicuruan (Gcu)	Mataco–Guaicuru [52]	100
Totonacan (Tot)	Mixe-Zoque (MZ.)	Totozoquean [53]	50
Indo-European (IE.)	Uralic (Ura)	Eurasiatic [18]	100
West Papuan (WP.)	Timor–Alor–Pantar (TAP)	No	100
Nakh-Daghestanian (NDa)	Northwest Caucasian (NWC)	North Caucasian [54]	6

The signals and the noise in the meta analysis of p-values: Pairwise TLF results and their clusters: We apply harmonic mean p-value analysis to all possible pairwise comparisons between WALS top-level families and display the results (14368 pairwise TLF results excluding the results between the same TLFs) in the online Supporting Information S7 File. The use of harmonic mean p-values leaves only 16 observations out of 14368 with $p < 0.0001$. With the table in the online Supporting Information S7 File, we reach the core of the analysis of our results in the context of signals and noise. The table delivers connections between TLF with low p-values, most of which are clearly due to chance. How do we differentiate signal and noise? The four results with extremely low p-values are very clear. The other lower results are a mixture of members of existing hypotheses and members of completely unrelated connections. When we analyze hypotheses, which consist of only one pair of TLF, the differentiation between signals and noise is not possible. The contemplation of a pairwise result in the context of neighbouring unrelated results can be useful to evaluate how low a TLF pair is, for which a hypothesis exists.

When we consider clusters of more than 2 TLFs, we become far less signals, but they become easier to differentiate from noise. We inferred all the 3- and 4-members clusters

with TLF to TLF connections supported by $p < 0.002$ and displayed them in the "Long-range clusters" tab of the online Supporting Information S7 File. Out of 791,489 potential clusters with three members, only 45 fulfill this condition. Out of these 45 clusters, we can form only 5 four-members clusters with all mutual connections with $p < 0.002$. Another list of 6 clusters with more than 3 members can be listed from the 45 three-members cluster list, if we accept the p-values of their remaining connections with $p > 0.002$. Ranking these 11 clusters by their p-values, we get two Nostratic and one Austric clusters in the top 5 list (details in the online Supporting Information S7 File, "Long-range clusters" tab).

Analyzing results:

In the pairwise TLF to TLF results of the online Supporting Information S7 File, four TLF relationships outside the WALS reference deliver a very clear result: Quechuan to Aymaran, Panoan to Tacanan, Mande to Niger-Congo and Indo-European to Altaic, all of which are part of existing long-range hypotheses. The other long-range hypotheses we address are among the pairwise TLF comparisons with the lowest harmonic mean p-values, but share their positions with clearly unrelated TLF pairs. This does leave us within the range of "the signals and the noise" dilemma but delivers at least strong clues, which can be combined with other facts in the discussion. We analyze some of the long-range hypotheses our system unveils both in the bootstrap analysis of the inferred phylogeny and the harmonic mean p-values analysis.

Eurasiatic [19] and Nostratic [17] [18] [20]

Eurasiatic and Nostratic form a fascinating but also highly controversial hypothesis. As a member of Nostratic, Eurasiatic typically includes Indo-European, Uralic, Altaic, Eskimo-Aleut and Chukotko-Kamchatkan, with variations by different authors. Nostratic is a wider family, also with variations by various authors, with Eurasiatic, Dravidian, Kartvelian, Koreanic, Japonic and Afroasiatic as core members. Our system has a very clear support both in the phylogeny/bootstrap and in the p-value analysis for a core part of Eurasiatic: Indo-European, Uralic and Altaic proper (Turkic, Mongolic, Tungusic). No signal is visible for an inclusion of Eskimo-Aleut and Chukotko-Kamchatkan in Eurasiatic. Koreanic and Japonic, which are included in Altaic, Eurasiatic or Nostratic by some authors do not display any signal in this direction in our system. Beside the clear support for a core version of Eurasiatic, the p-value analysis supports two other members of the Nostratic family: Afroasiatic and Kartvelian, the later also with a noisy support (bootstrap value 44) in the phylogeny. Fig.14 shows the p-value analysis values for these connections.

Table 7. TLF pairs' support by HM p-values (complete list see online Supp. Inf. S7 File)

TLF 1	TLF 2	Hypothesis	HM p-value	Rank
Quechuan (Que)	Aymaran (Aym)	Quechumaran [48] [49]	< 0.000001	1/14368
Tacanan (Tac)	Panoan (Pan)	Pano-Tacanan [50]	< 0.000001	2/14368
Indo-European (IE.)	Altaic (Alt)	Eurasiatic (Nostratic) [18]	< 0.000001	3/14368
Niger-Congo (NC.)	Mande (Man)	Blench, Dwyer. Vydrin [55]	< 0.000001	4/14368
West Bomberai (WBm)	Trans-New Guinea (TNG)	Usher (2020) [56]	0.000022	7/14368
Mayan (May)	Mixe-Zoque (MZ.)	Mora-Marín (2005)	0.000106	14/14368
Salishan (Sal)	Iroquoian (Iro)	Almosan-Keresiouan [57]	0.000127	19/14368
Austronesian (An.)	Tai-Kadai (TK.)	Austro-Tai (Austric) [51]	0.000157	24/14368
Austroasiatic (AuA)	Austronesian (An.)	Austric [51]	0.000186	25/14368
Tai-Kadai (TK.)	Hmong-Mien (HM.)	Austric [51]	0.000349	41/14368
Afroasiatic (AA.)	Uralic (Ura)	Nostratic [20]	0.000355	42/14368
Altaic (Alt)	Kartvelian (Krt)	Nostratic [20]	0.000389	47/14368
Wakashan (Wak)	Salishan (Sal)	Almosan-Keresiouan [57]	0.000468	55/14368
Afroasiatic (AA.)	Altaic (Alt)	Nostratic [20]	0.000492	57/14368
West Bomberai (WBm)	Timor-Alor-Pantar (TAP)	Usher (2020) [57]	0.000497	58/14368
Altaic (Alt)	Uralic (Ura)	Eurasiatic (Nostratic) [18]	0.000506	59/14368
Austroasiatic (AuA)	Hmong-Mien (HM.)	Yangzian (Austric) [51]	0.000553	65/14368
Matacoan (Mat)	Guaicuruan (Gcu)	Mataco-Guaicuru [52]	0.000554	66/14368
Trans-New Guinea (TNG)	Timor-Alor-Pantar (TAP)	Usher (2020) [57]	0.000619	72/14368
Totonacan (Tot)	Mixe-Zoque (MZ.)	Totozoquean [53]	0.000813	89/14368
Algonquian (Alg)	Salishan (Sal)	Almosan-Keresiouan [57]	0.000828	90/14368
Indo-European (IE.)	Uralic (Ura)	Eurasiatic (Nostratic) [18]	0.000846	92/14368
Indo-European (IE.)	Afroasiatic (AA.)	Nostratic [20]	0.001144	116/14368
Wakashan (Wak)	Iroquoian (Iro)	Almosan-Keresiouan [57]	0.001179	118/14368
Afroasiatic (AA.)	Kartvelian (Krt)	Nostratic [20]	0.001268	125/14368
Algonquian (Alg)	Iroquoian (Iro)	Almosan-Keresiouan [57]	0.001558	146/14368
Austroasiatic (AuA)	Tai-Kadai (TK.)	Austric [51]	0.001559	147/14368
Kartvelian (Krt)	Dravidian (Dra)	Nostratic [20]	0.002094	183/14368
Nakh-Daghestanian (NDa)	Northwest Caucasian (NWC)	North Caucasian [54]	0.0024	211/14368
Indo-European (IE.)	Kartvelian (Krt)	Nostratic [20]	0.002446	221/14368

Fig 14. Eurasiatic and Nostratic clusters in the meta-analysis of p-values

Austro-Tai, Sino-Austronesian, Yangzian [51] [58]

Our data shows a clear cluster with a proximity between the Austronesian, Tai-Kadai, Austroasiatic, Hmong-Mien and Sino-Tibetan top-level families. Austronesian and Tai-Kadai form a sub-branch, Austroasiatic-Hmong-Mien an other one, with Sino-Tibetic close to it (especially to Hmong-Mien). Since 1906 with Wilhelm Schmidt and 1942 Paul K. Benedict, various hypotheses have linked some or all of these families, sometimes with extensions to other ones. These hypotheses are known under the name "Austic". A sub-branch of Austic, Austro-Tai, linking Austronesian and Tai-Kadai show a proximity in the phylogeny and a strong support by the p-value analysis (Fig 15). Such a connection is mentioned by numerous authors, with more recent works in 2004-2006: Ostapirat (2005), Sagart (2004) and Reid (2006) supporting them. The Austroasiatic-Hmong-Mien connection is also well supported in our data, both in the phylogeny (bootstrap value: 100) and in the p-value analysis. Stanley Starosta's [58] Sino-Tibetan-Yangzian family corresponds to our cluster "Austronesian-Hmong-Mien-Sino-Tibetan" and our data also hints at his East Asian hypothesis, connecting Austro-Tai and Sino-Tibetan-Yangzian. Our Austro-Tai and Yangzian connections also fit as parts of Sergei Starostin's Dene-Daic macrofamily but the position of Sino-Tibetan is in this case too close to Yangzian. This proximity as inferred in our system is due to a Sino-Tibetan-Hmong-Mien-Japanese cluster which is probably due to early language contacts. Japanese and Chinese have a low HM-p-value support to the members of the Austic cluster other than Hmong-Mien, whereas within the Austic cluster, the mutual support is stronger. This can be interpreted as the signal of a differentiation between macrofamily (Austronesian, Austroasiatic, Tai-Kadai, Hmong-Mien) and macro-area (the latter with Chinese and Japanese). However, even with these results, this interpretation should be made with great care, as early contact within the ancestor languages of the Austic group cannot be ruled out.

Fig 15. Larger Southeast Asian clusters in the meta-analysis of p-values

The main elements of the Nostratic and Austic hypothetical macrofamilies appear as the few reliable signals in form of TLF clusters with 4 and more members, which clearly distinguish themselves from the abundant negative signals and statistical noise generated by our analysis of potential links between top-level families of languages (Fig 16). In the final loop of selective analysis, they deliver the best results out of a set of only 11 TLF clusters. Of these 11 clusters, 3 belong to the Nostratic and Austic hypothetical macrofamilies, two contain four core members (Wakashan, Salishan, Iroquaian and Algic), which are part of existing but contested hypotheses: Mosan,

Almosan and Almosan-Keresiouan. The remaining 6 clusters reflect clearly unrelated TLF connections and as such represent statistical noise in the list, albeit with 5 of them at the bottom of the list when ranked by p-values.

Fig 16. The Nostratic and Austric macrofamilies as inferred by our system

Fig 17. Inferred macrofamilies and long-range connections: Summary on world map

The Americas

The classification of the languages in the Americas leaves the biggest number of primary language families in one continent: 86 in our list, accounting for 23% of the TLF to TLF pairs. Very few hypotheses that link some of these TLF seem to move in the direction of reaching consensus among scholars. The most comprehensive hypothesis, J.H. Greenberg’s Amerind [57] includes all native languages of the Americas in one macrofamily, excluding Na-Dene, Haida and Eskimo-Aleut. This hypothesis has not been welcomed by the community although Greenberg’s previous results on the classification of languages in Africa had been successful and is now widely accepted. This situation is reflected in our system, which does not support any wide-scale connection on the American continent but does display a very strong support for the African classifications. Amerind as a whole does not display quantitative signals. However, in the top 40 results with lowest HM p-value in the 3367 TLF to TLF Amerind list, 19 are such for which a long-range hypothesis exists (see Table 7 and Fig 18). It is clear that the last word on the classification of TLFs in the Americas is not spoken and that results in quantitative research shed light on wider connections.

North Caucasian [54]

A connection between the Nakh-Daghestanian and the Northwest Caucasian top-level families is supported by a bootstrap value of 6 in our tree. In the p-value analysis, Northwest Caucasian and Nakh-Daghestanian share an average distance with $p = 0.0024$. This result is still in the range of statistical noise, with 4 unrelated connections to these two families out of 347 exposing a lower p-value.

Other connections

Our TLF to TLF results in the online Supporting Information S7 File can be used to check other hypotheses. Considering only the 16 results with $p < 0.0001$, two other connections unfold which are subject of discussion among scholars: Mande and Niger-Congo (Blench, Dwyer) and the connection between West Bomberai and Trans-New Guinea (Holton and Robinson). This last connection forms with Timor–Alor–Pantar one of the few clusters with all their connections with $p < 0.002$. This is in line with Timothy Usher’s current research on New Guinean languages [56].

Discussion

Materials and methods:

To make the discussion about our system and its results easier, we provide a graphical overview of the steps involved as well as the different kinds of results the system infers in Fig 18.

Fig 18. Overview of the processing steps and results of the system

A first particularity is that modeling the basis elements of the system (sound change rules, word list, etc.) is based primarily on result optimization through error reduction and not on existing findings: tuning the way we modelize the basis elements has an impact on how the system performs with the classification of languages. The principle is the same as for machine learning: training a system with the part of the data where the output is known, avoiding overfitting and inferring a model that performs well with new data.

The second particularity is the sole use of consonants. This choice has also been part of the error reduction process, which showed that not using vowels decreases the performance of short-range classifications (internal classifications of young subfamilies like Romance, Slavic or Germanic within Indo-European) but increases the long-range performance. The smaller number of possible vowel clusters compared with the consonants cluster list [59] in use would increase the overall exposure to chance. The exclusive use of consonants also reduces the complexity, allowing us to use simple alignment rules, which were also tuned using the error reduction process. Developing systems that challenge the results against chance is a more accessible task when the models get simpler.

Results:

An important note about the bootstrap values in the phylogenetic trees is that they should always be interpreted as a stability indicator within the very same respective experiments: they are not a confidence value: they just measure how often a result (node) remains stable with the addition of random values in a given context. This stability indicator cannot be used for interpretation across different experiments (e.g. global tree versus subfamily trees). A similar remark has to be repeated regarding p-values, especially Harmonic Mean p-values: they have to be interpreted relatively to each other within the very same analyses.

We find it useful to reflect on three aspects of our results, which offer potential for discussion:

- The system cannot differentiate the nature of the signals behind the inferred long-range connections: relatedness or early language contact. However, as we can see throughout the research, the word list in use is highly resistant to borrowing.
- Browsing the worldwide phylogeny in the online Supporting Information S5 File we see that well documented languages of Eurasia and Northern Africa (at the bottom of the file) lead to cleaner results. More noise interferes in the classifications of less documented languages like those of New Guinea, Australia or South America. Better quality of the data in use leads to a better differentiation between signals and noise.

Conclusion

We have presented a new approach for automatic language classification completely based on computer and statistical methods. It reaches a high level of precision, close to human based reference classifications and to one of the best automatic classifications so far available: Gerhard Jäger's one. The system has a strong ability to address the chance issue, not just challenging the results, but also increasing the ability to explore long-range relationships and delivering data for debates about proposed macrofamilies, disputed top-level families and internal classifications.

The top-level families known today arise from the level of visibility we have with the available information and technology in use until now. Opinions diverge on the time scope we can trace back, 8.000 to 10.000 years BC being a widely mentioned limit. Prior to this limit, language history has certainly been as dynamic as thereafter, but most signals of relationships between language families as we use them with classical methods may have disappeared forever. With newer technical possibilities, we can hope to extend the time scope we shed light on. The use of computer techniques for this task is a data science challenge, where our systems deliver signals but also noise. As in most other computer implementations, the system does not replace human expert judgment. The figures alone cannot explain the very complex phenomena behind them. Figures need to be interpreted and wherever possible, linked to other facts: they can support research from other disciplines. Statistical and classical methods are complementary and bring their contribution in interdisciplinary research. Convergence in results deserves a particular attention. In this sense, our results on the Nostratic/Eurasiatic as well as Austric macrofamilies, along with other findings on various distant relationship form a consistent contribution to the debate about deeper relationships between established top-level families of languages.

In the balance between signals and noise, the quality of the data plays a major role. The varying quality of the transcription and word availability, the inhomogeneous record of synonyms, root comparisons versus whole words comparisons as well as the undocumented and unknown loan words are sources of noise, increasing the variance of the results and reducing the precision of the system. Without the tremendous efforts by various institutions and scholars to compile word lists and make them available freely, research like ours would not be possible. The increasing quality of these contributions will be of decisive importance for future improvements of computer-based systems.

Supporting information

S1 File. Alignment rules and low points filter Source code of the *c#* application which generates the distance matrices. The alignment rules and low signal filters are clearly visible in lines 112 to 231. osf.io/qs2py/ (C# as TXT)

S2 File. Sound correspondence Inferred best sound correspondence and point systems with matching probability. osf.io/u2jgx/ (PDF)

S3 File. Conversion ASJP-Our project R script for the conversion of the ASJP source in our format (consonant classes of this project) osf.io/8v9tw/ (R file as TXT)

S4 File. Classification benchmark Benchmark vs. reference classifications (WALS top-level families and Genus, Glottolog, Ethnologue) and Jäger osf.io/pxj3y/ (XLS)

S5 File. Worldwide Tree Output phylogeny of the project (raw, bootstrap values) osf.io/3nwqf/ (PNG)

S6 File. Internal classifications Trees of the subfamilies of top-level families (internal classifications, low bootstrap support excluded) osf.io/s86wq/ (PDF)

S7 File. Long-range analysis Pairwise analysis of top-level families osf.io/2rw6a/ (XLS)

S1 Appendix. Pairwise comparisons Query form language to language (WEB)

S2 Appendix. Complete data and scripts osf.io/7g269/files/ (WEB)

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Author contributions:

Conceptualization, data curation, software, visualization: Vincent Beauflis
Methodology, validation, writing - review & editing: Vincent Beauflis, Johannes Tomin

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