Studying Language Evolution in the Age of Big Data

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Abstract

The increasing availability of large digital corpora of cross-linguistic data is revolutionizing many branches of linguistics, while at the same time uncovering new challenges. Overall, it has triggered a shift of attention from detailed questions about individual features to more global patterns amenable to rigorous, but statistical, analyses. This engenders an approach based on successive approximations where models with simplified assumptions result in frameworks that can then be systematically refined. More importantly, these simplified analyses still make explicit the methodological commitments and the assumed prior knowledge. Therefore, they can resolve disputes between competing frameworks quantitatively by separating the support provided by the data from the underlying assumptions. We describe here this evolving methodological shift, attributed to the advent of big data, covering briefly both randomization tests for detecting patterns in a largely model-independent fashion and phylolinguistic methods for a more model-based analysis of these patterns. We foresee a fruitful division of labor between the ability to computationally process large volumes of data and the trained linguistic insight declaring worthy prior commitments and interesting hypotheses in need of comparison.

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1 INTRODUCTION. The evolutionary relationships of languages have been a lively field of research for nearly two centuries, ever since Schleicher's evolutionary trees (Schleicher, 1853) and Dumont d'Urville's attempt to introduce a quantitative aspect into the comparison of Oceanic languages (see Hymes (1983) on d'Urville's work in 1834). These early roots predate Darwin's first sketch of an evolutionary tree of species, possibly drawn in 1837. Early work on phylogenetics in biology has been grounded in detailed expert descriptions of morphology. The advent of a deluge of molecular data and the relative simplicity of the mechanisms underlying sequence evolution has transformed molecular phylogenetics into a data-driven, computational science.

In contrast to biological evolution, the detailed forces and mechanisms shaping language change over time are much less thoroughly understood. Nevertheless, it seems safe to assume that spoken languages include a set of core features that are mainly uniparentally co-inherited with occasional horizontal influences from other speech communities. Such vertically inherited features range from phonetics to individual lexical items and entire grammatical structures. Just like the genotype comprising a biological system has a core subset of housekeeping genes that form a bundle that is frequently, but not always, co-inherited, it is likely that language has a core that can be used to define a VERTICAL DESCENT. Many other traits would be more or less coherent with respect to this bundle of features, with deviations defining HORIZONTAL admixtures. One may find clusters that, like pathogen islands in a bacterial genome, are also mutually co-inherited, but along a different lineage than the housekeeping genes. Pre-eminent among these are, obviously, cultural complexes that get borrowed along with the entire related vocabulary (Field, 2002). In addition, in language, we also have grammatical and various other typological features that may or may not follow the same lines as the core bundle. For a more detailed discussion on parallels in both disciplines see List et al. (2016).

In the following, we do not consider questions that pertain to which of these features SHOULD be defined as GENETIC INHERITANCE, in fact we shall studiously refrain from privileging a single co-inheritance bundle as THE defining feature of genetic relationship of a cultural trait such as language, but, instead, will concern ourselves solely with reconstructing the phylogeny of any of these sets of features. When we are confident that a set of features belong to the same bundle, a phylogeny built primarily on the basis of evidence from one set of features can provide a historical reconstruction for the other features. In any case, we consider all these features as useful subjects for historical inquiry, though their relative merit for answering a given question of interest to individual researchers will vary. For concreteness and because of large amounts of available data, we shall talk about PHYLOLINGUISTIC analysis of lexical features but much of the discussion also translates to phylogenies constructed from other features.

An important issue to consider in the choice of traits to analyze is the importance of synapomorphies, or shared derived traits that set a genealogical family apart. Certain traits such as grammatical paradigms may be complex enough that a particular system has a very low chance of arising more than once. If such traits are vertically inherited and maintained over time, they can provide clear and convincing classification. On the other hand, other features such as individual sound-meaning correspondences (Blasi et al., 2016b) or high-level typological variables (such as word order and the presence of certain marking strategies, (Dunn et al., 2005)) might be more prone to homoplasy, i.e., they may arise independently more than once. The combined evidence from a large number of such co-inherited units can provide the same or higher degree of confidence

in a classification. Here, we shall not prejudge whether one or another of these provides the larger body of relevant evidence, but rather consider ways of evaluating the evidence quantitatively in light of confounding processes like contact phenomena, areal diffusion, and sound symbolism and other psycholinguistic effects.

One of the key take-home lessons from phylogenetic studies in both biology and linguistics is that a detailed understanding of the mechanisms of change is helpful, but NOT a necessary prerequisite, for the reconstruction of phylogenetic relationships. The causal structure imposed by vertical inheritance on a branching TREE dictates that similarity of randomly originating features follows a hierarchically nested structure consistent with the partitions of the tree. If the feature set under study happens to contain enough independently evolving, vertically inherited neutral traits, their similarity alone can be used to reconstruct the phylogeny. While detailed stochastic models of mutational change have become the method of choice at the level of DNA and protein sequences, perfectly valid phylogenies can be obtained by investigating complex phenotypic characters such as specific shapes of bones, the presence or absence of particular neurotransmitters, or the spatial organization of neuronal networks. In fact, when there is no mechanistic understanding of the patterns of change, robust, non-parametric approaches to tree reconstruction are often the method of choice (Waegele and Bartholomaeus, 2014; Dunn, 2015). Of course no method is infallible with respest to the features chosen. If these are either too noisy to convey retrievable information or are not strictly vertically transmitted to begin with the resulting tree might not depict the actual relationships. An extreme example in the phylogeny of animals is the strange case of *Xenoturbella*, which was placed at vastly different positions in the animal tree based on different choices of data sets and taxa included for comparion (Bourlat et al., 2006; Rouse et al., 2016). DELETE: This unimpressive worm-like animal was classified as close relative of molluscs based on DNA that, as it turned out later, represented its food rather than the animal itself. It was later placed based on genome-wide sequencing data within the Deuterostomes, the animal clade that also includes vertebrates (Bourlat et al., 2006), only to be DEMOTED again earlier last year to one of the most basal bilaterian branches by means of data for related species (Rouse et al., 2016). This underlines the fundamental importance of basing phylogenetic reconstruction on multiple, independent feature sets because it is often not obvious *a priori* which features are informative and which taxa are relevant for comparison in a given context.

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I fail to see that the example of Xenoturbella underlines this conclusion. It just seems to illustrate that one needs to be able to correctly identify the data used and that the phylogenetic placement of a leaf will be wrong if not all relevant clades are included in the analysis.
I do understand the argument of the reviewer since it is wrong data rather than really wrong feature. What about a less fancy example like CCA-adding enzyme?
For example, the class of CCA-adding enzymes is essential for organisms. Consequently, CCA-adding enzymes are found in most organisms in all three kingdoms of life. However, building a phylogeny based only on the sequences of the CCA-adding enzymes would misplace the group Holozoa (animals and *Choanozoa*) as a sister group of the Proteoalphabacteria (Betat et al. 2015). The reason is the loss of the original CCA-adding in Holozoa and the horizontal gene transfer of the CCA-adding enzyme of the Proteoalphabacteria into Holozoa. On the other hand, when using the nucleotide sequences of 2 ribosomal RNA and the amino acid sequences of 6 protein coding es in Paps et al., the correct phylogeny can be retrieved (Paps et al 2013). The CCA-adding enzymes example might be a tad too technical for the intended audience - what about reducing the Xentourbella example to one or two lines?
I tried above. The whole point of the example is that it is not always/often clear *a priori* WHICH data and taxa are the correct/relevant ones.

Just like language evolution, biological evolution is not purely vertical and hence not completely tree-like. Even in higher organisms, horizontal gene transfer, convergent adaptive evolution, incomplete lineage sorting [1], and random noise in the data introduce deviations from tree-likeness in the data. What is lineage sorting? I have inserted a footnote Lineages are not always well-separated, as in the case of RING SPECIES (Irwin et al., 2005) in biology and DIALECT CONTINUA (Heggarty et al., 2010; François, 2015), making the tree model only an approximation (see (Geisler and List, 2013) for further models for language relationships). Although horizontal transfer, like any other causes of incorrect tree estimation, may bias quantities such as divergence time estimated from trees (Greenhill et al., 2009), there are nevertheless many important events in the evolutionary history that are correctly expressed by trees because they are primarily conserved vertically. In fact, even in the presence of other forms of relationships, trees are a useful representation of evolutionary relationships whenever there exists a dominating set of vertically inherited features. Several measures that quantify the of tree-likeness of a data set are available that do not presuppose a particular tree and hence can be employed without biasing subsequent phylogenetic statements (Bandelt and Dress, 1992; Nieselt-Struwe, 1997; Misof et al., 2014).

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This is a circular assessment (trees are useful when the data is sufficiently tree-like). Don't understand the issue here. It is exactly what we want to say, isn't it? I'm with Lydia here.
Indeed: treelikeness can be quantified independent of phylogenetic reconstruction – I included as review paper we recently wrote about this very issue. We should answer that this is indeed NOT circular.
NB: The use of the term "other forms of inheritance" does violence upon the term "inheritance". Presumably it refers to the mentioned cases where "lineages are not well-sorted" but it's never explained what that means in terms of an evolutionary process and whether it's a form of inheritance. – the well-sorted should be explained with the footnote for the previous TODO. I also replaced the 'other forms of inheritance' with 'other forms of relationships'. May be more generell and thus more inclusive. I'm not sure I agree with this. We need to decide whether we want to use inheritance ONLY for *vertical inheritance* or if we also want to use the term inheritance for horizontally transmitted material. (The term "horizontal inheritance" is indeed used in the bio literature, but we can avoid it if necessary. If so, we should mostly replace vertical inheritance with *vertical transmission*, however.

Models of evolution that allow an arbitrary network as representing the evolution are, of course, available, `NeighborNet` (Huson et al., 2010) being by far the most popular choice. Such networks, however, do not necessarily directly model an evolutionary process. Nevertheless, they can be very useful to visualize and quantify the contribution of non-vertical transmission (Holden and Gray, 2006; Bowern, 2010). Network graphs reflect relationships between languages given a distance measure. Other than tree producing algorithms LONG BRANCH ATTRACTION, that is, of two languages that are both dissimilar to all other languages are usually grouped together, is no problem since the problematic languages would be branching from the center directly. In particular this means that languages without any information on mutual history would result in a star-like `NeighborNet`. In contrast, languages that share a root are grouped together via rectangular branches. Hence, for languages that share unusually long branches than would be expected, borrowings are a reasonable explanation.

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(I am assuming "non-vertical inheritance" should be "non-vertical transmission".) The conclusion, however, does not follow from the citation. Bowern (2010) could have done the comparison between the borrowable and non-borrowable subset in the absense of any visualization at all, and the visualization used did not allow anyone to distinguish between retention/innovation and certainly did not give any quantification. see Fig. 3 in this paper plus its Discussion in Results; maybe an explanation is needed how one could detect something like borrowings in these networks? see text. I also added Holden & Gray on Borrowing in Bantu Languages, that explicitly makes use of network graphs yes for non-vertical transmission

As in other loosely constrained statistical estimation problems, phylogenetic networks may be over-parameterized so that it is often difficult to discern whether they uncover patterns of the underlying linguistic history, or are merely describing the random and idiosyncratic noise inherent in any particular data set. It is often better, therefore, to stick to a tree-based phylogenetic techniques but express the potential existence of reticulation or conflicts by measures of goodness of fit, for example, through low likelihoods in particular branches, a wide spread in the posterior distributions in Bayesian settings or explicit measures of reticulation when network approaches are

applied to the same data (Robinson and Holton, 2012). This is an important point which, unfortunately, is not developed in the paper. It would be great to be told how measuring the goodness of fit of various tree-models tells us whether a non-tree model fits better or worse. Also, the suggested paradigm of looking at the posterior in Bayesian settings conflates effects due to the desired quantity (tree-like-ness) and other things estimated (branch lengths, rates of change etc). I disagree - the text is already too gigantic! Added some references where people can see some (suboptimal) strategies used in linguistics, e.g. compute reticulation in the same data. Wide posteriors are taken as abscence of evidence for the relation but rarely used to discuss against the tree-model. The key question, then, is not whether one can devise a complete and sufficiently richly parameterized model of language evolution that takes all horizontal effects into account. Instead, we have to ask whether and how it is possible to reliably disentangle the vertical phylogenetic signal from superimposed horizontal influences. The advantage of this approach is two-fold. First, it allows us to identify the cases where *the underlying tree-like structure induced by the vertical process of inheritance is such a strong regularity that it can be recognized and, at the very least, approximated from the observable data.* Second, as the amount of data increases, it allows one to *systematically* improve the model using techniques like ancestral recombination graphs (Hudson, 1991; Griffiths and Marjoram, 1997; Arenas, 2013; Rasmussen et al., 2014), well known in the biological phylogenetic literature. The logic here is unclear. Cf. the comment above that we never actually told how only using tree-models tells us whether they are appropriate or not. But suppose we did, then the authors suggest we can systematically improve the tree-model by extending it to become ARGs. Then why not use ARGs to begin with? (That would be systematic, rather than ad hoc). I feel the whole discussion on the tree/non-tree like tension is too long already...

The purpose of this contribution is to demonstrate that quantitative statistical approaches that have become widely accepted and used in the life sciences can be generalized and adapted to the analysis of languages and their relationships. Of course, the use of such methods is not new in linguistics and many linguists indeed make extensive use of quantitative computational techniques. Nevertheless, we argue that the field stands to gain a lot from systematically adopting and adjusting the workflows of data driven (bio-)sciences. Not only can quantitative methods answer linguistic research questions but they also suggest additional research questions.

2 Lexicostatistics and language phylogenetics. is mislabeled because half of it is devoted to non-lexical phylogenies.good point: I'd go with Linguistic phylogenies alone

Although phylogenetic signal is present in virtually all aspects of language, computational work so far has concentrated primarily on cognate loss, following Swadesh's original comparison of cognate loss to radioactive decay (Swadesh, 1952). Languages manage to be expressive by a combinatorial process: meaningful utterances are open-ended compositions grammatically derived from a finite underlying lexicon. Swadesh proposed that a part of this lexicon consists of a core of similar concepts across the world's languages. Data has been collected on this core vocabulary for a large number of languages, and linguists have, often painstakingly, classified these words into cognate classes, that is, groups of words from various languages that share a common origin. After linguistic identification of cases in which the patterns of sound change or known historical contact events pointed to horizontal transfer (borrowing), the remaining loss of cognacy, presumably due to language internal processes, is quantified and modeled as a discrete random

process—usually, but not always, as a constant-rate and memory-free Poisson process (Sankoff, 1973). Once one allowed different rates for cognate replacement in different parts of the lexicon, and when the analysis used only the core concepts belonging to the Swadesh lists swadesh is just one of such lists - Jakarta-Leipzig is way more common these days, for instance. I'd say axe this reference to Swadesh.—assumed to be the most closely co-inherited roots, refractory to horizontal transfer—or, at least, weighted their evidence more, this gave a very good fit with known linguistic history (Lee and Hasegawa, 2011; Gray et al., 2009; Dunn et al., 2011) What is meant by "very good fit"? The whole paper argues we should use quantification to answer such questions but for some reason when we need it and it is easy to do, they don't do it. For example what is the Robinson-Foulds distance between the computational and "known linguistic history"-tree topologies in the cited papers? (And why cite these, esp Dunn et al 2011, rather than all studies with this metholodogy).agree with removing Dunn et al's ref here. As for the claim: I propose we replace "very good fit" for "qualitatively agrees most of the time with" although, as a matter of fact, most of the fit is simply topological in nature (e.g. a particular branch is recovered, or two close variates show up as close sisters in a tree.) , and provided a credible starting point in discussions on language relationships (Bouckaert et al., 2012). It is important to realize, though, that all these approaches crucially depend on manually determined cognate classes. There is not yet an equally reliable automatic method to determine cognacy, although contemporary automatic methods achieve reasonably good rates of classification (List et al., 2017a) it is fair to comment here on the automatic cognate detection algorithms, some of which achieve efficiency comparable to that of humans - I added Mattis' most recent paper. Any progress in the development of such methods has to rely on a good inference of sound correspondences, which seems to require larger datasets.

Beyond lexical data, there have been many attempts to use other kinds of linguistic data for the reconstruction of language history. A lack of reliable cognates among Papuan languages in Island Melanesia (apart from obvious borrowings from nearby Austronesian languages) on which to base a more standard lexicostatistic comparison, prompted Dunn et al. (2005) to use grammatical and phonological data, but the existence of enough independent traits in such data that evolve neutrally on a tree has been questioned (Albu, 2006; Cysouw et al., 2008; Wichman and Saunders, 2007; Wichmann et al., 2010). Other proposals have involved comparing morphological material (Nichols, 1992), syntactic features (Longobardi and Guardiano, 2009), as well as the phonetic distance between word forms within a cognate set (Heggarty, 2000).

In addition, machine learning approaches have been used in reconstructing ancient word forms (Bouchard-Côté et al., 2013) This information belongs in the section about lexicon. and in phylogenetic analysis of typological features (Gell-Mann and Ruhlen, 2011; Dunn et al., 2011). There is no machine learning in the standard sense of the term in the two cited papers.The sentence starting with "In addition..." seems to be out of place to me. I vote remove.

One must note, however, that even when there appears to be a phylogenetic signal in such data, there is much less consensus about the nature of any vertically-inherited CORE and how that relates to the vertical inherited bundle of features traditionally used to define genetic relations in linguistics (Dediu, 2015). In using such data, care must, therefore, be exercised.

3 MODERN WORK FLOWS FOR SOUND DATA. Since computational approaches so far have relied heavily on lexical data like cognate lists, the input data required extensive manual curation to separate

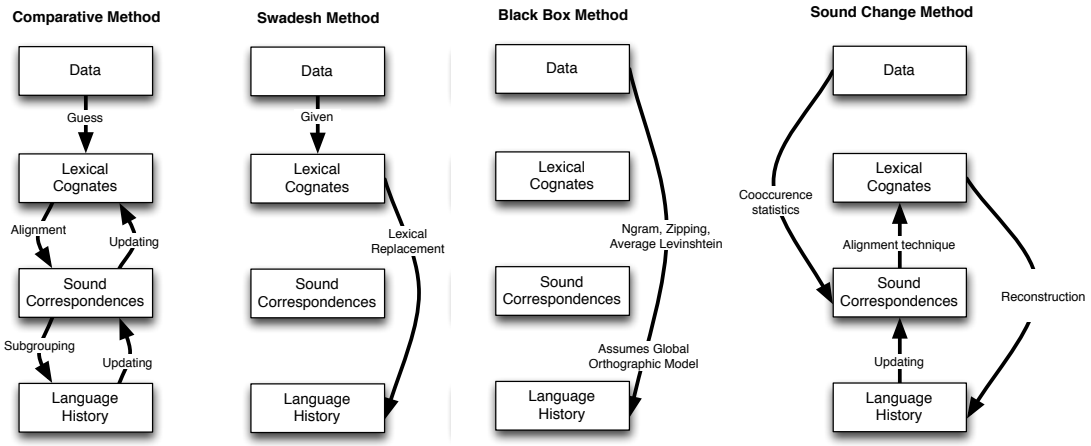

Figure 1: Comparison of workflows to study language evolution. The comparative method and the sound change methods are explained in detail in the following sections, where we show how those methods produce relevant and reliable data. We assume that the traditional Swadesh Method is so well known that it does not need to be recapitulated in detail (Campbell, 1998; Crowley and Bowern, 2010). Early computational approaches were mainly 'black box methods', and merely provided reasonable phylogenetic trees without a deeper understanding of the evolutionary events and processes explaining the phylogenies they predicted.

the bound grammatical affixes and identify cognates. These require a large amount of linguistic expertise for their preparation, thereby severely limiting both the scope and the statistical power of computational approaches. I remove the following sentence and comment because making statements about "number of cognates" in a given dataset is relative to the size of family, purity of data, time depth, etc, all things hinted before. BEFORE: Small or moderate size word lists contain only very limited numbers of cognates, particularly for the more distant languages. What do you mean by "the more distant languages"? I could imagine this being true for poorly attested languages, and languages in families where the general level of documentation is poor.

The recognition of cognates between distant languages often requires the intermediate reconstruction of ancestral forms, and it is difficult, if not impossible, to properly account for uncertainty propagation if these tasks need to be carried out manually. As a consequence, cognate recognition becomes a central issue for large-scale language phylogenetics. See (Ellison, 2007; Jäger, 2013; List, 2016) for automated approaches on cognate identification.

3.1 IDS AS AN EXAMPLE OF WORD LIST DATA. Throughout this manuscript, we will repeatedly make use of word list data from the *Intercontinental Dictionary Series* (Key and Comrie, 2007) to demonstrate how quantitative method can answer relevant linguistic questions. Instead of the IDS data, any word list data could in principle be used.

The IDS word lists are currently available for 241 languages. The set of languages is regularly extended. For example, Arabic is currently in progress and has not yet been released at the time of writing. The written form of the entries varies across the languages. For most languages, a phonemic-style transcription using IPA, Americanist, or extended Cyrillic traditions is used. For others an established orthography is used.

All word list are kept in the same format, and the organization is based on Buck's dictionary (Buck, 1949) which was topically subdivided into 23 chapters and had in total about 1200 potential entries for each word list. The IDS revised the chapter structure such that the IDS word lists have potentially 22 chapters and in total 1310 potential entries. Entries for which no word exists in a language are left blank for this language. Chapters are semantic groups such as 'The physical world' (chapter 1) or 'Emotions and values' (chapter 16). Each entry is assigned to exactly one chapter. Entries within each chapter are roughly sorted by their semantics, with semantic concepts assigned identifiers of the form 'chapter.meaning'. Both chapter and meaning are numerical values with the entries within each chapter intuitively sorted by their meaning. Furthermore, each entry has translation into English and at least one additional language, for example, Spanish.

In order to bypass manual cognate identification as the initial step one may start with a much more accessible set of data, namely comparative word lists not yet subjected to etymological analysis (Fig. 1). These compile, for a collection of languages, words with roughly corresponding meaning, but make no effort to single out cognates, let alone to distinguish borrowings from vertical inheritance.

The core or basic vocabulary remove reference to Swadesh list: comprising the Swadesh concepts when compiled into such word lists is particularly suited for the phylogenetic enterprise for two reasons. First, it is composed of many items of proven genealogical persistence (Calude and Pagel, 2011), with some of them potentially conserved beyond the conventionally assumed 10,000 ybp limit of the comparative method (Pagel et al., 2013). Even though Swadesh lists offer an initial starting point, the manner in which they were created and compiled had its shortcomings (Hoijer, 1956) These studies do not "prove genealogical persistence", they are circular in this respect since they assume families established on the assumption of genealogical persistence of the very same vocabulary items... I agree - however, do we really need this whole section on IDS? I don't think so IMHO Lexical replacement rate seems to be linked to frequency of use, which is fairly comparable, at least across languages from the largest lingustic families in the world (Calude and Pagel, 2011, 2014). Similarly, basic vocabulary is composed of the lexical elements that are the most resistant to borrowing (Haspelmath, 2009). For all these reasons, *ceteris paribus*, basic vocabulary items are often considered to provide a more reliable phylogenetic signal than other non-basic elements.

As we shall see below, it is possible to extract very good approximations to cognate sets from such data. Importantly, though cognate judgments made purely from the phonetic structure captured in these semantically aligned word lists can be improved with specialized linguistic knowledge, in recent tests on 'simple' language families, the difference was found to have no systematic structure that could bias the reconstruction of phylogenies based on this data (Steiner et al., 2011; Hruschka et al., 2015). Rephrase from Importantly on. For a comparison of different cognate detection algorithms see List et al. (2017b).

Nevertheless, it is difficult to overemphasize the importance of carefully curated data sets that are accurate, reliable, uniformly transcribed, and correctly glossed. Such cleaning of data and making them digitally accessible needs specialized linguistic knowledge and is time intensive. One may argue that one can avoid this step because pattern-free isolated errors in data are unlikely to confound major results. This would, however, be a mistake when the computation is expected to produce fine-grained results or is dealing with weak signals. This is the case, for example, when

one is interested in time depths at the limit of resolution of these methods, or when many threads of intense AREAL contacts need to be disentangled from each other and from VERTICAL transmission. In what follows, we will always assume that the data has been curated to the degree appropriate for the resolution required of the results, and comparable encodings of the wordlists and similar meaning assignments are used consistently.

3.2 IDENTIFYING SIMILARITIES.

WORD ALIGNMENTS AND THEIR SCORING. The first ingredient in determining historical relatedness of languages is a means of measuring the similarity of words. Human languages form words by a combinatorial composition of a basic repertoire of sound-tokens, called phonemes, that vary between languages. To be useful, computerized word lists need to encode the phoneme distinctions accurately using distinct characters; they often also record additional phonetic differences that are linguistically unimportant in identifying the words or under-represent crucial distinctions. A related issue is that transcriptions often use digraphs for single segments, and their usage is sometimes inconsistent across the orthographies used for the various languages and various sources of data, even after unicode normalization. Thus, for example, an ejective may be denoted by superposed apostrophe <ḱ>, postposed apostrophe <k'>, postposed palochka <k| >, or special letters <ƙ>. Depending on the encoding, these might be represented either as digraphs or unigraphs. If the language specific segmentation is available in the data source, these can all be converted to special characters—for example, in the private unicode space—before analysis. Most often, however, such information is missing from composite data sources and one chooses a suboptimal solution of leaving these as a sequence of characters to be handled later. An example for how to solve this issue will be discussed in section 3.5 below.

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An example for how to solve this issue will be shown later in this section. Leaving the sequences of characters to be handled later leaves the reader wondering, at this point in the paper, how this will be resolved. A reference to where it is resolved would be useful. I would change the last two sentences for a final reference in the previous sentence: "before analysis (although chances are such information is missing from composite data, which requires different strategies, ref. CHAPTER)

A very natural starting point, then, is to regard words as sequences of characters that correspond, at least approximately, to phonemes. The most direct approach to comparing sequences starts by aligning them. In bioinformatics, alignments are a nearly ubiquitous first step in comparative sequence analysis, so that efficient algorithms and ample experience can be imported from this field. In fact, such techniques for character-based alignments of words have been used to measure similarity, for example, by Kondrak (2000), Cysouw and Jung (2007), Kondrak (2009), and Steiner et al. (2011).

In contrast to the world of biological sequence analysis, where scoring systems are relatively simple and the algorithmic problems of efficiently computing alignments of large data sets dominate (see, e.g. Notredame, 2007), it is the construction of good SCORING MODELS,that is, a function or look up table providing a measurement for the similarity or distance of observed phonemes/characters, that is most difficult in language comparisons. his is the first mention of the term "scoring model" in this section, I believe. Because this is a very important concept for

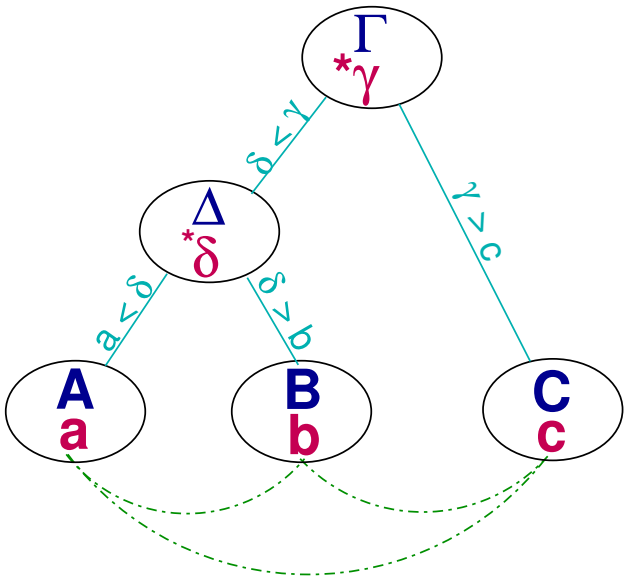


Figure 2: A hypothetical language tree for 5 (proto-)languages (dark blue) and one (proto-)sound (pink). Greek letters correspond to reconstructed proto-languages and proto-sounds and Latin letters to the observed sounds and languages. Sound change laws (typically used by linguists, turquoise) and scoring models (used in quantitative methods, dark green) describe both changes between languages in sounds/characters. However, while sound change laws describe the changes in the sound system from the ancestral language to the descending language, scoring models describe the cumulative effect of the sound changes in the languages under investigation. For example, the scoring model (dashed-dotted lines) would state that a from language A is often found at those positions in the words where language B has sound b. It thus indirectly implies that a and b originate from the same proto-sound. The sound change laws (straight lines, i.e. branches of the language tree) would state that there is a proto-sound $^*\delta$ which changed into a in language A and b in language B.

this section I recommend that you introduce it in caps (in keeping with other technical terms), and provide a brief definition. Alternatively the term could be introduced in the first paragraph of the sub-section, since it is indeed the focus of this sub-section. The fundamental reason for this is that unlike phonemes, the elementary tokens of biological sequences are uniquely identifiable across the taxa; for amino acids this is rooted in their distinct, functionally salient, chemical properties, and for nucleotides it follows from the extremely slow change of the genetic code over evolutionary time. In languages, on the other hand, the phonetic representation of the corresponding phonemes is the fastest process of change, and needs to be inferred from the data. If alignments of the cognates were known *a priori*, one could simply use log-odds ratios of co-occurrence counts as the scoring model.

It is important at the outset to distinguish the two related concepts of a scoring model for alignment and the laws of sound change. The score between character a in language A and character b in language B indicates a and b form a match in an alignment of two cognate words. Thus it quantifies the likelihood of obtaining b in B in a place where language A has a as a consequence of the evolution of both A and B from their common proto-language. No statement is made about whether this development was a regular correspondence or, indeed, what the proto-sound might have been. In contrast, the laws of sound change describe how the changes along the branches

of the language tree happen and, more precisely, how the proto-sounds of the proto-language changed into the sounds of the languages A and B under investigation. The scoring model therefore describes the cumulative effects of the sound changes, including statistically the effects of apparently irregular developments of individual words. Furthermore, the scoring model subsumes different sound changes and proto-sounds as long as their end points are the sounds a in A or b in B.

As an example, let us assume that we have three languages A, B, and C. The proto-language of A and B is Δ and the proto-language of Δ and C is Γ as shown in Fig. 2. Furthermore, assume that the proto-language Γ has a proto-sound ${}^*\gamma$. The reconstructed sound laws along the phylogeny are $\Gamma\ {}^*\gamma > \Delta\ {}^*\delta$, $\Gamma\ {}^*\gamma > C\ c$, $\Delta\ {}^*\delta > A\ a$, and $\Delta\ {}^*\delta > B\ b$. The corresponding scoring model would not know about the proto-sounds ${}^*\delta$ and ${}^*\gamma$ but would simply assign high scores to the cumulative effects. Thus, matching a of language A with b of language B, matching a of language A with c from language C, and matching b form language B with c from language C would receive high scores.

In a scenario more conducive to the analysis of large-scale data sets without *a priori* known alignments, two approaches have been developed. The first of them uses a small amount of linguistic knowledge to create an initial, crude similarity measure to propose a tentative alignment. The rule can be very simple. Steiner et al. (2011), for example, only discouraged matches between vowels and consonants, disallowed transpositions (metathesis), and put more weights on identities of consonants than vowels. Another example is is given by Heggarty (2000), who first used the manually curated proto-forms of the words under study to infer matches, and then counted the number of phonetic and articulatory features in which the aligned segments differ. It may come as a surprise that the model of Steiner et al. (2011), which is clearly over-simplified, nevertheless can identify an initial set of cognates between related languages. In fact, even these weak assumptions are actually unnecessary: an alternate approach with even fewer assumption described in subsection 3.2 can be used to infer the initial alignment. This works because phoneme evolution proceeds through small phonetic changes, and cognate pairs having a higher similarity score than two evolutionary unrelated words is a very low bar.

These methods ultimately utilize the strength of regularities in linguistic correspondence. Even a very rough and simplistic model for sound changes suffices to identify at least a proportion of the cognate pairs in the data set. Given the rarity of metatheses, the pairwise alignments of these cognates preferentially match corresponding sounds with each other. The key observation is that all this needs is an enrichment of cognates in the initial alignments. Even if a fraction of the candidate cognate pairs are false positives and some of the alignments of cognate pairs are wrong as a consequence of the oversimplified scoring model, there is enough signal in the correct alignments of real cognate pairs for the statistical machinery to identify the more common sound correspondences. What evidence supports this claim that there is sufficient signal in real cognate pair alignments for correct sound correspondences to be identified in spite of some false positives/wrong alignments? I agree on that the claim comes across as a bit vague.

It is interesting to note that the statistical approach accommodates many linguistic subtleties without explicitly building them into the method. Although the mapping of consonants to consonants and vowels to vowels in the PRE-ALIGNMENTS is a good working assumption, there is at least one clear set of frequent exceptions: Vowels often correspond to consonants belonging to the

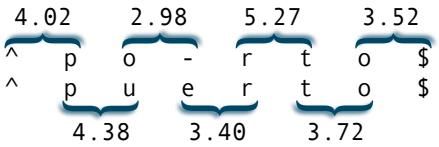


Figure 3: Example alignment for words from Italian and Spanish representing the concept 'port'. Each bigram pair in the alignment is scored separately, resulting in a total score $\sigma = 27.29$ in this example. Thus the normalized score is $nscore = 27.29/(8-2) = 4.55$.

classes often called glides and liquids, such as [w, j, l, r]. For example, [l] in the French words *plein, plaine, place* corresponds to [i] in Italian *pieno, pianura, piazza*. These consonants plus a vowel often also correspond to a single vowel. For example, /we/ in the Spanish words *bueno, puerto* corresponds to [ɔ] in Italian *bono, porto*.[2] These kinds of cases can be taken into account by relaxing the consonant-consonant and vowel-vowel correspondence constraint. At least some examples of this type appear in pre-alignments that are classified as candidate cognates even though scores were assigned, not trained in this alignment similar to editing operations with similarity scores. Hence in the second step they are assigned favorable log-odds scores without the need to model liquids and glides explicitly from the outside.

A more sophisticated scoring model that takes into account the neighboring phonetic context can also be estimated from the initial alignments of cognates. Here, we explore the utility of a bigram-based scoring model and compare it to a simpler model with unigram scores. The idea behind the computation of the scoring function is the same for both models. Likely correspondences of sounds will appear more often than expected by chance in an alignment of cognate words. This holds true for both unigrams and bigrams. In either case we therefore start from the collection of all alignments of the cognate candidates identified in the pre-alignments of the word list candidates for a pair of languages A and B. For each pair of sounds α in language A and β in language B (where α and β can be unigrams or bigrams as well as gap symbols) we compute their occurrences $occ_A(\alpha)$, and $occ_B(\beta)$ in the pairwise alignments. Similarly, we determine the co-occurrence $occ_{(A,B)}(\alpha,\beta)$, that is, we count how often α and β appear in the same alignment column of the pre-alignment of the languages A and B. The next step is to convert the occurrence counts into relative frequencies $p_A(\alpha)$, $p_B(\beta)$ and $p_{(A,B)}(\alpha,\beta)$. In a random alignment of unrelated words we would expect $p_{(A,B)}(\alpha,\beta) = p_A(\alpha)p_B(\beta)$. Statistically speaking, $\alpha \in A$ and $\beta \in B$ are likely to be related if they occur more often together in an alignment than expected. It is customary, therefore, to define the score as

$$\sigma_{(A,B)}(\alpha,\beta) = \log\left(\frac{p_{(A,B)}(\alpha,\beta)}{p_A(\alpha)p_B(\beta)}\right). \quad (1)$$

This so-called log-odds score is theoretically justified by a simple model of independent evolution (Durbin et al., 1998; Altschul et al., 2010) if there is enough data for training.

Character-based, that is, unigram alignments of words have been described repeatedly in the literature (see, e.g. Kondrak, 2000; Cysouw and Jung, 2007; Kondrak, 2009; Steiner et al., 2011). The alignment is often computed by means of a recursive scheme known as dynamic programming in computer science. The same idea readily extends to bigrams. Since the syllable structure is

rarely known, it appears prudent to consider *all* bigrams, and since the beginning and the end of words are often subject to different sound changes, it is desirable to treat them separately. The bigram scoring algorithm can be easily extended to handle this by introducing two additional symbols, ^ and $, before the first and after the last character of each word. Thus the word $w =$ ^ $w_1w_2w_3w_4$\$ of length 6 (four characters along with the word beginning and end markers) consists of the 5 bigrams ^ $w_1, w_1w_2, w_2w_3, w_3w_4, w_4$\$. An example of an alignment and its scoring is shown in Fig. 3. From an algorithmic point of view, bigram alignments are a fairly straightforward generalization of the well known Needleman-Wunsch algorithm (Needleman and Wunsch, 1970) used to solve unigram alignments (see Appendix A).

The text and formulas here are ambiguous as to whether sigma and nscore are defined of a pair of languages or a pair of words from two lgs. Presumably the latter but actually the sigma formula as written contains free variables that ranged over the full set of pairs between two languages on the previous page. Formulas are used for clarity so please be explicit as to what is defined over what and the domains of free variables. Based on this, one can proceed to define the total score of two words u from language A and v from language B $\sigma(u, v)$ as the sum of all bigram scores of all aligned bigrams $\sigma(u, v) = \sum_{\alpha\in u,\beta\in v,\alpha \text{ aligned to } \beta} \sigma_{AB}(\alpha, \beta)$ together with the contributions of all gaps,that is, insertions or deletions of characters, and then a normalized score (*nscore*) obtained by dividing σ by the number of score contributions. Note that the similarity score $\sigma_{AB}(\alpha, \beta)$ for bigram α from language A and bigram β from language B is defined in the scoring model. In the case of bigram alignments this amounts $nscore = \sigma/\ell$, where ℓ is the length of alignment without ^ and $. Such a normalization makes alignments of words with different lengths comparable by reporting an average score per aligned position. The reader may be left wondering about situations where one sound/symbol in language A corresponds to two in language B (e.g. Spanish puerta - Italian porta, or instances where two symbols correspond to a single sound in one language). This is one of the reasons that I recommend consolidating the discussion of representational issues and being more explicit about what "gaps" are in this method. For this todo maybe point to Fig. 3? maybe I can find another alignment where there is no deletion score used even though there obviously is one.Would be cool if we could use the examples above, e.g. bueno and bono. Do we have an fitting scoring model for this?

From alignment scores to cognates. These normalized alignment scores can be used to distinguish cognates from non-cognates. In Fig. 4 (left), we show histograms of both the simple unigram scores and the bigram scores for all pairwise alignments of words from 11 Indo-European languages (Table B3). Which 11 I-E lgs and why those (and, not, say, a single pair). This matters as the results should look quite different for distantly vs closely related pairs of languages. For both scoring models we observe two clearly separated peaks. The peak on the left, centered at negative score values, corresponds to alignments of unrelated words, that is, non-cognates, while the peak centered a positive score values corresponds to cognates. The right panel shows analogous data for the Guaycuruan language family. Here the separation between cognates and non-cognates is much less perfect than in Indo-European, but the two peak structure is still visible.

Note that the peaks are smoother and more clearly separated from each other when the bigram score is used. The use of the bigram score thus improves the capability of the normalized alignment scores to distinguish cognates from non-cognates. This is not unexpected since regular

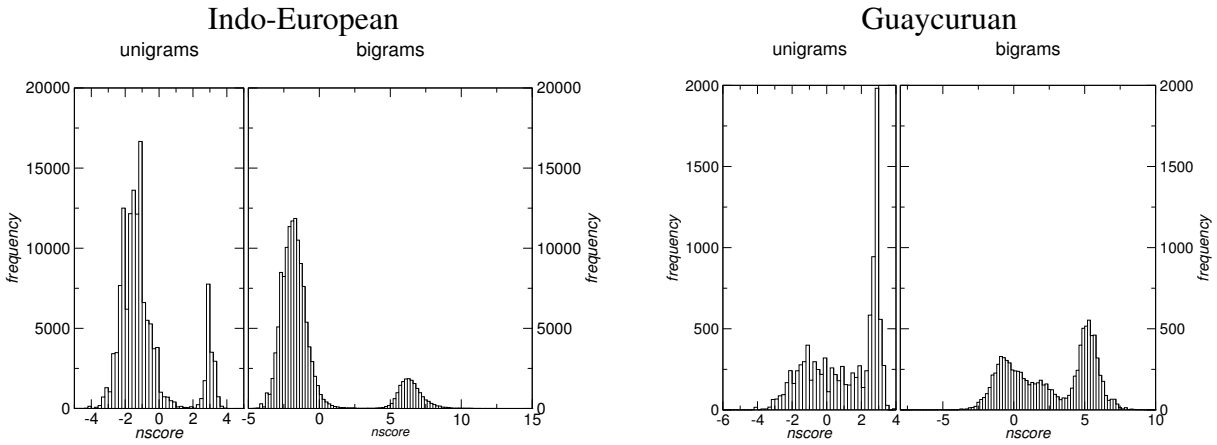


Figure 4: Distribution of pairwise alignment score for 11 Indo-European (Table B3) (left) and 3 Guaycuruan languages (Toba, Pilagá, Mocoví) (right) with a simple unigram scoring model (left in each panel) and a bigram scoring model (right in each panel) trained on the initial alignments obtained with the simple unigram scoring model.

correspondences are often sensitive to neighboring phonetic contexts, and a large amount of the context sensitivity can be accounted for by looking at one neighboring sound along with word boundaries. However, neighboring sounds are an imperfect proxy for syllable boundary. Word boundaries aren't really an 'imperfect proxy' for syllable boundaries. Rather, they are a restricted subset of syllable boundaries that are recoverable from orthographic representations.seriously??? In more difficult cases, such as the Guaycuruan example, the situation is far from perfect. Here the cognates are not completely separated from the non-cognates by the *nscore* even for the bigram scoring model. This leaves us with two possibilities: (1) We can seek to further improve the scoring model. Below we will briefly discuss a few ideas in this direction. (2) We can accept that the computational method does not provide us with a perfect way to identify *all* cognates, that is, we are left with a trade-off between false positives (false cognates: word pairs that are not truly cognates despite their good score) and false negatives (unidentified cognates: word pairs that we fail to recognize as cognates because their score is not large enough). The choice of the threshold is left to us. Depending on the analysis for which such cognate identification is needed, we may opt for a conservative strategy and minimize the false positives at the expense of missing some cognate pairs, or we may choose to be more inclusive and allow some false positives to sneak in and contribute to disruption of expected patterns at these later stages. Importantly, however, the automatic cognate recognition path provides these later stages of analysis not merely with a binary decision of whether or not a pair is a cognate, but rather with a score that represents the weight of phonetic evidence in favor of cognacy. But cognacy is a yes/no property and modeled as such in the work the authors cite, so the inability to provide a yes/no answer is incompleteness rather than a virtue. Any further deductions obtained from such putative cognates can weight the evidence by this score, thereby lowering the deleterious effect of false positives. Alternatively, of course, the permissive cognate list could be post-processed to identify and remove false cognates based on expert knowledge, with manual effort being allocated more to cognate pairs with low scores. Erroneous cognate detection may also result from erroneous or inconsistent orthography, manual effort

may also therefore be useful in improving the transcription, so that better cognate recognition will be achieved by the automatic procedure. It is also important to note that although the choice of the score cutoff is left to the user, it is not arbitrary. The shape of the score distribution provides quantitative information on the expected number of false positives and false negatives for each choice of the cutoff. We will return to this point again several times throughout this contribution.

We have seen that the improved scoring model leads to refined cognate identification. In principle we could now iterate this workflow again, using the alignments of the revised cognate pairs to recompute a refined scoring model. Somewhat surprisingly, Steiner et al. (2011) observed that the method converges already after a couple of iterations and only the first step from a crude pre-alignment to detailed scoring model yields a dramatic improvement in the accuracy of alignments and cognate identification.

Further improvements to the scoring model are possible in principle. In order to capture more of the correlations implied by the phonetics of the languages in question it may be desirable to go beyond bigrams to k-grams for $k \geq 3$. Such a model would also take care of local transposition These were assumed to be so few as to negligible earlier in the paper so that is not much of an improvement. But if it were important to capture them, k ¿= 3 is not necessary as adding transposition operations to the Needleman-Wunsch algorithm still keeps it polynominal. and regular sound changes dependent on longer contexts, or even word harmony features. The definition of scores described above generalize in a straightforward manner since the symbols α and β may signify arbitrary combinations of sounds. In practice, however, the sparsity of the available data is a limiting factor: not all 3-grams that are possible in given language will appear sufficiently often in word list data to get reliable estimates of their frequencies. A possible remedy is to use 'mixed' scoring models that use k-grams with variable length depending on their frequency in the data. Related techniques have been used in bioinformatics as means of describing sequence patterns (Begleiter et al., 2004). The use of such methods, and, in fact, the entire issue of discovering statistically significant contexts automatically has, to our knowledge, not been explored so far.

A PROBABILISTIC MODEL OF LEXICAL EVOLUTION. The approach outlined above is designed to represent the relationships between the observable data as directly as possibly, without making *a priori* assumptions about how exactly languages evolve. An alternative approach is to start by approximating language evolution as a stochastic process acting on the phonetic and lexical structure of a language. From the definition of the stochastic process the conditional probability $P(D|\mathcal{M})$ of the observed data D—in our case word lists of a set of languages—can be computed as a function of a typically large set of model parameters $\mathcal{M}$. The idea of the maximum likelihood approach is to find the set of parameters that maximizes $P(D|\mathcal{M})$, that is, the set $\mathcal{M}$ that makes the observed data the most likely outcome. With this type of modeling, one makes two fundamental assumptions: (i) the underlying stochastic processes capture the dominating processes of language evolution and (ii) the observed data are typical. In practice, the maximization of $P(D|\mathcal{M})$ is achieved by iteratively estimating: (1) the probabilities of non-regular sound changes from ancestor to observed phonemes, (2) a table of regular correspondences and (3) alignments between words across a set of related languages.

A priori the model allows for an arbitrary amount of phoneme evolution. Just as described in section 3.2, one needs to start the process with an initial alignment. As an example, one can

start with all words in one language that contain a certain phoneme and identifies the most over-represented phoneme in the corresponding words in related languages, compared to expectations based on the overall observed phoneme frequencies in those related languages. It uses these estimates of excess representation to initialize sporadic sound change probabilities and a regular correspondence table, and then uses this information to align the words in related languages. The non-regular sound change probabilities and regular correspondence table are then refined by looking at only the aligned positions and the process is repeated until the iteration converges. This method of alignment was used to obtain the regular correspondences in the Turkic language family in Hruschka et al. (2015) (Table B2). We use the data set used in that paper to demonstrate that a high fraction of cognates can be correctly found by choosing an appropriate cutoff for the best alignment score between randomly chosen words from different languages. The main advantage of using the Turkic languages as an example is that relatively comparable phonetic transcriptions were available, the language family has a relatively shallow time depth, and words had already been categorized into probable descendants of common ancestors, It should be mentioned that i) the results do not necessarily generalize to deeper families/cognacy and ii) that cognates in the Hruschka et al 2015 come in sets whereas the method described in the paper identifies cognates pairwise and may thus give inconsistent results of the type A is cognate with B and B is cognate with C but A is not cognate with C. so that the results could easily be compared against expert linguistic judgements.

Since cognates are known for this data set, we can compute the sensitivity and specificity of the cognate assignment for each choice of the score cutoff value: sensitivity is the fraction of the true positive cognate pairs with an alignment score at least as large as the cutoff value; specificity measures the fraction of non-cognates with an alignment score smaller than the cutoff. Each cutoff value thus yields a pair of sensitivity and specificity values that quantify how well the score-based separation between cognates and non-cognates performs. One can summarize the values in the form of the *Receiver-Operator-Curve* (ROC) shown in Fig. 5. It's more customary to present the f-score of the precision/recall corresponding to the different threshold values... replaced 'It is customary to' with 'One can' Each point on the line corresponds to a cutoff value and is placed according to the cutoff's sensitivity and specificity in the plot. The diagonal line indicates equal values for sensitivity and 1 − specificity. This corresponds to a completely random classification. ROCs below this line are worse than random. The closer the ROC approaches the upper left corner of the diagram the better the classification works. As a quantitative measure of goodness, one usually calculates the area under the curve (AUC), which is 1.0 for an ideal test. Mathematically, the AUC represents how often the test assigns a higher score to a random cognate pair as compared to a random non-cognate pair, and is, therefore, a threshold independent characterization of the quality of the scoring system. In Fig. 5 the AUC is 0.9.

The method can, obviously, be refined in ways described in previous subsections to detect changes conditioned by known phonetic contexts, for example, position within the word, neighboring phonemes or harmony. It is also possible to weight the commonly used words belonging to the core vocabulary more than the rare words in deriving the correspondence table, reflecting the expectation that the proportion of cognates and the regularity of correspondence is higher in this part of the vocabulary.

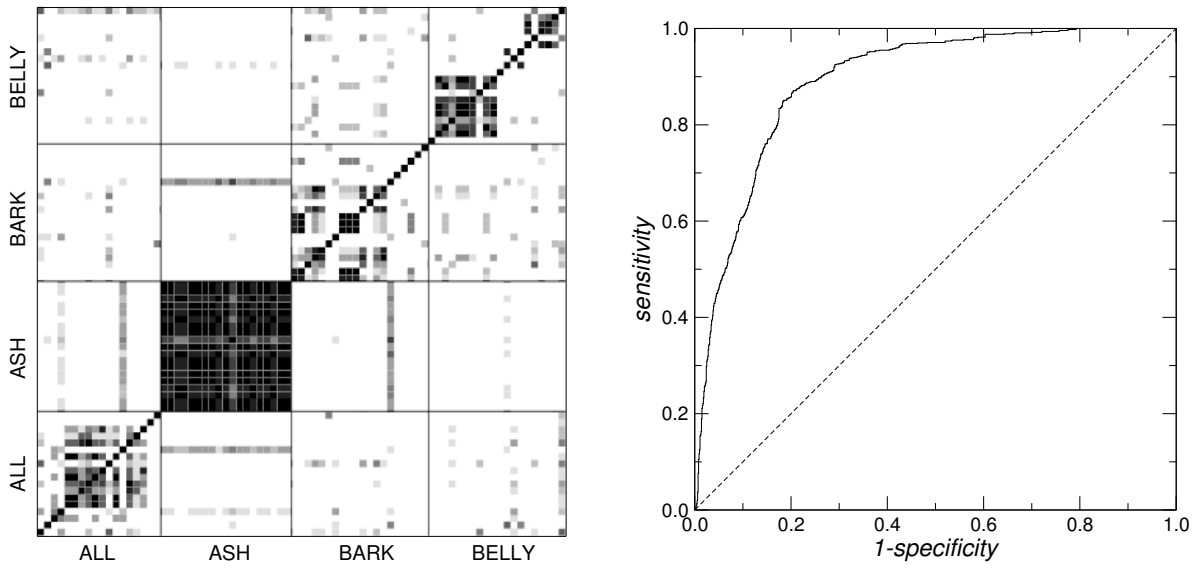


Figure 5: Aligning words using a likelihood based method can be used to detect cognates. Left: Data for 4 Swadesh meanings (all, ash, bark, belly) across 20 Turkic languages were aligned and the best alignment scores for each pair of words were converted to a distance measure and shown as a heatmap: black pixels: small distance between words (between 0 and 2), white pixels: large distance between words (> 14), gray pixels: intermediate distances between words (between 2 and 14). Islands of darker pixels along the diagonal reflect cognate classes. Right: An ROC curve for detecting cognates within 50 meaning classes in Turkic shows it is possible to find an alignment score cutoff with high sensitivity and specificity in separating cognates from non-cognates (Area-under-the-curve AUC= 0.90).

Comparing the two approaches. At face value the two approaches outlined above are quite different. The focus on alignments and their scores conforms more closely to the paradigm of sequence comparison in computational biology, while the comparison of probabilistic models focuses on the evolutionary processes and is somewhat closer to the traditional conceptualization in linguistics. do you mean the "alternative" Nevertheless, the two methods are largely equivalent and can answer essentially the same questions, albeit using different mathematical and computational techniques. These methods aren't equivalent from a traditional historical linguist's perspective, and probably wouldn't deserve any lengthy discussion as alternatives if they were truly equivalent. Perhaps a different word choice or a modifier on "equivalent" would make more sense here.

The likelihood method, for example, does not directly produce a scoring model. The results are, however, consistent with a scoring model. First, it is obviously possible to simply use the alignments to derive a scoring model as outlined above. Second, one can also use the transition probabilities between inferred ancestral sounds and their extant descendants to compute the probabilities of sound correspondences directly from the underlying stochastic model. Conversely, the scoring system derived in the first approach does not directly provide reconstructed proto-sounds. Well understood methods from computational biology are available, however, to infer ancestral states given observable transition probabilities (Pennisi, 2005; Liberles, 2007). Brown et al. (2013) investigated the inferrence of sound change rules from a scoring model even though the direction of the change was not labeled. Mathematically this should be possible, however, and

we take it on as an interesting open research question to solve this problem.

In principle, the two approaches can therefore be compared with each other at all relevant levels: the individual alignments, the inferred scoring systems, the reconstructed ancestral sounds, and the estimated language phylogenies. Such detailed comparisons of different computational techniques are important in their own right since they provide a measure of sensitivity to the varying assumptions inherent in these methods.

Both methods are alike in that they are almost entirely data driven. The alignment scoring, and hence the regular correspondences, are extracted from the data and represent only information that is contained in the data set that is actually used in the analysis. As such, one might miss regular correspondences that are not sufficiently prevalent in the word lists. Furthermore, the scores are explicitly dependent on the languages that are compared. Alternative approaches using a scoring system based on linguistic expertise also exist (Covington, 1996; Kondrak, 2003) and such models could also be designed to be more or less specific for particular language pairs or language families. Later in the paper sound change processes are argued be universal (a la Ohala) which means that there is a specific answer to the incertitude expressed in the above passage. The ”regular correspondences” you refer to here are the same as the ”table of regular correspondences” you mention on line 41 of page 12, correct? I suspect that some historical linguists will expect that all uses of the term ”regular” in relation to sound changes/correspondences will mean ”regular” in the strict Neogrammarian sense. It would be good to be explicit somewhere in this sub-section about whether ”regular correspondences” does in fact mean ”exceptionless” as in the Neogrammarian usage.

3.3 Phylolinguistics.

Trees and their reconstruction. Decades of practice in bioinformatics, in particular phylogenetics, has shown that the process of evolution by error-prone propagation of information very robustly generates tree-like signatures that can be retrieved from a wide variety of data by means of an equally diverse collection of methods without the need to have a detailed mechanistic model of actual processes of evolution (Waegele and Bartholomaeus, 2014). Many of these methods refer to indirect measures such as (dis)similarities, or employ approximate criteria such as the parsimony principle of cladistics. In fact, phylogenetics in the pre-molecular era was based entirely on ‘characters,’ that is, descriptions of characteristic features of organisms. This approach has been tremendously successful without any recourse at all to an underlying mechanistic theory of character change in biology. Clearly, it suffices for phylogeny reconstruction that the underlying evolutionary process causes the divergence of features and that distinct lineages are affected by changes in an approximately independent manner. We will return to violations of the assumption of predominantly vertical inheritance and limitations of phylogenetic reconstruction later in this section.

A thorough application of the comparative methods requires the *simultaneous* estimation of the language history tree, of the proto-languages corresponding to the interior nodes of the tree, of the associated regular correspondences, and of the cognates that are invoked in their support. This amounts to a comprehensive stochastic model of language evolution. While this approach is certainly the gold standard, it requires sufficient data to actually parameterize the model with

sufficient accuracy, and sufficient computational capacities. While this is becoming feasible at least from a computational point of view, Reference here is needed to Bouchard-Cote's book but, even more so, a justification for the totally unspported claim that it is feasible from a computational point of view is needed... no book found for the "computationally feasible" part we can point to the Bayesian phylogeny reconstruction methods and recent methods for reconstruction of ancestral states (Bouchard-Côté et al., 2012; Joy et al., 2016) which solve essentially the same problem in a biological setting.

it may not be the most efficient approach to analyzing the data. In the context of biological phylogenetics it often pays to subdivide the GOLD STANDARD inference task into individual components that can be solved independently from one another.

It is common practice in computational biology to compute sequence alignments first and to use them as starting point for the reconstruction of phylogenetic trees. The reconstruction of ancestral genomes (Pennisi, 2005) and ancestral sequences (Liberles, 2007) is then performed on a given tree. Inferred trees may then help to improve alignments, which in turn yield a better tree in an interative manner. In complete analogy, word alignments can be performed independently of cognate identification and the identification of regular sound changes (see also (Kondrak, 2009)). One may meaningfully start by first identifying regular correspondences between pairs of extant languages and then use the fact that these regular correspondences are by definition the result of sound changes from the same proto-language along the two independent lineages to piece this information together to approximately reconstruct proto-languages and then the regularities of sound change. This is an important question, but unfortunately not prudently discussed in this passage. Since the components depend on each other, it is not probabilistically correct to do it in the iterative manner, and, as argued elsewhere in the paper (p 16) it is not a correct approach from the perspective of propagating uncertainty. This separation of tasks is merely a matter of computational efficiency and expediency. In fact, both maximum likelihood and maximum parsimony methods necessarily use this kind of separation internally: likelihoods or parsimony scores are computed for a given tree, and then used to compare trees. Experience from computational biology, furthermore, shows that it is often pragmatically favorable to perform as much of the analysis as possible on directly observable data. For example, it can be helpful to identify regular correspondences between extant languages as a first step rather than trying to infer proto-languages and phylogenetic trees directly. Please explain what experience from computational biology shows how this is helpful if not for computational efficiency and expediency? As the text stands this claim is completelty unsupported. hab es gedruckt

Depending on the research question, it is often not even the necessary to attempt a full reconstruction of language phylogeny. Instead, robust and reliable statements on language evolution can be derived with much more modest approaches at both the level of modeling and at the pragmatic level of computational methodology. For example, reliable reconstruction of the subgrouping within a language family or identification of macro-families can be conducted on the basis of presence and absence of cognates without the necessity to model sound changes explicitly (Bowern, 2012; Bowern and Atkinson, 2012). How do you know the subgrouping in Bowern, 2012; Bowern and Atkinson, 2012 is reliable? The data is not given, the tree inference method uses exactly the tree priors taken over blindly from biology that the present paper warns about, and is squarely at odds with the flat subgrouping espoused by the earlier non-computational work.

NB: reconstruction of the subgrouping is misphrased, presumbly just ”subgrouping” is meant as there is no reconstruction in those papers.

In the *Classical Comparative Method* carried out manually, a valid reconstruction is usually interpreted to be a single highly likely solution. Likelihood based methods, on the other hand, emphasize the propagation of uncertainties. At its root, a likelihood based method proposes reconstructions at intermediate nodes and scores the tree based on the sum of the likelihoods over all possible reconstructions. The inclusiveness of the likelihood-based approach contrasts with approaches that have become traditional in manual reconstruction simply through exigencies of the labor required. To the extent that the data and our prior knowledge, in a likelihood context, concentrate the support of the posterior probability on or near a unique reconstruction, likelihood based methods can be reduced to the traditional interpretation without a significant loss of their content. On the other hand, when possible reconstructions are inherently uncertain, likelihood methods propagate the errors consistently, something that no reconstruction limited to only a single instance can do. Very similar statements can be made about parsimony or distance based methods in their domains of validity.

Beyond computational biology. Despite the conceptual parallels between biological phylogenetics and phylolinguistics, there are several practical concern that make it necessary to adapt and modify computational methods from bioinformatics and computational biology. As a consequence, computational tools from the life sciences are not readily applicable but need careful modifications and adaptations. For instance, regular correspondences are inherently directional and thus non-symmetric, while classical similarity measures are symmetric by construction. It is easily possible, however, to modify alignment algorithms so that they can work with asymmetric scoring models, allowing for the incorporation of directional changes between languages. Another complication is that while sequence alignments in bioinformatics can be content with substitutions, insertions, and deletions as basic operations, additional types of changes appear to occur rather frequently in language evolution. From an algorithmic point of view the inclusion of contractions, expansions, and metathesis is straightforward (Kondrak, 2000); it is a statistical question, however, when the additional uncertainty arising from the estimation of extra parameters is justified by the better fit that the model engenders.

Just as in the case of alignment algorithms, there is no reason why the scoring of trees should rely on symmetric similarity measures. Indeed, a few recent studies show that regular correspondences can be used just as well. In Bouchard-Côté et al. (2013), for instance, a family of probabilistic models of sound change is described. These were then applied successfully to the automatic reconstruction of Proto-Austronesian and its daughter/descendant Proto-Oceanic. A complete Bayesian approach to tree reconstruction, incorporating context-independent directional regular changes, was described by Hruschka et al. (2015). Similarly, the parsimony approach used by Steiner et al. (2011) inherently yields non-symmetric models of regular sound changes.

Another difference between the phylogenetic problem in computational biology and linguistics arises from the nature of the evidence. Genetic material being analyzed comes from individuals in a population, and the computed phylogenetic tree is an approximation to the genealogical relations between these individuals. As such, the splits in the tree represent survival of sibling lineages in the data set, and do not represent moments of special change. In contrast, linguistic material is

usually a record of a conversational norm in a society. Splits in a linguistic genealogy thus approximate to splits in linguistic communities. In this respect, linguistic analysis is more like analyzing morphological traits in the biological literature, and language evolution parallels evolution of morphological traits in biology. In both systems one finds evidence of punctuated evolution (Atkinson et al., 2008) as well as population size effects on rates of evolution (Bromham et al., 2015). Similar remarks apply to uncritical assumptions about uncorrelated Poisson nature of changes in various linguistic features.

There are additional problems for some Bayesian analyses that try to use information about the expected shapes of phylogenetic trees (Kingman, 1982). These expectations are based on finite variance birth-death models maintaining large populations. There is no *a priori* reason to believe that linguistic community splits will lead to similar trees. Nevertheless, Bayesian methods are useful in propagating uncertainties and can properly incoporating non-linguistic constraints such as arising from known histories of population movements and lack of contact over certain time ranges.

These cautionary remarks apply only to a blind application of programs developed for the biological domain to linguistic data. What is needed, instead, is a reformulation of the problem for the linguistic domain taking into account its particularities. Such an approach carries over the mathematics already developed to deal with historical processes in biology to this domain without a false reduction of linguistic or cultural traits to genetic sequences or genes.

DEEP PHYLOGENY AND ITS LIMITATIONS. Similarity serves only as a first filter for relatedness. In fact, the rate of 'random' mutations variously affecting the sounds in individual words is so low that the method of comparative historical linguistics stipulates that only regular correspondences can be invoked to support the recent relatedness of languages. It is not entirely clear what this sentence means, or how to evaluate the claim here without knowing exactly what you mean by 'random' mutations in this linguistic context. Do you mean sporadic changes? Either some clarification or a reference to some supporting discussion would be very helpful. But at deeper time scales, not only these 'sporadic' sound changes, but also fusion of morphemes, morphological analogy, lexical diffusion, frequency effects, dialect mixture, inherent variations, borrowing from other registers, etc., build up and reduce the observed regularity. The view of many linguists is that when the cumulative effect of these intrusive events obscures the regular correspondences, reconstruction of chronologically deeper families is futile. This is especially problematic since a desirable, though not strictly necessary, result of the application of the comparative method is the reconstruction of a proto-language invariant from which the descendant languages can be deduced via a set of regular phonetic laws.

A variation has been advocated that reconstructs proto-languages using a step-by-step reconstruction sequence, where intermediate reconstructions on a smaller time scale are then compared with each other (Whorf and Trager, 1937; Haas, 1969). This is useful when due to layers of accumulated phonetic change, ancestral states of great time depth are not easily deduced from modern languages, but it throws away possibly informative information carried in the *variation* of forms within clades of shallow time depth, not allowing information from sister subgroups to inform the reconstruction (Hockett, 1958; Greenberg, 1987; Fox, 1995). Instead of choosing one extreme over another, a probabilistic framework can be designed to admit effectively irregular changes at a

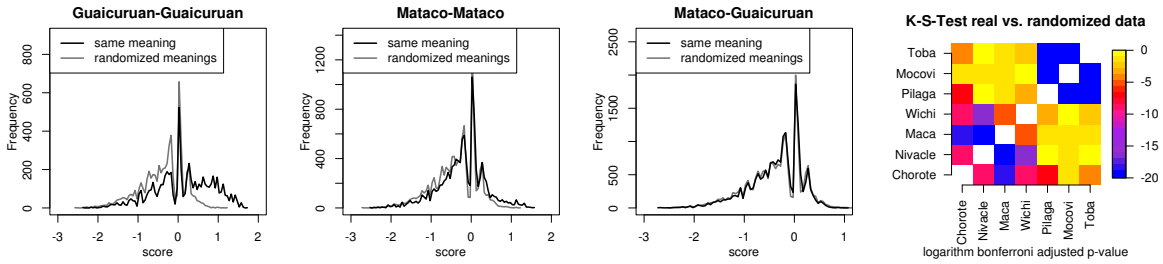
low rate, but favor a regular explanation when the data demands it.

There are, of course, inherent limits to the resolution of chronologically deeper branches in phylogeny. All signals that can be used to infer trees from extant data (e.g. sound changes, lexical replacement, and turnover of typological features) are necessarily cumulative and therefore will eventually saturate. Deep phylogeny applications in biology, therefore, focus on slow-evolving characters and disregard features that evolve at faster time scales. It is at present not completely clear whether sufficient phylogenetic signal has been retained by languages in the different well-established families to disentangle their deep phylogenetic relationships. This is, however, a question that can be addressed and answered by quantitative statistical methods in a systematic manner using the available data sources.

Many key questions of deep phylogeny in biology have recently been addressed very successfully not only because genome projects have provided access to much larger data sets for individual taxa but also because methods have become available to combine different data types from molecular sequences to detailed morphology character tables (Waegele and Bartholomaeus, 2014). Maybe even more importantly, denser taxon sampling leads to considerable improvements in the quality of phylogenies due to noise reduction (Zwickl and Hillis, 2002), helping in particular with the resolution of early branches. Analogous approaches can be envisioned for language comparisons. The expansion of word list well beyond Swadesh sets, the integration of slow-evolving language features, and the addition of more languages together are likely to lead to major progress in deep phylogenetics of languages. The need for a drastic expansion of the data sets in phylolinguistics implies that efficient computational methods are needed to help with preparation and quality control of the input data sets at an early stage. Thus, for example, typological errors often introduce rare characters or unusual sequence of characters into the data; a hidden Markov model could be trained to learn the probabilistic patterns in the sequence of characters composing the words of a particular language and extremely rare occurences of characters or sequence of characters can then be flagged for manual verification. Do you mean ”typographical errors”? As written, the meaning of this sentence is unclear.

THE EFFECTS OF BORROWING. Not all language change can be attributed to vertical inheritance. It is an important function of a good alignment method to seed language comparisons with the correct regular sound correspondence, rather than a false correspondence suggested by borrowed forms. Whether this is achievable, and how much linguistic knowledge may be required to supplement the data for a particular comparison, depends on the structure and coverage of available data from the languages being compared. In particular, extensive contact and borrowing might make it impossible for purely computational methods to disentangle vertically and horizontally inherited words. This is also an issue in bioinformatics, where Hidden Markov Models have been quite successful in recognizing sequences that have been acquired by horizontal transfer (Dufraigne et al., 2005). It will remain to be seen whether a similar approach can also be successful in cases of large scale borrowing. Please explain what this HMM does? (HMM is an extremely general technique for sequences and it is not obvious how they can be used in the manner mentioned).

It is generally believed that the vertically transmitted patterns of sound change between two language lineages form consistent systems applying to all or nearly-all words they affect, even if the sounds themselves have diverged widely. Isolated loan words may show similarities of sound



(a) (b) (c) (d)

Figure 6: Distribution of pairwise alignment scores for languages from the Mataco (Nivaclé, Maca, Wichí, Chorote) and Guaycuruan (Toba, Pilagá, Mocoví) languages. In panels (a-c), pairs of words with the same meaning according to the input word lists are compared with scores for pairs of words with independently randomized assignments to meanings. For comparisons within each language family (panels a and b) a clear shift to the right is observed for meaning-matched word pairs: that is, more meaning-matched pairs with large scores are observed compared to pairs with randomized meanings. In contrast, the two distributions are nearly identical for comparisons of one Mataco with one Guaycuruan language. Thus, there is a clear statistical signal for relatedness within Mataco and within Guaycuruan, but not between the Mataco and Guaycuruan families. (d) In a more detailed analysis, each pair of languages is compared separately and the statistical support for the difference of distribution is measured by the Kolmogorov-Smirnov test. We find strongly supported blocks (cooler colours) within the Mataco and Guaycuruan language families, but little signal across the family division. Data were recomputed from Steiner et al. (2011).

patterning with other languages, but they should not in general assemble into a system with the same degree of internal consistency as the system produced by vertical descent. For example, Russian *molozivo* 'colostrum' is cognate to German *milch* 'milk' and shows more consistency with the regular correspondences, rather than the borrowed form *moloko* 'milk' which is semantically more similar to *milch*.[3] In this sense the emphasis on regularity is believed to reflect more fundamentally the way language structure causes relatedness due to common descent to be expressed in lexical comparisons. Note that we use the term lexical comparison to explicitly include the comparison of phonemes/characters comprising the cognates in addition to the more traditional analysis of the presence or absence of cognates with a given meaning. Similarity of non-loanwords can carry information about timescales in a context defined by the system of regular correspondences. In practice, however, whether the internal system coherence produced under vertical descent can be distinguished from BORROWED COHERENT CORRESPONDENCES will depend on the number of words that have been borrowed from individual sources, the way these are distributed among core and peripheral vocabulary items, and whether influences on other language features such as morphology have influenced the use of either vertically transmitted or loaned words.

3.4 THE VIRTUE OF STATISTICAL TESTS. In the last section we sketched the basic tools and procedures that take us from raw data to the estimate of trees, regular sound changes or alignments. However, the whole enterprise relies on the assumption that there is a bona fide phylogenetic signal in the data. Furthermore, we have listed a few factors that might account for the absence of a such a signal. It should be noted that the methods discussed before will yield an answer even if the data at hand is essentially structureless noise—in other words, the fact that a tree can be produced is not a guarantee that it bears any meaningful information with respect to genealogy.

For the purpose of distinguishing structureless from potentially informative data, statistical thinking plays a central role. The key notion is the NULL HYPOTHESIS. Roughly speaking, a null hypothesis is a scenario or a collection of scenarios where there is no signal in the data. This would answer the question of 'how would a tree, regular sound change, or an alignment look like when there is no phylogenetic information at all?' The goal is to have a concrete baseline against which one compares the empirical results: if the results found in the analysis of data do not differ in any meaningful way from the uninteresting case of the null hypothesis, then we have no case for our analysis, unless strong external evidence could be invoked. To give an extreme example, if we align two series of words from a pair of languages that are believed to be related and find that their similarities are not so different from what would be found in a random collection of strings, one has to either drop the idea of genealogical relatedness, or there must be good arguments (for example, genetic or anthropological data suggesting that the populations were related) to persist in the quest for genealogical relatedness. Even then, for such a postulate of relatedness to be entertained, an explanation, such as a large time depth, for the absence of a signal has to be given.

Let us flesh out a concrete example in more detail. In the case of cognate judgments based on similarity scores, for example, one could construct a null model to test that pairs of cognates are more similar than pairs of non-cognates. Let us assume that we know, for a particular scoring model that we want to use, the probability $P(s)$ that the score s is the similarity score of a pair of non-cognates. This distribution, then, can serve as the null model: if the results we find are comparable to what one would get with non-cognates, there is little motivation for pursuing the matter any further. We can then calculate the similarity score $\bar{s}$ for a word pair ω and ask how likely it is to find such a score or a more extreme score under the null model, that is, under the score distribution of the non-cognate word pairs. In the case of the similarity scores, MORE EXTREME means scores that are even larger than the observed score $\bar{s}$. Thus, the probability that our word pair ω has a score of at least $\bar{s}$ when the words are not cognates is $P(score(\omega) \geq \bar{s}) = \sum_{s \geq \bar{s}} P(s)$. This probability is called the p-VALUE and quantifies how likely it is to obtain the observed similarity score if the null model was true. The smaller the p-value, the more confidence we have that the observed score does not come from the null model.

A null model can be particularly detailed if we know precisely what the no-signal case is. In this respect, it can be as complex as the alternative hypothesis we entertain. However, there are shortcuts to null hypothesis construction based on the empirical data itself, a prominent example being PERMUTATION TESTS. The general idea behind a permutation test is to construct the null model by randomly rearranging the observed data in an attempt to destroy all the regularities that can be suspected to be related to the effect under consideration (see Oswalt (1970) for an example on permutation tests in linguistics).

Let us consider again cognacy as an example. Given word lists of two languages, we expect cognates to be much more frequent among words that share similar or identical meanings. The corresponding null-model thus consists of randomized word lists, where words with different meanings are matched across languages (Baxter and Manaster-Ramer, 2000). If meaning-matched words are more similar to each other than words from unrelated meanings—ignoring horizontal transfer and sound symbolic shared patterns (Dingemanse et al., 2015)—a statistically significant difference between real and permuted similarity distributions supports a non-trivial genealogical relationship between the languages. This idea is limited by regularities in the meaning space of

the kind discussed in 4.1-4.2 (as well as synonyms). The paper would make an actual contribution if this was taken seriously for a correct assessment of number emanating from a permutation test.

The data is again taken from the IDS. For each language, we have about 1000 words in the word list and unique identifiers for the meanings across all word lists. We took the similarity scores from (Steiner et al., 2011) and calculated the similarity of a word pair as the alignment score of the best alignment between the two words with respect to the scoring model. While this can be done in theory for all word pairs, we only chose word pairs with identical meanings originating from different languages. Furthermore, we split up the data into alignments within Mataco, within Guaycuruan, and between Mataco and Guaycuruan. The distributions of the scores, that is, the frequency of each score, is then shown as black lines in Fig. 6 (a)–(c). The entire procedure was then repeated with the permuted word lists. As explained above, the permutation is performed by re-assigning each word of the language to a meaning randomly and independently for each language. In this way, we measure how much similarity we would expect between words that typically do not have the same origin, that is, non-cognates. In other words, we estimate the NULL MODEL for the score distribution and show them as superimposed gray lines.

If we now want to answer the question of whether there is a non-trivial relationship between two languages, we need to test whether the score distribution of the real data is different from the score distribution of the permuted data. For this purpose we performed a Kolmogorov-Smirnov test (Smirnov, 1948), which basically tests the null hypothesis that the difference in distributions is only due to sample-to-sample fluctuations expected of finite samples. Once more, a small p-value hints to the fact that the null hypothesis is a bad assumption for the data at hand. Therefore, we performed the test for each pair of languages in the data from the Mataco-Guaycuruan group of languages and obtained a p-value for each language pair. Recall that the p-value measures how likely it is that we obtain a value at least as extreme as the observed. As we discussed before, if a single test is performed, small p-values suggest that the null hypothesis might not fit the observed data well. If several statistical tests that produce p-values are performed instead, then naturally from time to time a system that complies perfectly to the null hypothesis will yield a small p-value.

Therefore, one has to correct the p-values of the m independent tests. In our example, we have 7 languages and thus 30 different language pairs. Is the math correct here? 7 x 6 / 2 = 21 according to me. To illustrate the problem, let is consider 0.1 as our significance cutoff for the p-value. Then the probability that we call a result significant even though it is not, is exactly the p-value and thus at most 0.1. Now if we observe all 30 p-values from the 30 tests are 0.1, we can still correctly conclude that for each test the chance to call the result significant, if it is not, is 0.1. Vice versa, the probability that a test classifies the result correctly as significant is 0.9. Consequently, the probability that all 30 test classify the results correctly as significant is $0.9^{30} = 0.04$, which leads to the conclusion that the probability that we call at least one insignificant result as significant is $1 - 0.04 = 0.96$. In other words, even though we find 30 significant p-values, it is very likely that at least one out of 30 test is incorrectly identified as being significant. A traditional way to correct for this effect, known as multiple testing problem, is the Bonferroni family-wise correction (Bonferroni, 1936) which simply multiplies the p-values with the number of independent tests m or, equivalently, divides the cutoff by m. The Bonferroni correction is extremely conservative and other methods of correcting for multiple testing also exist in the literature, and may be used in cases where we have more tolerance for false positives (Holm, 1979; Hochberg, 1988; Hommel,

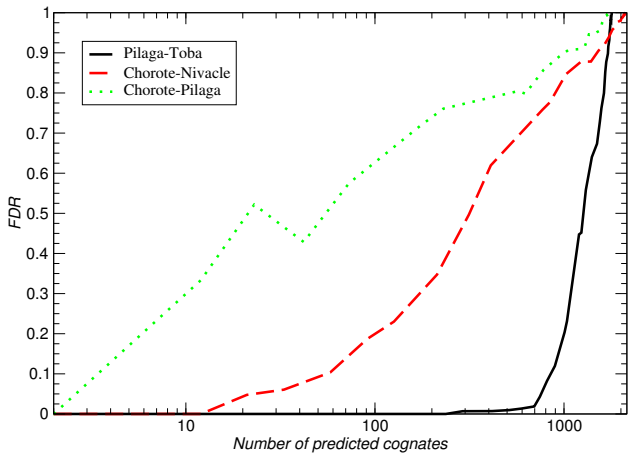


Figure 7: Estimates of the false discovery rate as a function of the predicted cognates for three pairs of languages. As the score cutoff θ decreases with the number of predictions, the FDR increases approximately monotonically. For the closely related Pilagá and Toba hundreds of cognates can be identified without much danger to make mistakes. Larger cognate sets for the related, but much more diverged languages Chorote and Nivaclé cannot be extracted without contamination by false positives, roughly 20% within the top 100 predictions. For the presumably unrelated languages Chorote and Pilagá, the FDR increases even more rapidly.

1988; Yoav Benjamini, 1995; Storey, 2002).

We depict the corrected p-values in Fig. 6(d) as heatmap where yellow corresponds to the highest possible p-value of 1 and blue corresponds to the lowest observed p-value of 10^{-20}. We can see that there is a very strong signal of relationship within the group of Guaycuruan languages. Also within the Mataco languages, we observed a significantly strong signal. Thus, for both groups we obtained the signal and can conclude that the languages have a relationship stronger than expected. Between Mataco and Guaycuruan there is, if at all, only a weak signal between Chorote and Pilagá. Thus, a non-trivial relationship between Mataco and Guaycuruan is not supported. While the results in this case are not surprising, they nevertheless demonstrate the power of permutation tests and statistical testing.

Of course, the usefulness of permutation tests depends on the quality of the test statistic. In our example, how well does the measure of word similarity represent the true relationship? The better the numerical value of similarity correlates with evolutionary distance, the more sensitive will the results of our test be. Thus, a similarity measure that depends on inferred patterns of regular correspondences is likely to provide a better inference of genetic relationships than a similarity measure that depends only on shared sound features in individual words. Nevertheless, statistically, any permutation test that gives a statistically significant result, after correcting for the number of independent tests performed, points to a non-random underlying process.

Both, the permutation test and the test of significant difference in the distributions, are model independent. In the case of the test for difference in the distribution just the empirical data is used without making any assumption on the underlying theoretical distribution of the data. Consequently, the Kolmogorov-Smirnov test can be used even if the theoretical distribution is unknown.

The results of permutation tests in our example have another immediate use, namely the iden-

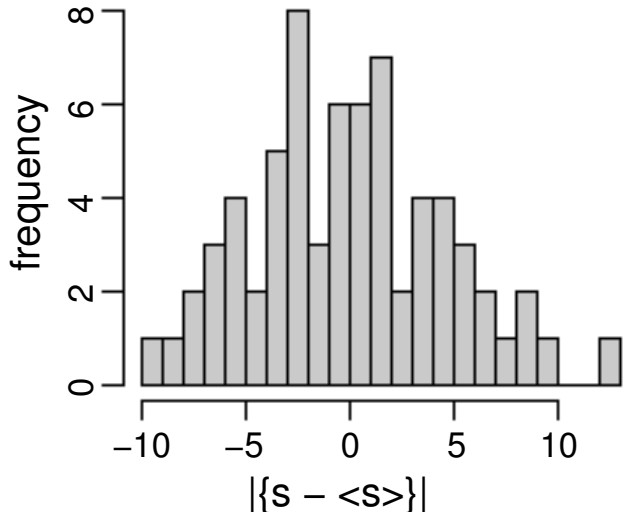


Figure 8: Comparison of 70 South American languages with English. The histogram shows the number $s - \langle s \rangle$ of words that are more similar than the randomized baseline.

tification of likely cognates. Retaining only those word pairs with a similarity score larger than some cutoff θ provides a set of candidate cognates. The randomized distribution tells us how many false positives (namely how many unrelated pairs of words are incorrectly classified as cognates) we have to expect at this level of similarity, namely as many as the number of pairs with a score larger than θ in the randomized distribution. In the examples in Fig. 6, we find virtually no expected false positives for scores above $\theta = 1$. As the cutoff is lowered, we expect to find more true positives, but only at the expense of a contamination of the candidate set by false positives. A common way to control this trade-off is to determine the false discovery rate (FDR), that is, the fraction of positive test results that are incorrect. The set of word pairs with a similarity $> \theta$ will contain both correct cognate pairs and incorrect ones. Since it is plausible to assume that word pairs from two different meaning categories will rarely be cognates, we can estimate the number of false positives as the number of word pairs with a similarity $> \theta$ after randomizing the assignment of words to meanings. Fig. 7 shows how the FDR increases with number of predictions. The acceptable level of the FDR depends of course on the purpose of the study. In many cases an FDR of 0.1 is often deemed acceptable but a more stringent value may be desirable, for instance, to limit the predicted cognate pairs to a number that is managable for an expert linguist to carry out an in depth analysis on.

Fig. 8 shows an example of an expected negative result. To check if there is signal of similarity between English and South American languages, we compute for each language the number of words of the same meaning that are more similar to English than the background similarity estimated by randomizing the assignment of meanings. The symmetric distribution around 0 shows that there is, as expected, no signal. The power of statistical testing, however, lies in the fact that a Kolmogorov-Smirnov test as described above can be used to assign this conclusion a precise evidentiary value characterized by the p-value of the test.

3.5 QUANTIFYING REGULAR CHANGE: THE IMPORTANCE OF REPRESENTATION. The ease with which sound similarities or regular correspondences can be discovered depends on the encoding used to represent the sounds of the language. For languages with a single dominant script, one can choose to use the established orthographies; but this is often not an ideal representation. Scripts and languages are often inherited from different sources, and orthography often encodes orthographic history, in addition to current distinctions. It also frequently fails to indicate important distinctions, or represents distinct sounds in ambiguous ways. Finally, many non-alphabetic writing systems do not directly encode the phonetics at all. Do alphabetic scripts do that? Or is segmental phonology rather than "phonetics" intended?

Using a fine-grained, subphonemic, transcription to represent the pronunciation accurately brings its own set of problems. Phonetic detail plays a role not only in distinguishing different words, but also to signal emotions, status and ethnicity. These differences lead to individual speech variations much of which can be represented in a sufficiently fine grained phonetic markup. Linguistically, however, the sounds that we are often interested in analyzing are the ones that contrast different lexical items. The overloading of the phonetic medium for carrying both linguistic meaning and extra-linguistic signals, and lack of strong constraints from an underlying physical substrate, naturally leads to a VIRTUALIZATION (Doyle and Csete, 2011), where the perceptual tokens map onto speech sounds in a labile but rule-directed fashion. Since these tokens, or phonemes, are the linguistic building blocks for lexical items, a word list encoding only the phonemic structure can retain the linguistically salient sound differences removing the less useful variation. A phonemic transciption is also useful in erasing ALLOPHONIC phonetic differences that are completely predictable from neighboring phonetic structure. Such a structure also has the advantage of making similarities and regularities across languages easier to detect.

Of course, it can be argued that the different sound values carried by each phoneme in closely related languages also provides information that can be used to measure the amount of divergence between the languages. Analysis of such data sets based on similarity alone is often difficult, without projecting to a representation that erases small but frequent phonetic shifts. On the other hand, if the data set is large enough to parameterize a sound change model and evaluate its goodness of fit, the information in such fine grained data can be properly used.

In summary, to find the relations at a certain depth, it is useful to encode the sounds in a system that erases distributional distinctions that are important at a shorter time scale but preserve slowly varying features that are useful for the classification.

To demonstrate that effects of different encodings is small we consider two examples. First we test the effect of minor inconsistencies between transcription systems. To this end we selected Mocoví and Pilagá, two of the three Guaycuruan languages also used for the analysis shown in Fig. 6 and artificially introduced some changes that mimic different interpretations of phonemes. We used the original data of Mocoví from the IDS database and replaced [i] by [e], [k] by [c], and exchanged [a] and [o]. Thus, while in the initial encoding [a] of Mocoví and [a] of Pilagá were likely the same sound, in the artificially recoded data this is not longer the case. In addition we have erased the difference between [k] and [c], and [i] and [e], respectively. We prepared two data sets. One data set contains Pilagá and the Mocoví in the encoding provided by the IDS. The other data set contains Pilagá and the artificially recoded wordlist of Mocoví. For both data sets, we trained a bigram-model as described above and obtained pairwise alignments with the

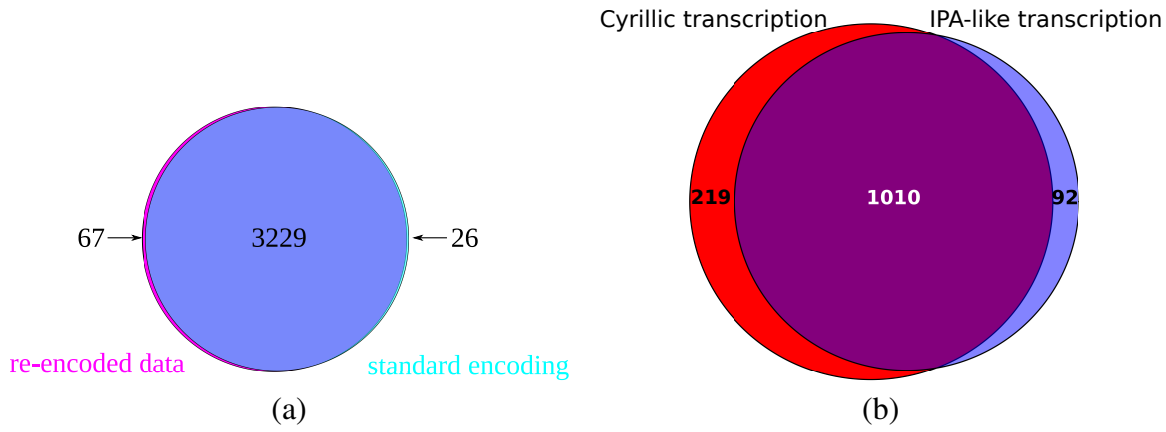


Figure 9: Overlap between the pairwise cognates: (a) Pilagá and Mocoví and Pilagá and the re-encoded wordlist of Mocoví. 97.2% of the cognate pairs are found in independently of the encoding. Reducing the FDR to 0.001, 97.5% of the pairs are found independently of the encoding. (b) Tsez Mokok (IPA-like and cyrillic transcription) and Tsez Sagadin (cyrillic transcription).

trained bigram-model. It is important to note that the score values are not directly comparable between different data sets. We therefore used permutation tests on each data set to obtain the score-cutoff that corresponds to an FDR of 10% and used these score cutoff values to make the cognates assignments for each dataset. Then we compared the results between the native and the artificially recoded set. We found that 97% of the cognates pair called in at least one data set, are also called in both cognate sets (see Fig. 9a). The final sentence of this paragraph needs to be reworded for clarity.

The second example was chosen to show that even drastic changes in the encoding have only very moderate effects on the alignments and the subsequent cognate identifications. To this end we use two different transcriptions of the IDS wordlist of Tsez Mokok. One uses an IPA-like transcription and the other one uses a cyrillic encoding. The wordlist were obtained from different versions of the IDS. Thus we removed all entries that are available in only one of the two transcriptions. Again, we prepared two data sets, Tsez Mokok and Tsez Sagadin in cyrillic transcription and Tsez Mokok in the IPA-like transcription and Tsez Sagadin in cyrillic transcription. As for the artificial example, we trained a bigram-model and used a permutation test to find a score-cutoff corresponding to a FDR 10% to produce a cognate judgements for both data sets (see Fig. 9b). Most of the cognates were found independently of the encoding (76%). Using the same encoding, that is, cyrillic transcription for both wordlists, yields additional 16% cognates that were missed when different encoding were used for the two wordlists. For this experiment we used only one iteration to train our bigram-model. The ability to detect cognates based on the alignment score would likely increase when running multiple iterations. No attempt was made to check whether the transcriptions are self-consistent, that is, whether different signs were used to encode the same sound within a given transcription. We also note the some noise in these data arises from differences in the entries such as alternative suffixes or prefixes which are sometimes provided within parentheses instead as an separate entry.

These experiments demonstrate that automated cognate detection is very robust against small

differences in the encoding used for the word list and thus tolerates occasional errors in the data. In our 'easy' example we found a residual level of about 3% discrepancies, This conclusion should be qualified by the fact that only closely related languages were used in the tests. Of course, then a small amoutn of error drowns in the flood cognates. More interesting would be to assess the impact in a case where the error amound would compete against a similarly small amount of cognates. which is small enough to be tolerated in further analysis. Even for completely different encoding schemes that follow different traditions we observe that the majority of cognate call is independent of the encoding scheme. Substantially different encodings, furthermore, mostly lead to a loss of sensitivity, that is, an underprediction of cognates. In cases where the residual levels discrepancies might be problematic, the automatically produced cognate calls provide at least a very good starting point for further manual curation of cognate assignments. And, of course, there is the possibility to choose a smaller FDR value to obtain a smaller but more accurate set of cognate pairs.

3.6 From non-parametric overviews to detailed probabilistic models. The approaches discussed so far were non-parametric. In the case of the alignments, this in particular means that it was not necessary to include prior knowledge about evolutionary process to obtain similarity measures between words. There is no need to know how the languages are related to each other, which proto-languages existed and what they looked like. This becomes important if no clear model for the phylogeny is established yet, the phylogeny could not be completely resolved, or the different models of the phylogeny are still hotly debated. We, furthermore, showed that one does not need to include the sound changes but can infer them indirectly from the scoring model. The exact scores for matching the observed characters can also be estimated based on the data. All these parameters, namely the phylogeny and scores, would be defined *a priori* in a parametric method but do not need to be specified in the non-parametric case.

When applying the non-parametric approaches we discussed before, one needs to choose the similarity measure that can be used to classify the related languages. Since language change is a composite of many underlying processes, the similarity measure almost always captures a composite of many different pieces of evidence. For example, different words change at different rates (Pagel et al., 2007), and consonants are perceptually different from vowels in word recognition (Cutler et al., 2000). [4] The most efficient use of lexical data for determining deep language relationships, therefore, should weight the stable words and consonantal identity more. Is this a language independent result? The signal from vowels is more informative when the vowel inventory is larger than average. In the non-parametric approaches, such choices of variously weighting the evidence are choices external to the evidence, and made *a priori.*

In contrast, likelihood approaches depend on detailed models in which all the parameters are simultaneously and consistently estimated. It can be shown statistically that likelihood based estimation of models and their parameters has many desirable asymptotic properties: in particular, they automatically re-weight the data to answer each posed question efficiently. In other words, the likelihood method 'forgets' the initial weighting of the data as the optimization progresses and reaches the same end results irrespective of the the starting point. Consequently, there is no need to choose a specific start point; instead any random choice will do. These asymptotic properties, however, hold only if the amount of data is large and the true generative model, that is, the true

evolutionary processes that lead to the observed languages and sounds, can be well approximated by one or more of the models under consideration. Such an approximation may take the form of ignoring the correlations introduced by a set of complex unmodeled processes, replacing them with uncorrelated random variables, or, instead, reducing the randomness by endogenously specifying the correlations. As an illustration, consider the example of modeling sound changes along the branches of the tree. Often sound changes are conditioned, for example, they occur only in specific contexts. What if those contexts are not known? We could simply model sound changes as rules that are always applied if a specific sound occur. In this case we would recognize that the model of unconditional sound changes cannot fit the data. Let us assume, furthermore, we cannot model the unknown context-dependencies since we do not have enough data to allow the model to choose from all possible context-dependencies. The remedy in this scenario is to ignore the context dependency and instead assume that a change occurs only with a specific probability. Now we can fit the data. Even more, the statistical procedure provides us with its best estimate to where a sound change occurred and where it did not. Hence we can calculate the correlations between the inferred sound changes with position, context, and even with another sound change. In a refined model, one would condition the probability of the sound change on these confounding factors.

The likelihood based models do not, in general, degrade gracefully as we deviate from the condition that a tested model is an effective approximation of reality. With vastly incomplete knowledge, therefore, the choice between the likelihood based parametric approaches and the non-parametric approaches described earlier is, essentially, a trade-off between efficiency and robustness against model misspecifications, that is, producing the correct results even though some aspects or parameters of the model are wrongly estimated.

Both classes of approaches—the parametric likelihood based models and the non-parametric estimates based on similarity measures—ultimately rely on a notion of uniformitarianism: that the process of language change and diversification does not change over time. Only in very heterogeneous, rapidly changing, or extremely long time durations the rates of this process can be averaged over and approximated by an additional uncorrelated noise. At intermediate times that is often the most interesting, however, non-stationarity of the process is an important problem. Non-stationarity in these cases usually means that the probability distributions of sound changes change over time or that the scoring model are different depending on the age of the words. Two partial solutions ameliorate this somewhat. First, one can test the assumption of uniformity (Hruschka et al., 2015) in the data set under consideration, so that this and other modes of model failure can be quantified and incorporated in the final confidence interval.[5] Second, models that allow a drift of the underlying process parameters, such as rates of change (Thorne et al., 1998) or patterns of covariation (Penny et al., 2001), have been developed and used, and with enough data, the extra parameters introduced can indeed be estimated.

3.7 Computational methods and inference. Since computational methods today implement almost all of the traditional methods of historical linguistic reconstruction, they have the large potential to aid the traditional linguists in their research. The major strength of computational methods is, however, the estimation of approximate models from vast amounts of linguistic data. The output of such a method is often presented as a properly scored choice between alternative histories.

For the likelihood-based approach of estimating Bayesian posteriors, the final score can be interpreted as a measure of the rational certainty arising from prior beliefs about model approximations and the data at hand; such scores from various diverse evidence can, therefore, often be combined to provide a composite picture without much additional calculations.

These scores, moreover, are intended to formalize standard linguistic understanding. The scoring method for a recently implemented likelihood based method (Hruschka et al., 2015) can, for example, be described as proposing sound correspondences, reconstructing intermediate ancestral forms probabilistically and evaluating the ability of such a model to explain the data with a minimum of extra random, that is, unexplained, changes. These methods can be easily extended to simultaneously evaluate the proposed intermediate sound systems and other features of the reconstruction, but many rare processes are left out of models as a practical consideration.[6]

Relative to this, the strength of manual curation lies in being able to handle less data but many more particularized situations by inductively drawing upon one's experience in various areas of linguistic, philological and cultural knowledge that currently remain untapped by computational methods (Starostin, 2010). Though this approach suffers from the well-known problem of over-fitting—seeing patterns in random noise—the alternative of computational methods are only expected to be correct on average. Individual nodes of a phylogenetic tree, reconstructions of particular word forms, or determination of specific regular correspondences can, always, be affected by model approximations. Even here, however, the computational methods can be easily set up to 'explain' its answers: to provide, for example, not only a phylogenetic tree and the confidence we ought to assign it, but also a list of evidence in favor of such a reconstruction and conflicts that are left unresolved by the result. Such evidence and conflicts, as well as a score indicating their significance for the proposed reconstruction, can focus the attention of linguists and guide further research.

While the methods sketched here complement and assist the labor of traditional historical linguists, they constitute the only alternative available in cases where information is scarce or contradictory. A prominent case is that of the Tasmanian languages, discussed in detail in Bowern (2012) (which we follow in the next paragraphs). After the settlement of British settlers in the island (mostly during the 19th century), native population experienced a sharp decrease in number followed by what is usually perceived as a decomplexification process in their material culture. "After the settlement of British settlers in the island (...), native population experienced..." Little evidence about the cultural organization of the Tasmanian people has survived, with different accounts differing in the degree of unity or diversity across the island. "...with different accounts differing in..." To worsen the situation, few Paleolithic archeological sites exist, and the climatic conditions of the island do not favor the conservation of artifacts. The genetic information provides limited help since considerable European admixture occurred after colonization. The linguistic evidence is not outstanding either. There are a few wordlists (with a widely varying number of elements) from all over the island, sometimes without precise information about the location or any ethnographic or demographic information about the speakers that served as informants. Based on this data, researchers have argued about the unity or diversity of Tasmanian languages, with perhaps the most widely accepted opinion being that linguistic analysis can lead at most to rejecting the idea that Tasmanian languages constitute a single linguistic family (Crowley and Dixon, 1981).

By using a combination of methods from evolutionary biology—prominently, phylogenetic inference—Bowern was able to gather enough evidence for 4/5 groupings (tentatively referred as macro-families) present in the wordlists that correspond somewhat with earlier archaeological classifications, while at the same time lending support to the idea that Tasmanian languages are not all directly related, at least to the time depth accessible to the methods and the data. Not only did the usage of methods from evolutionary biology allow Bowern to determine the number and extension of putative genealogical groups among the Tasmanian languages, but, more importantly, the usage of those methods lead to a natural quantification of uncertainty—so, for instance, while the evidence for a common ancestry of two of the inferred groups (those from Bruny Island and Oyster Bay) is strong, the estimate of the common root age is extremely imprecise, ranging from anywhere from 2,000 ybp to 20,000 ybp or more.

3.8 Putting dates on language trees. One important aspect of statistical modeling is that different aspects of the result have different confidence intervals and even different requirements on the underlying model. This is as true for computational methods as it is true of manually derived phylogenies: one often attributes a much higher certainty to the identity of the various large subfamilies of Indo-European than to their relationships to each other. In computational linguistics, one piece of the result—the absolute dates of various events—is often more uncertain and controversial than the classification. This mimics similar controversies that have arisen in molecular dating of the origin of biological taxa. The reconstruction of the phylogenetic tree, specifically its topology, requires only that the underlying process conforms to a so-called additive tree, that is, branch lengths measure the total amount of change that has occurred along them (Semple and Steel, 2003). As a consequence, a large array of rate variations occurring independently along the different branches of the tree do not affect our ability to correctly reconstruct them. Dating, on the other hand, requires an explicit clock and hence a way to explicitly model rate variations so that an ultra-metric tree can fit to the data.

Dating in phylolinguistics is a complex subject where methodological consensus has not been reached yet (Heggarty, 2006). Ultimately, since dates rely both on linguistic and non-linguistic evidence, this is not entirely unexpected. To convert the relative divergence times of the various branches to absolute times, information for some of the splits has to be in-built into the prior structure, which later permits to infer dates (and rates) along with branch lengths (Gray et al., 2011). For instance, Gray and Atkinson (2003) fixed the ranges of coalescence of most of the Indo-European sub-families based mostly on historical records from the Roman Empire and Medieval Europe period, and in Gray et al. (2009) they studied the expansion of the Austronesian family while constraining the age of some of its sub-families on evidence from archeology.

To obtain the dates of unknown events from the dates of a few known events requires a model about the rates of change; equally, however, the known dates allow one to evaluate any assumption one makes about them. The original proposal of glottochronology was to assume that the number of cognate retentions of two languages diverging at a given time decays exponentially with constant rate (Swadesh, 1955)—which is analogous to the strict molecular clock hypothesis in molecular evolution. Rate constancy has been severely criticized since early on (Bergsland and Vogt, 1962; Blust, 2000), although some support for the idea still exists in other contexts (Ehret, 2000; Starostin, 2000, 2013; Holman et al., 2011). None of these paper support the idea of rate

constancy, they support (emprirically) the idea of rate regularity. Within the context of a likelihood based approach, the relative constancy of the rates of various features can be tested (Hruschka et al., 2015), as can particular hypotheses about factors affecting changes in the different branches (Atkinson et al., 2008).

A natural extension of this idea is to allow individual pairs of languages or whole branches to have their own independent rates (Embleton, 1986). Such an unconstrained model, however, introduces too many degrees of freedom, which leads immediately to estimated parameters with large variance. A widespread solution to this conundrum is the application of some kind of regularization constraint on the different rates, in such a way that large variation of rates within lineages is penalized (Sanderson, 2002), though alternate statistical methods that fix the probability distribution of the rates, rather than the rates themselves, can be easily implemented in a Bayesian framework (Korber et al., 2000). Again, to the extent that the data does not contradict them, simple approximate models involving rate constancy, but allowing unmodeled sources of dispersion, are expected to outperform more realistic, but complicated models, in terms of providing valid estimates with defensible error bands. With respect to the actual processes used to model cognate loss and retention, researchers, therefore, usually adopt simple parametric models taken from evolutionary biology (Nichols and Warnow, 2008), although some more realistic alternatives have been developed as well (Nicholls and Gray, 2006; Starostin, 2007). Even when such approaches fail to answer the methodological question of how reliable molecular clocks are expected to be in a given situation, they do allow one to come up with more realistic confidence intervals for the inferred dates.

4 Models of meaning. It is never declared how synonyms are treated in the IDS and in the experiments of Section 4 and how prevalent that is.

Discussion of lexical connections between different languages often suffer from the fact that the meanings expressed by these lexical items have not yet been formalized. A word meaning covers a region of a multidimensional conceptual space; it is difficult if not impossible to identify discrete word senses (Croft and Cruse, 2004; Koptjevskaja-Tamm, 2008). Semanticists ideally use stimuli representing particular situation types (images, video, questionnaire sentences) to elicit a range of points in the conceptual space (e.g. Berlin and Kay, 1969; Dahl, 1985; Levinson and Meira, 2003; Majid et al., 2008; Croft and Poole, 2008). However, historical linguists rarely if ever do so, in part because they frequently must rely on secondary sources and documents from extinct languages for comparison. Although historical linguists recognize the problems of discrete word senses in considering lexical reconstruction, in applying the comparative method they implicitly assume a model of discrete word meanings or at least of semantic overlap across the words in languages to be compared (Fox, 1995). In effect, English (or another language used by the historical linguist) functions as the semantic metalanguage for comparison of word meanings. Word meanings also overlap with other word meanings in a language, and shift both gradually (e.g. extension and retreat in a semantic domain) and discontinuously, via processes such as metaphor and metonymy (Sweetser, 1990; Traugott and Dasher, 2002); and little cross-linguistic research has been done on the likelihood of various types of semantic shift, except in restricted domains such as body part terminology (Brown, 1976, 1979; Witkowski and Brown, 1979; Wilkins, 1996), cardinal directions (Brown, 1983), perception verbs (Viberg, 1983), concepts associated with fire (Evans,

1992), and color metaphors (Derrig, 1978). As a result, outside a very restricted domain, comparison of words to obtain cognates is often done primarily based on the validity of regular sound correspondence with little weight on semantic content (Nichols, 1996). A complete probabilistic model for inferring language relationships, however, needs to include probabilistic aspects of meaning correspondences as well.

4.1 PARALOGOUS WORDS. This element of cognacy across meaning category is analogous to an important mode of biological evolution—the duplication and subsequent functional divergence of genes. Indeed, a large fraction of the protein inventory of most organisms has arisen in this manner. It is largely unknown whether a similar mechanism is at work in human languages, that is, to what extent a given language harbors cognate words with different meanings. English language examples of such PARALOGOUS COGNATES *tell/talk*, *lay/lie*, and *raise/rise* demonstrate that such word pairs exist.[7] The loss of ancestral morphological forms together with the retention of FROZEN word forms as NEW words provides a mechanistic explanation for such examples. Again we will, for the sake of this contribution, not pursue the issue of possible mechanisms. Instead we ask here a much simpler question: Is there evidence for PARALOGOUS WORDS as a wide-spread phenomenon? In other words: do data sources accessible to us contain sufficient information and signal to start investigating paralogous words in a systematic manner? For the purpose of this position paper we will demonstrate how these questions can be addressed by means of a suitable statistical approach. We will leave a more detailed analysis of the topic, which is ongoing work, for a subsequent publication.

We have to make one single assumption about paralogous cognates, namely that they inherit both their phonological form and their meaning from a common ancestor. Conversely, we assume that a simultaneous similarity of meaning and phonological form, if not explanable by chance, can result only from paralogous cognates: As it is written this is two assumptions. Actually the first is the definition of paralogous and what you assume is the second one (that only paralogous cognates have sim in form and meaning). that is, processes like sound symbolism are sufficiently weak that they can be ignored for this purpose. If paralogous cognates exist, they will therefore be recognizable in the data as similar words that also fall into the same broad semantic groups of meanings. We have already seen above how phonological forms can be compared in the context of computational cognate detection. We will adapt this approach to become applicable to words from the same language. The comparison of meanings is conceptually more difficult. However, we do not need a detailed theory or representation of meaning. For our purposes it is sufficient to be able to decide whether some word pairs are semantically closer than others. We can therefore make use of the semantic classification of the words in word list data. As discussed above, the IDS data (Key and Comrie, 2007) are grouped into 'chapters' that correspond to very broad semantic categories. We can therefore structure our analysis in the following manner: If two similar words are completely unrelated and accidental, then they will appear at random places in the word lists. On the other hand, paralogous cognates will retain some semantic similarity and hence predominantly appear within the same chapter of the IDS word list. It is important to recall that our purpose is to check whether there is evidence for paralogous cognates in the first place, not to understand them in full detail. We therefore devise a simple test for the association of similar words with similar meanings: we simply ask whether there are more pairs of similar words within

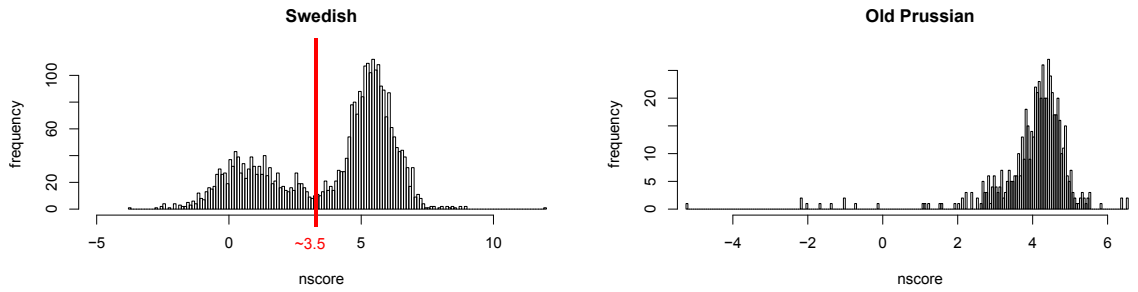


Figure 10: Distribution of normalized alignment scores for (left) Swedish and (right) Old Prussian. For alignment scores of Swedish words, a bimodal curve can be seen. The left hill is assumed to represent scores of unrelated words, while the right one mostly contains alignments of similar words. Therefore, the cutoff is set to 3.5 as this score separates the two hills. The distribution of alignment scores in Old Prussian shows that the data here is rather sparse. Hence, no cutoff can be chosen and the dataset was removed from this experiment.

a chapter than between chapters, and if so, whether the difference is statistically significant.

To do this in practice, we compare for each language two samples of 1000 pairs of non-identical words. We remove identical words with different meanings since we only interested in paralogs, that is, words that are distinct, not in words that have simply expanded their semantic scope. The removal of identical words is contrary to the stated interest which was "This element of cognacy across meaning category is analogous to an important mode of biological evolutionthe duplication and subsequent functional divergence of genes.". Surely identical words are (always or sometimes) instances of this process. For example, mouse is an animal and now also a computer device, with its own life in the different senses (e.g., the computer device can have a different plural). The first sample comprises word pairs from the same chapter. In the second sample we only include word pairs from two different chapters. Then we determine, separately for each sample, the number of word pairs that are phonologically similar using the same alignment scores that we have employed already for cognate detection in section 3.3. More precisely, we consider two words x and y from the same language A as similar if $score(x, y) > \theta(A)$, that is, if their similarity is larger than a language-specific threshold $\theta(A)$. This threshold value is also estimated from the word list data in complete analogy to the thresholds used earlier for cognate detection. Again, the bimodal form of the distribution of the scores of all word pairs for language A is the key, and we remove languages from this study when the bimodality is not obvious , that is, there is only little data for these languages (see Fig. 10). Our pairs of similar words therefore have the same statistical characteristics as cognates, except that they are taken from the same language, and may not correspond in meaning too closely.

The results of this sampling procedure are two numbers n_s and n_d for each language A: the number n_s of pairs of phonologically similar words among 1000 word pairs from the same chapter, and the number n_d of pairs of phonologically similar words among 1000 words from different IDS chapters. For each language, the parameter $\delta = (n_s - n_d)/1000$ therefore measures (as a fraction of all word pairs) the excess of similar words with similar meanings over similar words with unrelated meanings. A positive δ-value consequently indicates that a language contains more non-identical words with similar meanings than expected. For a single language we might observe a positive

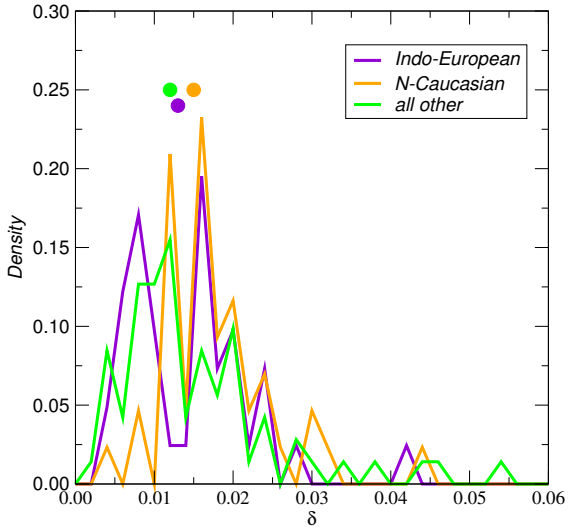


Figure 11: Distribution of δ in Indo-European, Northern-Caucasian, and all other languages (see Table B1). Medians of the distributions are shown as filled circles. We did not observe δ-values smaller than zero. If there would not be a signal, the δ-value would distributed symmetrically around zero as, for example, in Fig. 8.

δ-value by chance. In Fig. 11, we therefore plot the frequency distribution of the δ-values for large language groups, including Indo-European and Caucasian languages, as well as for a sample of 155 languages from the IDS. If similar, non-identical words do not systematically have similar meanings we expect that this distribution is centered around zero.

We find, however, that for all languages $\delta > 0$, even though the values are close to 0 for some languages (Fig. 11). This is extremely unlikely if the values are drawn from any distribution centered about zero. In fact, the probability that 155 independent numbers from such a distribution all end up with the same sign by chance is less than 10^{-46}. This indicates that there is indeed an an association between similarity in meaning and similarity in the form of the words. The distribution of δ for language groups shows medians around $\delta = 0.014$ providing an estimate for the fraction of words that have a similar copy with similar meaning. This simple analysis indicates that word paralogy is a pervasive phenomenon across essentially all language groups that deserves a more detailed investigation in the future since all languages have a δ-value larger than zero.

4.2 Polysemy. The concept of paralogous words is closely connected to the idea of polysemy: words acquire additional meanings with continued use, often due to culturally salient metaphors or widely used metonymies. Individual instances of these are extremely historically contingent, but the universal features that make languages useful and learnable are expected to be reflected in the statistical patterns of these changes. The signatures of such patterned changes should, therefore, be visible in the patterns of polysemy across the world's languages.

A recent work (Youn et al., 2016) provides a quantitative assessment of the patterns of polysemy using cross-linguistic dictionaries. When a word in a meta-language is translated to a language of interest, additional meanings may appear if the word is polysemous in the language. The study builds a collection of cross-linguistic polysemies for a few concepts chosen from Swadesh

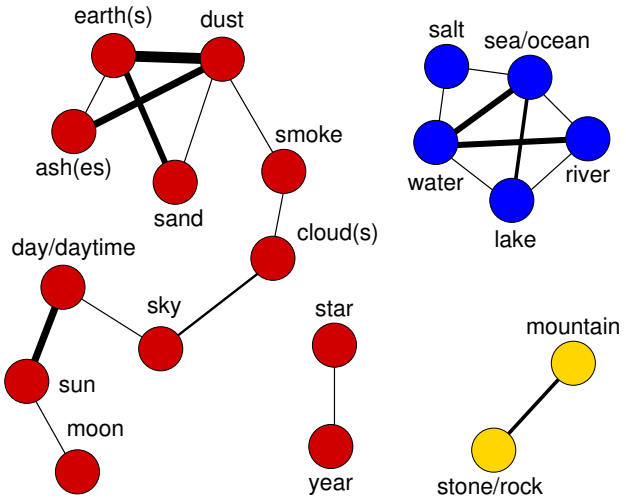


Figure 12: A portion of the lexical semantic network presented in Youn et al. (2016) showing the heterogeneous connectivity structure of the lexical semantic network. The nodes are Swadesh concepts linked if there exist languages with words polysemous between the two concepts. The links are weighted proportional to the number of such polysemies, and rare single polysemies are omitted for simplicity. The data are collected from bilingual dictionaries of eighty-one languages unrelated at the level of genus in the standard linguistic classification. As clearly shown in the diagram, some concepts like 'water' or 'earth' are involved in many polysemies, whereas others like 'moon' in very few. Further analysis reveals that these concept form three almost disconnected clusters shown here using different colors.

list across a set of languages sampled to be representative of worldwide diversity. Then, a semantic network is constructed for each language where nodes denoting concepts are linked if they are represented by a polysemy. Fig. 12 shows an aggregated network obtained from the entire set of languages. A randomization test showed that the polysemy relations were statistically universal across the languages—the network of relationships captured by any random subset of languages was significantly correlated with that obtained from the complementary subset, but different from what one would expect merely from the amount of polysemy observed for the different words. With further work, this should be translated into an empirical prior on the capacity of different meanings to be expressed by the same word.

When words change meanings, the process involves a number of intermediate steps as illustrated in Fig. 13. The intermediates involve the diversification of meanings of words leading to polysemies, and the meanings of different words overlapping, leading to synonymies. In addition, novel words arise by morphological processes or adoption of foreign words, and word senses get specialized by the loss of rarely used meanings especially when large clusters of synonyms exist. The detailed parameterization of this state process model has not yet started, but databases of attested meaning changes across the language families of the world are being assembled (Zalizniak, 2008). Careful study of polysemies and typologically frequent, or 'trivial', semantic shifts is of particularly vital importance to hypotheses of distant phylogenetic relationship, since the quantity of direct semantic matches between languages declines progressively, depending on the time distance that separates them. Some steps in that direction are currently being taken by members

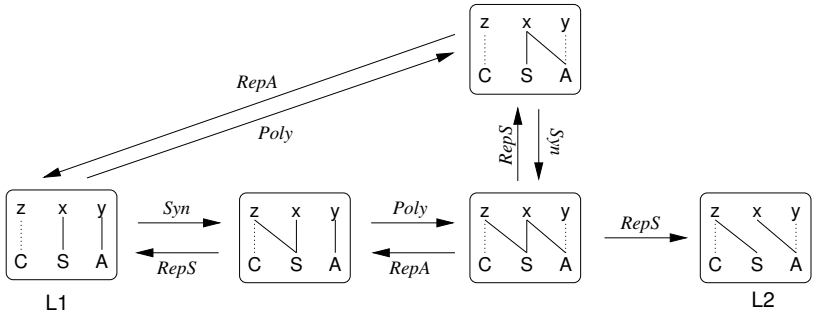


Figure 13: A model of how semantic shift takes place through intermediate polysemy and synonymy. Meanings, represented here by capital letters, are expressed by words represented by lowercase letters. Over time, polysemies (a word representing more than one meaning) and synonymies (a meaning represented by more than one word) are generated by additional word-meaning links being generated, whereas loss of word-meaning links leads to loss of polysemies and synonymies. The net result is often a word replacement in which a word with one meaning can shift to being used to express a different meaning. In the figure, the word-meaning associations that may be the focus of a study are depicted by solid lines, whereas dotted lines represent associations outside the study set that may not be directly observed. The possible paths arising from sense extension are labeled as *Poly* indicating development of a polysemy or *Syn* indicating development of a synonymy, and sense specialization leading to a word losing the sense *X* is indicated by *RepX*.

of the EHL program (EHL), working on algorithms for automated comparison between expanded word-lists consisting of a fixed 400–500 elements, as compared to Swadesh's original 100–200. These algorithms take into account the possibility of 'trivial' semantic shifts, based on a preset listing of such shifts that is being extracted from polysemies and indisputable low-level semantic change, elicited within the comparative-historical databases created by various members of the program. I cannot find any information on the EHL website cited here on the work being done there on semantic shift. If it is not possible to cite outcomes of that work it may be preferable to omit the discussion of that work in progress. Ich kann es auch nicht finden.

5 Measuring the success of statistical methods. In the previous sections we described several statistical methods and discussed their applications to different aspects of language evolution. We demonstrated in the sample application that the results are reasonable. One might argue, however, that we chose 'simple' cases where the answer is already known. This may not immediately convince the reader that the methods will also work in 'hard' cases, where the signal is weak and multiple hypotheses are still debated in the linguistic community. Thus, the question is how to prove that a method provides useful and reliable results in the hard cases? The problem of assessing the reliability of a method or a specific software tool has been well studied in the context of computational biology. In this section, we sketch these methods of verification with examples relevant to historical linguistics.

Statistics provides a measure for the confidence in the results produced by a computational method. Throughout this contribution we have used three of these measures: specificity, sensitivity, and the FDR (see Figs. 5 and 7). Sensitivity and specificity are calculated with respect to a known ground truth, often called the 'gold standard'. It is common practice therefore, to test

methods on well understood examples.

A good method has two features: (1) it works successfully on 'perfect' data, and (2) the results are robust against noise and errors of the kind that can be expected to be present in the input data. In computational biology, the robustness is often tested using simulated data. We have used the same idea above to test the robustness of cognate identification with respect to errors and differences in the encoding of word list data. The artificial data sets can be used to benchmark methods and to estimate their error rates. Since the noise is modeled explicitly, conclusions on the robustness of the method towards different noise can be estimated.

Such simulations, however, require a knowledge of the underlying processes to produce representative data. In cases where we know little of the underlying processes, we need to use a different approach. A particularly interesting method is called CROSS-VALIDATION. It consists of modeling the behavior using a subset of data and testing it out with the other subset. Even when one is unable to test the results on a left out set, the variation in the results as different random subsets are analyzed can be used to estimate the uncertainty inherent in the method.

As an example, imagine one would like to evaluate how good the likelihood method works but there is no model of evolution of sound systems and cognates that reproduces faithfully all relevant features expected in the data. If one has enough cognates, one can apply the leave-out approach. This consists of running the analysis method on sub-samples of the observed data. A robust method will show almost the same results for any large sub-sample. Furthermore, the result from any such sub-sample will agree with the result obtained from the whole data set. For example, the likelihood method described above results in a phylogeny with sound changes assigned to the branches. One therefore tests whether the phylogeny and the predicted sound changes are essentially independent of the sub-samples. Similarly, the correctness of the scoring model can be tested with this approach by training the model with sub-samples of the data. The test can be made more quantitative by observing that statistics can often predict how the uncertainty in estimation resulting from sampling biases and variances changes with sample size, and tests with sub-samples of various sizes can verify these predictions.

6 CONCLUSION. The conclusion contains information not in the body of the paper and should thus be reorganized.

Biological and language data share enough properties to argue that methods developed in one domain are also applicable in the other. Comparative methods are useful in both fields as a means to infer the evolution of species or history of languages. Words as well as genes, proteins, or RNAs are encoded in a linear manner, and their comparison is usually based on alignments. In biology, it is possible to formulate explicit models with just a few parameters that have to be estimated. The amino acids and bases at alignment positions change almost independently and thus almost identical models can be applied to all domains of life. This is not the case for linguistics, where the fundamental processes of evolution are not yet properly understood and modeled. This, however, merely cautions against the uncritical use of molecular phylogenetics programs directly for linguistics: not against reimplementing the tools and methods that have been specifically developed to discover the regularities from the linguistic data themselves. Furthermore, permutation tests, as shown in this paper, are model independent. They allow tests of phylolinguistic hypotheses even in the complete absence of mechanistic or detailed statistical models.

In our presentation above we have highlighted but a few aspects of language evolution. There are, of course, numerous others. Grammatical features, for example, are subject to evolutionary turnover as well. The work of Dunn et al. (2011) highlights an important issue, on the one hand, features of language may well be correlated. On the other hand, most regularities are of a statistical nature rather than absolute "universals". Phylogenetic relatedness naturally introduces such correlations. It becomes an important issue, then, to disentangle regularities in language evolution that are grounded in cognitive, physical, or biological constraints from those that are a mere reflexion of lineage-specific persistence. As a case in point, some of us recently revisted (Blasi et al., 2016a) the presumed independence of sound and meaning, which is widely believed to be a crucial property of human language. Surprisingly, a careful statistical examination of words from nearly two-thirds of the world's languages reveals that unrelated languages very often use (or avoid) the same sounds for specific referents. This effect cannot by explained by phylogenetic relatedness or geographic proximity but emerge independently. At present we cannot give a mechanistic explanation for most of the statistically signficant sound-meaning associations—but we could quite easily incorporate them into the background statistics used, e.g., for cognate detection, with the effect of increasing sensitivity.

Computational linguistics methods have the potential to carry out all the major steps of historical reconstruction starting with lexical data, especially when curated manually with detailed linguistic knowledge to separate the roots from the affixes. These methods can be used to determine when sound similarity is high enough to merit a closer scrutiny (Turchin et al., 2010), to infer regular sound correspondences (Hruschka et al., 2015) and cognates (Frunză, 2008; Kondrak, 2009; Hall and Klein, 2011; Steiner et al., 2011; Rama et al., 2013), to take phonetic context into account and reconstruct ancestral forms (Bouchard-Côté et al., 2013), and to use these—as well as cognate loss (Gray and Jordan, 2000; Gray and Atkinson, 2003; Pagel et al., 2007)—to classify language families and arrange them into a phylogeny (Hruschka et al., 2015). These methods infer and incorporate limited amounts of rate variation across the various lexical items and lineages, and provide a quantitative evaluation of various hypothesis, often in probabilistic terms that can be translated across different data domains. Even though these methods do not currently incorporate rare phonetic processes like metathesis and analogical change, nor do they evaluate the reasonableness of the phonetic system in their inferences, such additional processes and constraints are reasonably straightforward to add in when and where they become important. Though analogical change is sometimes treated as a "garbage bin" of marginal, non-regular changes, the phenomenon is really not that rare (certainly not in the same class of unusual "phonetic processes" as metathesis, though of course metathesis can happen by analogy...). Non-regular does not mean rare. Nor is it the case that analogical changes are inherently non-regular. It's a little unclear, therefore, exactly what you are trying to single out here as being poorly handled by these methods. The required parameters can again be learned based on the data. As long as the effect of each particular language contact on the lexicon is reasonably small, methods from biological phylogenetics (Griffiths and Marjoram, 1997; Arenas, 2013) can be used to factor them into the inference. More problematic is quantifying whether a reconstructed lexicon is reasonable. Work on quantifying lexical semantics, however, holds promise for modeling semantic shift, thus providing an avenue to approach this problem systematically.

It is important to highlight that the task of a statistical inference algorithm is never to param-

eterize the most complete and complex known model based on the data. Rather, it is to resolve the model into those parts that affect multiple independent pieces of data so that the correlations between them can be used to properly parameterize the model. Those processes that affect only a small number of independent facets of the data ought to be modeled as RANDOM EFFECTS since the data constrains the total strength and structure of the combined effects of all such processes far more than it constrains the correlation produced by any one of them. As the amount of available data increases, or our understanding of such processes increases, they can be added back, possibly under the control of priors that incorporate our independent knowledge of their strength and structure.

The major goals of quantitative modeling may be encapsulated in a few points. Each of these depends, in one way or another, on the ability of algorithms and high-performance computation to carry out sorting and tracking tasks at which computers are strong and humans are weak. The first is that quantitative models may simultaneously retain a large variety of hypotheses about history, and assign scores to them that result from explicitly stated criteria, consistently imposed. The second is that probabilistic methods may weigh joint evidence of relatedness from intermittently-preserved features in languages. While any single feature may be unreliable and carry limited information, the number of incompletely-preserved signatures of relatedness may be sufficiently larger than the number of strong signatures, that the weak signatures in aggregate provide a large or even leading part of the information available in the data. This is analogous to fingerprinting, in which both single features and the comparison of global parallels enable the assignment of similarity. The third is that formal models require the modeler to be explicit about premises, and provide systematic commitments to what it means to minimize bias over evidence that cannot be crisply formalized. This does not require the elimination of context or ambiguous premises; rather, it incorporates these in priors, so that the modeler asks 'what weight of evidence would be required to convince me that my prior premise was incorrect?' Fourth, quantitative methods permit efficient backtracking if results are obtained that conflict among methods, or that conflict with trusted knowledge from outside the linguistic problem. Backtracking means isolating the key assumptions on which differing conclusions depend, either enabling a study of the relative strength of differing positions, or signaling the kinds of currently-unavailable data that would best resolve them. Fifth, quantitative methods, simply by showing what can (and what cannot) be reliably computed from given assumptions and evidence, can expose different frames for questioning or different concepts for interpretation, which might have remained hidden from the perspective only of manual reconstruction. Sixth, even in the 'hard' cases where signals are weak or multiple signals overlayed, computational methods can come in handy. Computational methods do not simply return whether a hypothesis is true or not but rather how likely they are. Thus, when data are noisy, different hypotheses can be tested and unlikely hypotheses can be discarded. Discordant results from application of different methods may point to hypotheses resolving the apparently incoherent array of conclusions.

Formal methods never replace human thought, and the subset of premises and evidence that can be expressed formally is always incomplete within the domain available to human expertise. We should recognize, however, that the unaided human mind was never the widest possible window through which to experience the world. New devices for measuring, organizing, and computing have enlarged the power and also the conceptual scope of human thinking in all of the natural

sciences, often in unanticipated ways. The promise of computational methods to historical linguistics is likewise to allow minds to see the language world in all their existing capacities, and in new capacities as well.

What these methods, then, allow one to do is to take the tedium out of the work of linguistic reconstruction. The computational codes are not designed to supersede the knowledge and efforts of the careful historians and linguists: rather, its primary use, at least initially, ought to be in helping evaluating hypothesis. It is reasonably straightforward for these computational methods to output not only a scored list of alternative hypotheses, but also a scored list of evidence that supports and refutes any hypothesis. This can focus the valuable time of researchers in understanding and weighting the contradictions. This then is the division of labor that one can envisage: linguistic knowledge alone prescribes what questions are interesting and what constitutes adequate support for or against them—how this is done is what the focus on computational linguistics should be.

Appendix A: bigram alignment algorithm. Word alignments are performed with an extension of Needleman-Wunsch algorithm (Needleman and Wunsch, 1970) that computes optimal alignment for linear gap cost models such as the Levenshtein distance (Levenshtein, 1966). The linear gap model is not ideal, however. Instead, it is desirable to penalize longer gaps subadditively. The simplest such model uses affine gap costs, in which the opening of gap incurs higher costs than gap extensions. An efficient dynamic programming algorithm for this version of the problem was given by Gotoh (1982). In order to accommodate overlapping bigrams as the basis of the scoring model we further modify this method.

Consider two words $X = x_1 \cdots x_n$ (from language P) and $Y = y_1 \cdots y_m$ (from language Q) of length n and m. Denote by $M_{i,j}$, $D_{i,j}$, and $F_{i,j}$ the score of the best possible alignment of the prefixes $X = x_1 \cdots x_i$ and $Y = y_1 \cdots y_j$ subject to the constraint that alignment ends in a match or mismatch, in a gap in the first sequence X, and in a gap in the second sequence Y, respectively. These scores must satisfy the recursions

$$\begin{aligned}
M_{i,j} &= \max \begin{cases} M_{i-1,j-1} + \sigma(x_{i-1}x_i, y_{j-1}y_j), \\ D_{i-2,j-2} + \sigma(x_{i-1}x_i, y_{j-1}y_j), \\ F_{i-2,j-2} + \sigma(x_{i-1}x_i, y_{j-1}y_j)\} \end{cases} \\
D_{i,j} &= \max \begin{cases} M_{i-1,j} - \Delta_{PQ}(x_i), \\ D_{i-1,j} - \delta_{PQ}(x_i), \\ F_{i-1,j} - \Delta_{PQ}(x_i)\} \end{cases} \\
F_{i,j} &= \max \begin{cases} M_{i,j-1} - \Delta_{QP}(y_j), \\ D_{i,j-1} - \Delta_{QP}(y_j), \\ F_{i,j-1} - \delta_{QP}(y_j)\} \end{cases}
\end{aligned} \tag{2}$$

Here $\sigma_{PQ}(x_{i-1}x_i, y_{j-1}y_j)$ denotes the (mis)match score of the bigrams $x_{i-1}x_i$ from language P and $y_{i-1}y_i$ from language Q. The key difference to Gotoh's algorithm is that the scored bigram overlaps the previous match. Furthermore bigrams are scored only after gaps in either sequence. The parameters $\Delta_P(\,.\,)$ and $\Delta_Q(\,.\,)$ are the gap opening penalties, while $\delta_P(\,.\,)$ and $\delta_Q(y_j)$ are the smaller gap extension penalties.

The gap penalties may depend on the language pair and the sound, for example, to accommodate the systematic silencing of a phone. Here we use language and sound independent parameters (3.5 for gap open and gap extent). The (mis)match scores are estimated according to equ.(1). Since the amount of available data is limited, we use the well-established method of pseudo-counts (Lawrence et al., 1993) to relate the observed number of occurrences of bigrams $occ_{(A,B)}(\alpha,\beta)$ to their relative frequencies:

$$p_{(A,B)}(\alpha,\beta) = \frac{occ_{(A,B)}(\alpha,\beta) + \varepsilon}{N + \varepsilon} \tag{3}$$

Here N is the total number of bigrams. The small correction ε can be interpreted as the uncertainty about the probability of non-observed events. The use of pseudo-counts has the benefit that all scores remain finite. For the scoring model employed here we used $\varepsilon = 3$.

APPENDIX B: TABLES OF LANGUAGES Lists of languages used for different computational analyses.

Table B1: Languages used for calculating δ values in Figure 11.

Language Family	**Languages**
Indo-European (41)	Albanian Tosk, Eastern Armenian, Western Armenian, Avestan, Breton, Bulgarian, Catalan, Czech, Danish, Dutch, English, Middle English, Old English, French, German, Middle High German, Gothic, Ancient Greek, Modern Greek, Hittite, Irish, Old Irish, Italian, Judeo Tat, Latin, Latvian, Lithuanian, Old Norse, Old Church Slavonic, Persian, Polish, Portuguese, Romani, Russian, Sanskrit, Serbo-Croatian, Spanish, Swedish, Tokharian B, Welsh, Yiddish
North-Caucasian (43)	Northern Akhvakh, Southern Akhvakh, Andi, Andi Muni, Archi 1, Archi 2, Avar, Avar Andalal, Avar Antsukh, Avar Batlukh, Avar Hid, Avar Karakh, Avar Kusur, Avar Zakataly, Bagvalal, Bezhta, Botlikh, Botlikh Botlikh, Budukh, Chamalal, Chechen, Chechen Akkin, Dargwa, Dargwa Kajtak, Dargwa Kubachi, Dargwa Muiri, Ghodoberi, Hinukh, Hunzib, Khinalug, Khvarshi Inxokvari, Khvarshi Khvarshi, Lak, Lezgi, Lezgi Mikrakh, Rutul, North Tabassaran (Khanag), South Tabassaran, Tindi, Tsakhur, Tsez (Dido) Mokok, Tsez (Dido) Sagada, Udi
other (71)	Arabic, Ancient Aramaic, Hausa, Azerbaijani, Azerbaijani Terekeme, Kumyk, Nogai, Ignaciano, Mashco Piro, Trinitario Moxos, Hawaiian, Maori, Marquesan, Proto-Polynesian, Rapa Nui, Rotuman, Tongan, Tuamotuan, Limonese, Negerhollands, Toba, Basque, Cayuvava, Cofán, Elamite, Itonama, Seri, Trumai, Zuni, Chorote, Nivaclé, Cashibo, Chácobo, Shipibo-Conibo, Yaminahua, Araona, Ese Ejja, Tacana, Buyang Ecun, Buyang Langja, Central-Thai, Chadong, Dehong (TaiNüa), Kam (Southern Dong), Khün, Lakkia, Lü, Nung Fengshan, Nung Lazhai, Nung Ninbei, Shan, Sui, Thai Song, Zhuang Zuojiang, Guaraní, Guaraní (Eastern Bolivian), Mundurukú, Sirionó, Wayampi, Erzya, Estonian, Finnish, Hungarian, Khanty, Komi, Lappish (North Saami), Mansi, Mari, Nenets, Selkup, Udmurt

Table B2: Languages used in Section 3.2.

Language Family	**Languages**
Turkic	Yakut, Tuvan, Tofalar, Khakass, Shor, Altai, Kirghiz, Uighur, Uzbek, Kazak, Karakalpak, Nogay, Bashkir, Tatar, Kumyk, Balkar, Karaim, Turkmen, Azerbaijanian, Gagauz, Turkish, Khalaj, Chuvash

Table B3: Languages used for calculation of uni- and bigram score distributions in Figure 4.

Language Family	**Languages**
Indo-European	Spanish, Italian, Latin, French, Greek, GermanStandard, Dutch, Danish, Swedish, English, Breton

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Notes

[1]Incomplete lineage sorting describes the effect that for a small subset of the genome may contradicts the true phylogeny by being more similar to a more distant relative than to the, e.g., sister species. In the words of linguistics, some words in a language may be less similar to the cognate in the sister language than to the cognate in a more distantly related language.

[2]The /we/ is orthographically <ue> in Spanish.

[3]Even in word lists derived from standard orthography several automatic regularizations are performed that do not affect the detection of sound changes. Among them is the removal of capitalization. We report words here as given by the word lists, hence we write *milch* 'milk' instead of the orthographically correct *Milch*.

[4]Again, we include changes in presence and absence of cognates as well as sound changes in the word 'change'.

[5]The confidence interval describes the range of a parameter in which one expects the true value for this parameter to lie. For example, if we would know that there are differences in the rates with which sound changes happen, we could ignore the differences since they are very small. However, if we know about the size of the difference we could give the confidence interval for the results based on the size of the differences and observed data points.

[6]In a deeper analysis, the consideration is not only one of practicality but also of principle. Much of the purpose of quantitative methods is to demand a formal statement of the assumptions underlying a historical reconstruction. Ineffables, or evidence external to the data that can admit multiple interpretations, resist such formalization. Quantitative modeling forces the modeler to accept that if a few features cannot be explained without reference to a much more complex context than the evidence within the data itself, and if that context is ambiguous or subject to dispute, the model should adopt a least-biased assumption consistent with other assumptions that have been made in definite form as commitments of the model.

[7]We ignore for this discussion examples like *spring(verb)/spring(season)/spring(source)/spring(coil)* where the identity of form allows us to treat them either as paralogs or as semantic extension from a single sense.