

# Quantitative standards for absolute linguistic universals

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## Abstract

Absolute linguistic universals are often justified by cross-linguistic analysis: if all observed languages exhibit a property, the property is taken to be a likely universal, perhaps specified in the cognitive or linguistic systems of language learners and users. In many cases, these patterns are then taken to motivate linguistic theory. Here, we show that cross-linguistic analysis will very rarely be able to statistically justify absolute, inviolable patterns in language. We formalize two statistical methods—frequentist and Bayesian—and show that in both it is *possible* to find strict linguistic universals, but that the numbers of independent languages necessary to do so is generally unachievable. This suggests that methods other than typological statistics are necessary to establish absolute properties of human language, and thus that many of the purported universals in linguistics have not received sufficient empirical justification.

## Introduction

One of the primary goals of cognitive science is to characterize the mental representations and processes that are shared across all humans. Universal features of cognition are interesting in part because they lead to plausible candidates for genetically-encoded representations and processes, and in many cases characterize the uniquely-human features of thought. In cognition, universals have been proposed in nearly every domain, ranging from color naming (Kay & Regier, 2003) to high-level domains such as moral reasoning (Mikhail, 2007), geometrical intuitions (Dehaene, Izard, Pica, & Spelke, 2006), folk biology (Atran et al., 1998), and numerical reasoning (Pica, Lemer, Izard, & Dehaene, 2004), among others. Perhaps the most well-developed theories of cognitive universals come from the domain of language typology, which has long attempted to characterize the range of possible human linguistic systems. An understanding of the breadth—or lack thereof—of human languages is key for making sense of human thought and communication. For instance, the science of language should aim to uncover if all languages have properties such as recursion, lexical

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categories, or principles of binding theory. These types of linguistic features have motivated substantial cognitive theories about the representations learners bring to acquisition (e.g., Wexler & Manzini, 1987; Wexler & Culicover, 1983; Hauser, Chomsky, & Fitch, 2002, among others). Here, we study the amount of evidence necessary to make reasonable statistical inferences about such universals. While we focus on linguistic universals, our methods and general approach are also applicable to cognitive domains outside of language.

In linguistic typology, core universal representations have long been hypothesized. Greenberg (1963) described two different classes of universal patterns in languages (for discussion, see Bickel, 2007a). First, there are violable statistical tendencies, patterns which hold with higher than chance frequency across language. We refer to these as *typicality* universals<sup>1</sup>. An example is Greenberg (1963)'s first universal that subjects tend to precede objects in simple declarative sentences. This is not true of all the world's languages, but it is evidenced in the non-uniform distribution of word orders across languages. Typology also formalizes *absolute* constraints, meaning ones which strictly constrain the space of humanly possible languages. While nearly all instances of absolute constraints are contested (see Evans & Levinson, 2009), prototypical examples include the presence of linguistic features such as WH-movement and auxiliaries (Pinker & Bloom, 1992) or recursion (Hauser et al., 2002). There are also implicational absolutes, such as Greenberg (1963)'s universal that languages with VSO word order are always prepositional. Though some have argued that typicality universals are more informative and useful than absolute ones (Nichols, 1992; Dryer, 1997; Cysouw, 2005a; Bickel, 2007b) or that typological data is not relevant to universal grammar (Newmeyer, 1998, 2004; Haspelmath, 2004), we believe that the most substantive and interesting theories about cognition would come from absolute universals. Such universals—if any exist—would delineate necessary properties of human languages and thus characterize hard constraints on cognitive capacities. They also provide hypotheses about what knowledge or constraints humans bring to the problem of language learning—what makes humans distinctively human.

Statistical methods for typicality universals have been extensively developed and discussed previously (for an excellent review, see Cysouw, 2005a). A basic challenge with testing typicality universals is that the set of existing languages may not form a representative sample in the space of all possible human languages. For instance, if it is observed that SOV word order is more frequent than OVS, this might be due to chance rather than biology: perhaps SOV languages just happened to be the ones that survive to the present day. However, the problem is more serious than just the effects of random chance. The processes of language change and contact create languages with correlated features (e.g. Dunn, Greenhill, Levinson, & Gray, 2011), meaning that some word orders will be over-represented much more than would be expected just by pure random sampling<sup>2</sup>. Many authors have proposed addressing this problem by using a sample of languages which is as independent as possible, for instance looking at stratified samples (e.g. Tomlin, 1986), languages in distinct genera (Dryer, 1989, 1991, 1992), distinct geographical regions (Maslova,

<sup>1</sup>We differ from previous literature and Greenberg, which refer to these as *statistical* universals.

<sup>2</sup>This problem known as *Galton's problem*, after Sir Francis Galton, who first pointed out the issues it causes for comparative anthropological work (c.f. Ember, 1971). Some anthropologists have even argued that the problem is so severe, there exist only 50 to 75 cultures that can be examined in the whole world and treated independently (Naroll, 1973); Perkins (1989) argues similarly for linguistic typology.

2000; Dryer, 2000), or with distinct linguistic features (Perkins, 1989; Rijkhoff, Bakker, Hengeveld, & Kahrel, 1993; Rijkhof & Bakker, 1998). Such statistical tests are not clearly applicable to absolute universals, since they are designed to compare relative frequencies, not to determine when the true frequency of a feature is zero.

Indeed, absolute universals provide an interesting puzzle for scientific methodology: the presence of an absolute constraint can only be inferred from what has not yet been observed. But, as is often pointed out by typologists, it is always possible that an exception to a universal constraint might be observed with one additional language (Bell, 1978; Dryer, 1989; Bickel, 2001). Dryer (1989) describes the problem as

... no matter how many languages we examine and find conforming to an absolute universal, we can never know that there is not another language that fails to conform to the universal, either one that was once spoken or a hypothetical language that is possible but never actually spoken due to historical accident. What this means is that absolute universals are never testable<sup>3</sup>. ... No amount of data conforming to the generalization provides any reason to believe that there are no languages that do not conform. And no evidence from attested languages can provide any basis for believing that exceptions are not possible.

For Dryer this is both the logical problem of induction, and a statistical puzzle of how we can know whether features are low probability or zero probability. Bickel (2001) goes so far as to say that cross-linguistic analysis “cannot in principle contribute” to the discovery of what is possible and impossible in human languages since, “a probabilistic statement is not, and cannot be converted into, a possibility statement.” He recounts examples of linguistic phenomena which were previously—and erroneously—thought to be universally impossible, including for instance syntactic ergativity without morphological ergativity, and pronoun borrowing.

Dryer and Bickel—and before them, Bell—are correct in a strict logical sense: observed languages can never conclusively show that an unobserved feature is impossible. However, the point of this paper is to argue that nonetheless, absolute universals are still valid terrain for inductive scientific inferences. In particular we develop two methods for inferring when an absolute constraint is *probably* true—for when a reasonable inductive scientist should conclude that there is likely to be a cognitive constraint on possible languages. We first present a method centered around the frequentist idea of keeping a low *false positive* rate of proposing linguistic universals. Then, we develop a formal mathematical model that computes the degree of belief one *should* have that property of language is impossible, given a set of sampled languages. We also explore the bounds provided by the formal tools we develop. We will argue that the amount of statistical evidence required to justify absolute universals will typically be much more than is achievable with the present set of languages in existence. This is unfortunate for anyone seeking to justify universals by cross-linguistic comparison. But the real importance of this result is that apparently absolute typological patterns are themselves poor motivations for linguistic theories. For instance, even if every language in existence exhibited a feature such as recursion, movement, or auxiliaries, that alone would not be enough to justify these as cognitively *required* properties of all possible

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<sup>3</sup>Dryer uses “testable” as a technical term, meaning that there exists possible evidence to falsify the theory, and possible evidence to confirm it.

human languages. Following Tily and Jaeger (2011), we argue, instead, that other sources of evidence such as learning experiments are necessary.

This challenge of inferring restrictions based on what is *not* observed is faced much more broadly in cognitive and linguistic research. A key example is a classic learnability problem, the *subset problem* (Wexler & Manzini, 1987), which holds that learners may incorrectly hypothesize an under-restrictive linguistic system (e.g. grammar), and never receive contradictory evidence. For instance, learners might incorrectly guess that certain types of ungrammatical sentences actually *are* grammatical; if learners only change hypotheses when they hear counterexamples, their over-generalization will never be corrected. This problem appears in many areas of language acquisition, including syntax (Wexler & Manzini, 1987; Berwick, 1985), phonology (Smolensky, 1996; Hale & Reiss, 2003), and the learning of compositional sentences structures (Crain, Ni, & Conway, 1994). Our case is analogous: we want to know whether certain unobserved features are truly impossible. Like good learners of language, we would like to avoid both (i) positing necessary restrictions on human language, and (ii) missing good generalizations about what is truly disallowed. Perhaps unsurprisingly, the statistical tools we use are closely related to statistical models which provide sensible and rational solutions to the subset problem in language learning (Perfors, Tenenbaum, & Regier, 2011; Xu & Tenenbaum, 2007; Piantadosi, Goodman, & Tenenbaum, Under review).

The outline of this paper is as follows: in the next section, we formalize a frequentist framework for testing absolute universals. Then, after presenting a case study on word order which demonstrates several important methodological points, we apply a bootstrapping techniques to 138 features from the World Atlas of Linguistic Structures (Haspelmath, Dryer, Gil, & Comrie, 2005), and show that incorrect absolutes are often inferred by drawing fewer than around 500 independently sampled languages. We then present a Bayesian statistical model for this problem, and apply it to studying Greenberg’s Universal 20 (Hawkins, 1983; Rijkhoff, 1990, 1998, 2002; Cinque, 2005; Cysouw, 2010a), concerning the order of elements in a noun phrase. This example illustrates both the difficulty of justifying this universal, and ways in which formal modeling can nonetheless lead to nontrivial findings. In the conclusion, we discuss alternative approaches to discovering universals.

### Bootstrapping word order

In this paper, we focus on making inferences about the absolute constraints on some observed feature of language  $F$ . We suppose that  $F$  has  $N$  particular *values* that any language could exhibit, which exhaust the space of logically possible feature values<sup>4</sup>. For instance,  $F$  might be a language’s *word order*, a language’s preferred linear order of subject, verb, and object. For word order, there are seven different possible values for  $F$ : SVO, SOV, OSV, OVS, VSO, VOS, ND (no dominant word order).

Much work in linguistics attempts to find suspicious gaps of feature values that don’t appear in language. In reasoning from observed instances to hypothesized restrictions one might incorrectly infer a restriction on features (a false positive error). For instance, if fewer

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<sup>4</sup>This setup is similar in spirit to the *principles and parameters* approach to language acquisition (e.g. Chomsky, 1981; Wexler & Culicover, 1983), but is meant to be theory-neutral. The features we describe may be entirely descriptive—there is no assumption that the space of these parameters is, for instance, innate.

languages had survived to the present day, we might not have seen a language with OSV word order, and might have thought that this order was somehow impossible with human cognitive systems. Our first way of dealing with potential false positives is to control them—to estimate the rate at which we would false posit absolute universals if we examined a given number of languages. It is impossible to entirely avoid false positives; instead, we choose a method to keep the false positive probability below a bound, perhaps 0.05, the standard for publication in psychology. This means that 1 in 20 findings of universal constraints with this method will be false positives. However, for what are essentially non-repeatable experiments (since there are only finitely many languages to test), one may actually desire a much smaller false positive rate of 0.01 or 0.001.

It is useful to focus on the example of word orders in order to illustrate the logic of our approach. We can imagine that a naive scientist observed  $L$  human languages, and posited that any word orders unobserved in their sample were probably disallowed by cognitive mechanisms. Such a conclusion, we know, would be a false positive error since all 7 word orders actually *are* allowed. Through simulation (c.f. Haspelmath & Siegmund, 2006) we can determine what false positive rate this method would give as the number of languages observed,  $L$ , varies. A simple version of this computation was performed by Bell (1978). Ideally, to compute this, we would assume the scientist sampled  $L$  languages from the *true* distribution of possible human language<sup>5</sup>. However, we do not know the *true* distribution of word orders. Instead, we can use a trick known as *bootstrapping* (see Davison & Hinkley, 1997), where we approximate the true distribution with the empirically-observed distribution. In our case, we sample word orders from the distribution of word orders in a large database, treating this large sample as a “good enough” approximation to the real thing. Here, for simplicity, we sample from the empirically observed distribution in the World Atlas of Linguistic Structures (WALS) (Dryer, 2005). Importantly, the sampling is done *with* replacement in order to simulate sampling from the infinity of possible human languages.

Figure 1 shows how often one would conclude that each word order is impossible, as the number of languages sampled,  $L$ , varies from 1 to 2000 languages. In this plot, for instance, the line for OVS line represents the probability that a scientist who looked at  $L$  languages would incorrectly conclude that OVS is absolutely and universally outlawed. We are interested in making the probability of false positives small, below for instance the dashed 0.05 line or the 0.01 line. This graph illustrates several key points. First—and unfortunately—this figure shows that for word order, one must have examined a relatively large number of languages in order to make the false positive probability below 0.05. A linguist who looked at fewer than around 900 languages would have a false positive rate of greater than 0.05 of thinking that *OSV* is an impossible word order. To make the rate less than 0.01, one would have to look at around 1400 languages. For our purposes, these are even slightly conservative<sup>6</sup> estimate since we may be interested in the probability of *any* feature value rendering a false positive, not just the least frequent one.

<sup>5</sup>For simplicity, here we assume that the languages sampled are drawn independently, but the topic of independence will be addressed more in the next section.

<sup>6</sup>In this paper, *conservative* means we underestimate the number of languages required. This is conservative with respect to the number required, not with respect to the estimated false positive rate for any sample size.

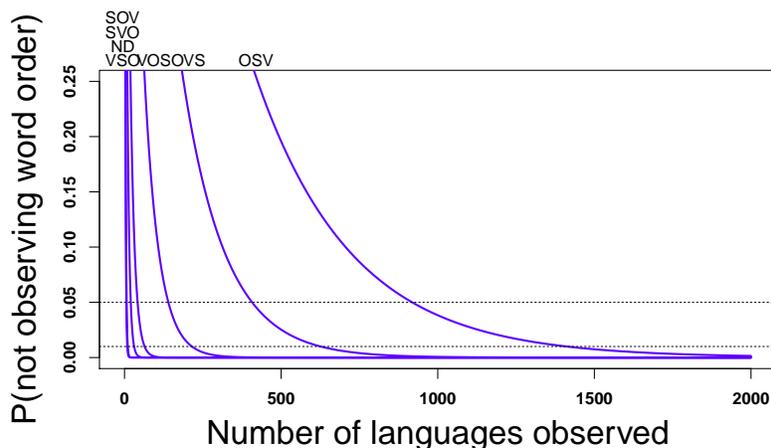


Figure 1. The probability of thinking that each word order is impossible, as a function of the number of languages observed.

Second, this graph illustrates that finding the least frequent feature values is hardest. This is because they are least likely to be drawn on any individual sample, and so are the most likely not to occur in a collection of  $L$  samples. This should be intuitive, and illustrates an often discussed problem for typology: rare feature values are more difficult to find, so it is never clear if a feature value is impossible—or rare and simply not yet observed (see Cysouw, 2005b; Wohlgemuth & Cysouw, 2010b, 2010a; Cysouw, 2010b, 2010a). In general, then, our degree of belief in an absolute universal should depend on how likely the rarest feature values are.

### Bootstrapping features from WALS

The analysis in the previous section raises two interesting issues. First, since the false positive rate depends on how rare the rarest features are, it is not clear that findings based on the distribution of word orders generalize to other features linguists might care about. It may be that rare word orders are much rarer than other typical features one would study, for instance. To address this, we study 138 features from WALS<sup>7</sup>, not just word order. Keeping the false positive rate low across this broader range of features should provide good guidelines for how to keep the false positive rates low for future linguistic features which are similar to those already in WALS.

Second, it is not clear that the raw distribution of features in observed languages provides a good estimate of the true distribution. Many of the languages in WALS are genetically and historically related, meaning that accidents of linguistic history may be driving the overall distribution of word orders (e.g. Dunn et al., 2011). This means that when we model sampling from the observed distribution, we are not correctly approximating the “true” distribution of word orders, and thus not approximating the correct false positive

<sup>7</sup>For simplicity, we take the particular WALS features values at face value and assume that they are a reasonable characterization of typical features linguistics would characterize.

rate. Here we consider four methods of approximating the true distribution:

1. **Flat sampling** – This uses the raw distribution of feature values observed in WALS.

2. **Family stratified** – Sampling from the true distribution is done by first sampling a language family uniformly at random, and then sampling a language within that family uniformly at random.

3. **Genus stratified** – Sampling from the true distribution is done by first sampling a language genus uniformly at random, and then sampling a language within that genus uniformly at random.

4. **Independent subsample** – This method constructs a set of languages which share as few features as possible, and treats sampling from the true distribution as sampling from that set of approximately independent languages.

The flat sampling method is the one used in the previous section, using just the raw feature counts from WALS. The family stratified method attempts to correct for the fact that imbalances in the number of languages observed in each language family are likely due to historical accidents (though see Maslova, 2000). We can partially correct for these historical accidents by increasing the probability with which we sample languages from language families with fewer languages; we do this by first sampling a family and then sampling a language in a family. The genus stratified sampling does the same thing, but at the level of genera rather than families<sup>8</sup>. The independent subsample method is meant to approximate the true distribution by the distribution of features in a sample of languages whose features are as uncorrelated as possible (see Perkins, 1989; Rijkhoff et al., 1993; Rijkhof & Bakker, 1998). This also attempts to remove artifacts of history, but does it by finding a sample of languages which is as independent as possible in their feature values. To do this, we used a simple greedy algorithm to find a diverse subset of languages<sup>9</sup>. We ran this algorithm to produce a set containing 255 and 639 languages, respectively 10% and 25% of languages mentioned in WALS.

With each of these sampling methods, we used a dynamic programming algorithm to compute the probability of making a false positive error, averaging across 138 features from WALS (Figure 2). Figure 2 shows the mean false positive rate for various  $L$ . The resulting value can be interpreted as the expected false positive rate for a new feature, given that the new feature we study is similar to the typical feature already included in

<sup>8</sup>We note that both family and genus-level sampling has been criticized methodologically (e.g. Bickel, 2008; Janssen, Bickel, & Zúñiga, 2006); in general, our basic bootstrapping approach supports is amenable to even more sophisticated means of generating independent subsets of languages, such as areal stratification (Dryer, 1989, 1991, 1992) or Bayesian phylogenetic methods (Daumé III, 2009; Dediu, 2011).

<sup>9</sup>Finding the *most* diverse subset of languages would require searching over the exponentially many subsets of existing languages, creating an instance of the NP-complete problem **SET-COVER**. Our algorithm is similar to the best polynomial time approximation to **SET-COVER** (Chvatal, 1979). The algorithm starts with an empty set of languages and considers adding each possible language in WALS. It first adds languages which decrease the number of unobserved feature values. This ensures that, with enough languages, all feature values are represented. To break ties, it adds languages which share the smallest proportion of their defined features with languages already in the set. Further ties are broken by picking languages which have the largest number of defined features. Note that after enough languages have been added so that all feature values are observed, additional languages never decrease the number of unobserved feature values, meaning that the decision about which language to add is based first on the proportion of features it shares with languages already in the set. This creates a set of languages with diverse feature values.

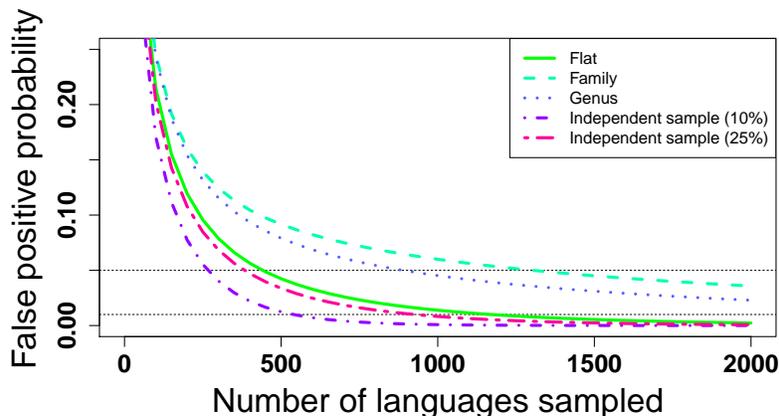


Figure 2. Bootstrapped false positive rates for 138 features from WALS. This shows the mean false positive rate across features, taking the average over particular feature values. Thus, this can be interpreted as an estimate of the false positive rate for a newly studied linguistic feature assuming that its distribution of feature value is like those observed previously in WALS.

WALS (e.g. similar number and distribution of feature values). This figure demonstrates that the number of languages necessary to achieve a false positive rate of 0.05 varies from around 250 to nearly 1500, depending on which sampling method is used to approximate the true distribution. The most optimistic curve, “Independent sample 10%,” drops below a false positive rate of 0.01 only after 500 languages; some of the others do not make it there even after 2000 samples. A rough heuristic one could draw from these plots, then, is that absolute universals are only likely to truly reflect strong cognitive constraints when they have been examined in at least 500 independent languages. Note that this provides only a *statistical* argument of the impossibility of a feature—a scientist who concluded it was impossible after examining 500 languages would tend to have a reasonably low false positive rate of positing universals.

It is important to emphasize one aspect of this analysis. The sampling procedure we use assumed *independent* samples from the true distribution. This means that what is really required is 500 independent languages, not 500 languages overall. For instance, Spanish and Italian do not count as two separate languages in this analysis since they are genetically related. This means that the *real* number of languages necessary may be much larger than 500 when sampling uses non-independent languages. Correlated samples will provably increase the number of samples needed to stay below a given false positive rate. Note, though, that the languages need not be independent in all respects: they need only be independent with respect to the relevant feature, which may be possible in some cases. To the best of our knowledge, it will *in general* not be possible to find 500 independent languages. There are, for instance, 212 language families in WALS, yet language families already are not independent samples. More aggressive independence methods—based on for instance geography (e.g. Dryer, 1989)—will likely arrive at much more independent samples, but orders of magnitude fewer of them. This means that it is very unlikely that

statistical analysis will provide sufficient evidence to justify absolute universals.

### A Bayesian approach

In the previous section we looked at how many samples are necessary to maintain a low false positive rate using the simulated false positive rates on current data as a proxy for false positive rates on future data. An alternative approach is to compute the degree of belief that one normatively should have that a feature is impossible. This is possible through a Bayesian model: with enough sampled languages that fail to show a feature value, the statistically better theory is one in which that feature value has zero probability.

The Bayesian approach specifies a probability model over unknown states of the world and links this probability model to the observed data. In our case, the unknown state of the world is the true, underlying distribution of feature values. Let  $x = \langle x_1, x_2, \dots, x_N \rangle$  be this true distribution on the  $N$  logically possible feature values. Here,  $x$  assigns each feature value a probability, corresponding to the chance that an independently sampled language will exhibit that feature value. For instance, if the features are word orders, then the  $x_i$  for *SVO* might be relatively high, say 0.35 and the  $x_j$  for *OSV* might be relatively low, say 0.05. We can use a model to “work backwards” from counts  $c_i$  of how often each feature value is observed, to the unobserved probabilities  $x_i$ . We will use a simple Bayesian model known as a *Dirichlet-Multinomial* model which makes parametric assumptions about the distribution  $x$ . In particular, it assumes that  $x$  has been generated from a *Dirichlet* distribution. This assumption is not uncontroversial—some have suggested linguistic feature values follow a negative exponential distribution (Cysouw, 2010b) or Pareto-like distributions (Maslova, 2008)—but to our knowledge no systematic model comparison has been undertaken on the distribution of feature values. Perhaps more importantly, the Dirichlet-Multinomial model is analytically tractable. Our formulation has a single free parameter,  $\alpha$ , which controls the degree to which we expect  $x$  to be uniform. As  $\alpha$  gets small, we expect that most of the probability mass in  $x$  is on only a few  $x_i$ : most feature values are low probability, and the distribution is far from uniform. Large  $\alpha$  means that the distribution  $x$  is very close to uniform: all feature values are equally likely. When  $\alpha = 1$ , this corresponds to no real bias, with all *distributions* on  $x$  being equally likely. We can also fit  $\alpha$  by seeing which value makes the observed counts in WALS most likely. For this we find  $\alpha = 0.9$ , a value close to uniform. In this case, all distributions on feature values are almost equally likely, with a bias towards distributions that assign most probability mass to relatively few values (e.g. that have some rare features). Note that  $\alpha$  close to 1 does not imply that all feature values will be equally likely—a uniformly sampled distribution on feature values will often contain some rare features.

We are interested in testing if, in the true distribution  $x$ , some feature values are fundamentally outlawed for human language. This is only sensible if some logically possible feature values are not observed in our sample. Suppose we have observed some number  $c_i$  of languages with the  $i$ 'th feature value. Since we are interested in the case where some feature values are unobserved, we will assume that only  $K$  feature values (out of the  $N$  possible ones) have been observed in existing languages. Thus,  $c_i > 0$  for  $i \leq K$  and  $c_i = 0$  for  $i > K$ . Given this, there are a number of hypotheses we might have. For instance, we might think that all of the unobserved feature values are impossible ( $\forall i > K, x_i = 0$ ). Alternatively, we may think that at least one of them is impossible ( $\exists i > K, x_i = 0$ ). Or,

we might think that only the second is possible, etc. In general, if there  $N - K$  unobserved feature values, then there are  $2^{N-K}$  different theories of this sort we might consider. We will denote each of these possible theories as  $M_b$  where  $b$  is a binary vector that characterizes what is allowed and disallowed in the theory. So for instance,  $M_{000\dots0}$  corresponds to the theory that all of the unobserved features are impossible;  $M_{010\dots0}$  corresponds to the theory that only the second unobserved feature is possible, and the rest are impossible;  $M_{111\dots1}$  corresponds to the theory that all of the unobserved values are really possible; etc.

It turns out that for the Dirichlet-Multinomial, we can directly compute the posterior probability of any particular model  $M_b$ , given a vector of counts  $c = \langle c_1, c_2, \dots, c_N \rangle$  of how often each feature is observed in our sample of languages. As we show in Appendix A, this probability is

$$P(M_b | c, \alpha) \propto \frac{\Gamma((K + n_b) \cdot \alpha)}{\Gamma(C + (K + n_b) \cdot \alpha)}, \quad (1)$$

where  $C = \sum_{i=1}^N c_i$  is the total number of languages observed and  $n_b$  is the number of 1s in the binary string describing  $M_b$  (e.g. the number of features that are unobserved, but actually possible). Here,  $\Gamma$  is the *Gamma function*, roughly a generalization of factorials to real numbers. This probability is easily normalized to give a proper probability distribution (see Appendix A):

$$P(M_b | c, \alpha) = \frac{\frac{\Gamma((K+n_b)\cdot\alpha)}{\Gamma(C+(K+n_b)\cdot\alpha)}}{\sum_{j=0}^{N-K} \binom{N-K}{j} \frac{\Gamma((K+j)\cdot\alpha)}{\Gamma(C+(K+j)\cdot\alpha)}}, \quad (2)$$

Note that to use this to compute the probability that *any*  $n_b$  features are allowed (as opposed to the specific ones in  $b$ ), we can multiply this equation by  $\binom{N-K}{n_b}$ .

This equation is powerful in that it allows us to say, if we observe some feature values, how likely is every possible combination of allowed and disallowed features according to an idealized statistical analysis. Before applying this to a widely studied set of feature counts, it is worth pointing out a few simplifications of (2) that make it more intuitive. First, in the case of one unobserved feature ( $K = N - 1$ ) and thus only two competing hypotheses ( $M_0$  and  $M_1$ ), it is more intuitive often to deal with a *Bayes factor*, which is the log of the ratio of the probability each model assigns to the observed data (the vector of counts  $c$ ):

$$BF = \log \frac{P(c | M_0, \alpha)}{P(c | M_1, \alpha)}. \quad (3)$$

Here, a value greater than zero supports the constrained model  $M_0$ . However, what matters more is the strength of this evidence. Somewhat analogous to how frequentist statistics standardizes p-values, Bayesians standardize how much evidence is required to conclude that one model is better than another. One commonly accepted standard is due to Jeffreys (1961) who considered Bayes factors in the 1.6–3.3 range<sup>10</sup> “substantial,” 3.3–5.0 “strong,” 5.0 – 6.6 “very strong” and  $> 6.6$  “decisive.”

Appendix A shows that when  $\alpha = 1$  and  $K = N - 1$ , this Bayes factor is simply

$$BF = \log \frac{C + K}{K}. \quad (4)$$

<sup>10</sup>Log base 2.

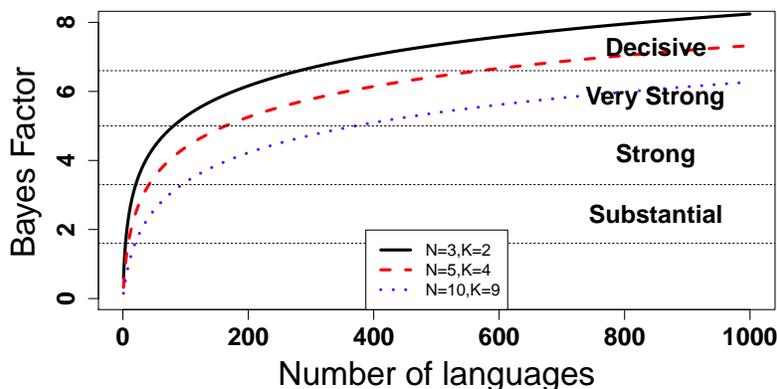


Figure 3. Bayes factor in favor of a constrained model, as a function of the number of samples for  $\alpha = 0.9$ .

For example, to get strong evidence—say, a Bayes factor of 4.0—in favor of a universal restriction against a single feature value when  $N = 10$  feature values are possible, we would require a sample of  $2^4 \cdot (10 - 1) - 10 + 1 = 135$  independently sampled languages not showing the feature. “Decisive” evidence, a Bayes Factor of 6.6, would require 864 samples. When  $C \gg K$ , the Bayes factor is approximately  $\log(C/K)$ , which indicates that doubling the number of possible feature values requires roughly doubling the number of samples, to maintain the same Bayes factor. Note that these results are still assuming that  $c_i = 0$  for  $i > K$ ; otherwise observing a language with  $c_i > 0$  for some  $i > K$  would falsify model  $M_0$ . One other important fact about (4) is that as  $C \rightarrow \infty$ , the Bayes factor in favor of  $M_0$ , with an outlawed feature, will also go to  $\infty$ . This means that as more and more languages are observed, evidence accumulates in favor of a universally outlawed feature—it is possible to go from frequency counts to statistical inferences of impossibility. This same fact holds for the more general case of (2): increased observations of languages will eventually push the evidence in favor of an absolute restriction, eventually beyond any fixed standard of evidence.

To understand this relationship between number of languages and amount of evidence, we can consider various  $C$  using our empirically-determined value of  $\alpha = 0.9$ . Figure 3 shows the Bayes factor in favor of a constrained theory for various  $N$  ( $K = N - 1$ ), as the number of independent languages in the sample varies. Here, the results qualitatively agree with our earlier frequentist analysis that very convincing evidence in support of an absolute universal is only found after around 500 languages. However, quantitatively this analysis is somewhat more optimistic, finding strong support for absolute universals after around 100 to 200 languages, and decisive support between around 500 and 800, depending on the number of features examined. Like the above analysis, these languages are required to be independent, meaning that even a few hundred languages may be unachievable.

We note, however, that the particulars of this Bayesian analysis are sensitive to  $\alpha$ , the parameter expressing how strongly we should expect a uniform distribution of features. For

instance, if  $\alpha = 0.5$ , a prior favoring the likelihood of rare features, the most optimistic line only approaches “very strong” evidence after about 800 samples. Conversely, if  $\alpha = 2.0$ , meaning that we expect all feature values are pretty likely, the lines all become “decisive” before even 200 samples. Unfortunately, this would still be a huge number of independent languages to find.

One additional advantage of the Dirichlet-Multinomial is that it allows for easy computation of relevant measures other than the Bayes factor. For instance, we can compute the expected value that the unconstrained model assigns to one of the  $N - K$  unobserved features. In this case, the probability distribution on feature probabilities given by the Dirichlet-Multinomial is a Beta distribution  $x_i \sim \text{Beta}(\alpha, (N - 1)\alpha + C)$ ; in particular, the unobserved features have an expected probability of  $\alpha / (N\alpha + C)$ . For instance, in the unconstrained model, with  $N = 5, K = 4, \alpha = 0.9$ , observing one missing feature value over 100 languages will lead us to believe that an unobserved feature has probability  $0.9 / (5 \cdot 0.9 + 100) = 0.0086$  of being found in a human language. This is a useful computation because it is applicable also to testing typicality universals—we can estimate how infrequent a feature value is likely to be, given that it has not been observed. Thus, the model can be used to compute other relevant comparisons and statistics, allowing for more precise inferences.

*Example computation: absolute constraints on NP constituent ordering*

We next demonstrate how the formal model can be applied to an open area of research. This example is intended to be illustrative and not conclusive: the right “answer” will depend on how many effectively independent samples are included in the world’s extant languages, a difficult problem that is beyond the scope of the current paper. A considerable amount of work has been done elaborating on Greenberg (1963)’s Universal 20 (Hawkins, 1983; Rijkhoff, 1990, 1998, 2002; Cinque, 2005; Cysouw, 2010a), which concerns the order of demonstratives, numerals, adjectives, and the head noun. Only a subset of the possible orderings are observed in human language. The proposals for *why* some of the noun phrase constituent orderings are unobserved are quite varied, ranging from explanations internal to Chomsky (1995)’s minimalism (Cinque, 2005), to statistical models based on the properties of the word order (for comparison of models, see Cysouw, 2010a). This means that the validity of this universal has theoretical importance.

For this potential universal, we can take Equation (2) and compute the posterior distribution for how likely it is that in a sample of languages we should believe any particular constraints on allowed features. We use the reported counts from Cysouw (2010a), building on Dryer (2006), who found that in a sample of 276 languages, 7 of the possible 24 orders (feature values) were unobserved. As above, this means that there are  $2^7 = 128$  possible theories for which subset of the unobserved orders is actually cognitively permitted. For simplicity, we will assume a uniform prior on these hypotheses<sup>11</sup>. In general, these 128 hypotheses can be grouped into  $7 + 1 = 8$  classes for *how many* of the unobserved orders really are possible. Note that each class of hypotheses is a different size: the class where 0 orders are allowed has only one hypothesis ( $M_{0000000}$ ) the class where one order is allowed

<sup>11</sup>An important caveat is that we might actually assign higher prior to  $M_{1111111}$  since it is in some sense *cognitively* simpler: it posits no constraints on word order. An analogous analysis could be applied in this case.

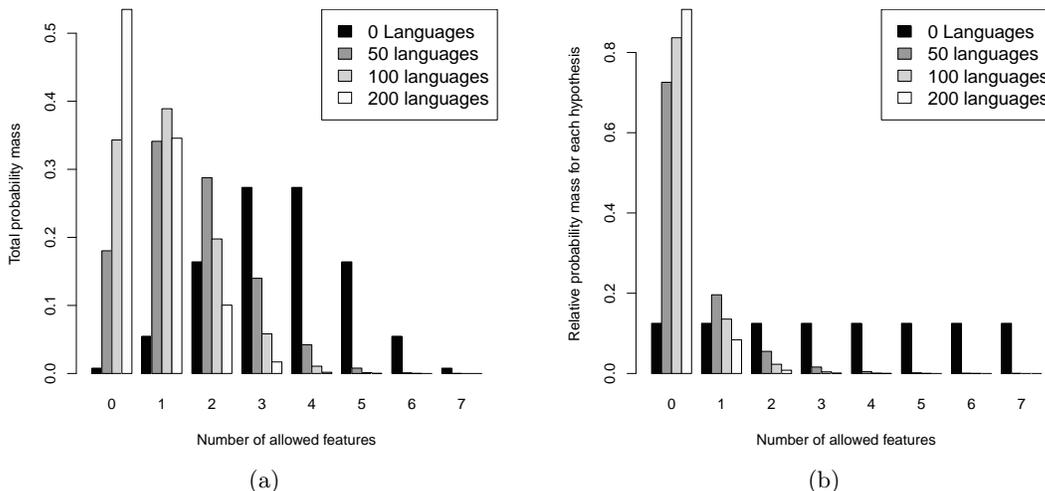


Figure 4. These plots show the probability ( $y$ -axis) of different hypotheses about the 7 unobserved word orders, as a function of the number of features orders which are cognitive permitted ( $x$ -axis), though unobserved in a sample of languages. (a) shows the total probability mass of all hypotheses with  $x$  of the unobserved word orders actually permitted, as a function of  $x$ , for various language samples of size 0, 50, 100, and 200. (b) shows the relative probability of the average hypothesis in each equivalence class (see text).

has 7 hypotheses ( $M_{0000001}$ ,  $M_{0000010}$ ,  $M_{0000100}$ , etc), and in general the class with  $i$  allowed orders has  $\binom{7}{i}$  hypotheses.

Figure Figure 4(a) shows the total probability mass for each class of hypotheses, as the number of languages observed varies. When 0 languages are observed, these posterior values simply correspond to the number of hypotheses in each class, according to the binomial coefficients  $\binom{7}{i}$ . This corresponds to a uniform prior on hypotheses, which becomes a binomial prior on classes<sup>12</sup>. However, as we observe more and more languages (with none of them showing the 7 orders), this distribution shifts towards the class 0, with none of the unobserved hypotheses possible. In the limit, the 0 class’s probability and thus can assign the observed orders higher probability (for analogous reasoning, see Perfors, Tenenbaum, Griffiths, & Xu, 2011). This illustrates that it may be easier to get statistical evidence against some hypotheses, without narrowing down exactly which one is the “right” one.

Figure 4(a) may be difficult to interpret in that the posterior distribution on the number of allowed orders depends on the number of hypotheses in that class. Figure 4(b) shows a different view of the same distribution, but which adjusts for the number of hypotheses in each class. Here, we plot the posterior probability of the *average* hypothesis in each class, relative to those in other classes. This can be interpreted as a plot of how well a typical

<sup>12</sup>Another modeling approach would have been to put a uniform prior on the *number* of orders which are allowed, instead of the specific set of orders. Doing so would require almost exactly the same derivations presented in the Appendix, and would have yielded a posterior distribution over the number of disallowed orders identical to Figure 4(b).

$i$ -orders-permitted hypothesis would compare to a typical  $j$ -orders-permitted hypothesis—a comparison of individual hypotheses rather than groups. Thus, this shows that when 0 languages have been observed, the average hypotheses in each class are all equally likely (even though the sum of probabilities in each class, Figure 4(a), is variable). Again, as we observe more data, this posterior distribution shifts towards zero, such that by 50 or 100 languages, very little relative probability mass is put on theories that posit all orders are allowed.

We can additionally use to model to compute other measures which may be more informative. It is useful to compare the probability of the constrained model to the probability of the best unconstrained model; for instance, only in transitioning from 100 to 200 languages does the “best” model switch to 0 allowed features being more probable than 1 allowed feature. We can additionally use this analysis to determine how many languages would be required before, say, 95% of probability mass was put on the “0” bar, corresponding to none of the unobserved orders are allowed. This would require around 3600 *independent* languages, suggesting that a universal outlawing of these 7 orders will never be justified with cross-linguistic statistics alone. It is therefore not sensible to construct explanations of why we fail to see exactly and only those 7 word orders—likely at least some of the 7 are cognitively allowed.

### Conclusion

We have shown through several kinds of analyses that absolute universals will be very difficult to justify based on cross-linguistic analysis. For reasonable scientific inferences, this is not due to a *logical* problem of inferring impossibility, but rather a *sample-size* problem of the large number of languages necessary. Indeed, statistical model comparison does not know the difference between theories based on probability and those based on possibility: they can both be translated into the logic of hypothesis testing. However, the amount of data to find absolute universals is likely to be extraordinarily large, at least relative to the number of languages in existence. Our application of Bayesian methods to Greenberg’s universal 20 points additionally towards a nuanced view, in which certain claims may be justifiable using cross-linguistic statistics—for instance that likely not all unobserved word orders are actually possible.

In general, though, other methods are required in order to test linguistic—and indeed cognitive—universals, before they are incorporated into theory. One possibility is that absolute universals may be deduced from *a priori* grounds, as part of the theoretical framework necessary for studying language (Bickel, 2007a). For instance, it may be a kind of definitional universal that all words consist of morphemes. However, many of the most interesting universals are simply empirical questions—are there, for instance, any hard cognitive restrictions on the ordering of NP constituents? In these cases, we strongly advocate the use of behavioral methods for testing the psychological reality of constraints. This point has been made recently by Tily and Jaeger (2011), who argue that multiple methodologies are necessary for drawing strong typological conclusions and that artificial language learning (Hudson Kam & Newport, 2005, 2009) in particular is one powerful method (see also Jaeger & Tily, 2011). Indeed, artificial language learning has been fruitfully applied to study a variety of universals (Culbertson, Smolensky, & Legendre, 2011; Tily, Frank, & Jaeger, 2011; Christiansen, 2000). Similar techniques on artificial function word learning

have been used to argue for the psychological reality of typologically observed constraints on determiners (Hunter & Conroy, 2009). The use of multiple methods is important because empirical uncertainty about which universals are “real” can lead to an exponential blow-up in the number of possible linguistic theories (see Gibson & Fedorenko, 2010). Even in the case of Universal 20 above, there are 128 different hypotheses for word orders are actually permitted, and any theorizing—in particular derivations of all and only the observed word orders (e.g. Cinque, 2005)—is likely to be premature over-fitting (see also Bickel, 2001).

In general, we also recommend that claims about linguistic universals should be accompanied by some measure of the strength of evidence in favor of such a universal—for instance, a Bayes factor or posterior probability for the constrained theory over the unconstrained theory. This is especially important when universals are taken to be relevant to theoretical debates in linguistics, since theories should not be evaluated by or depend on very weakly-supported “universal” properties. Our results demonstrate that a considerable amount of work is required in order to justify absolute universals and that skepticism is warranted when absolute universal are posited from no more than cross-linguistic patterns.

Appendix A: Derivation of Bayes factor

We apply a simple Bayesian model known as a *Dirichlet-Multinomial* model. We present a derivation for a model  $M_b$  Where  $b$  is, as above, a binary string describing which of the unobserved feature values are in reality impossible. Thus, for instance,  $M_{11\dots 1}$  corresponds to the theory that all unobserved features are possible, and  $M_{00\dots 0}$  corresponds to the theory under which none are possible. We assume a Dirichlet prior on  $x$ , the true distribution of features. The Dirichlet prior is:

$$P(x \mid \alpha, M_b) = \frac{\Gamma((K + n_b) \cdot \alpha)}{\Gamma(\alpha)^{K+n_b}} \prod_{i=1}^{K+n_b} x_i^{\alpha-1}. \tag{5}$$

where  $n_b$  is, as above, the number of 1s in  $b$ . For notational simplicity, our equations will all assume that the  $n_b$  ones in  $b$  occur in the first  $n_b$  digits of  $b$ : thus, we might have  $b = 1100$  or  $b = 1000$ , but not  $b = 0100$ . This assumption simplifies the notation greatly, but does not affect the math—the same derivations can be made by appropriately shuffling the indices of  $x_i$  based on which features are allowed via  $b$ . This simplification is why the sum can run to  $K + n_b$ , as opposed  $K$ , and then some subset of later indices.

This prior has two parts. The fraction out front term is simply a normalizing constant, written in terms of the  $\Gamma$ -function, a function that essentially generalizes factorials to non-integers. The product over  $x_i^{\alpha-1}$  formalizes the key part of the prior and is parameterized by the single variable  $\alpha$ . As  $\alpha$  gets large, this prior favors a uniform distribution,  $x_i = 1/(K + n_b)$  for all  $i$ . As  $\alpha$  gets small, this prior favors distributions which place probability mass on only a few  $x_i$ . Crucially, however, this prior treats all  $x_i$  the same, meaning that a priori we do not expect some feature values to be more likely than others<sup>13</sup>.

The second part of the model is the *likelihood*, which formalizes how likely the observed data are for any assumed distribution  $x$ . The likelihood takes a simple form as well. Suppose that the  $i$ th logically possible feature value occurs  $c_i$  times in the observed data. This happens with probability  $x_i^{c_i}$  since each instance occurs with probability  $x_i$ , and there are  $c_i$  of them. Taking into account the fact that the data points can occur in any order, this means that  $P(c \mid x, M_b)$  is then

$$P(c \mid x, M_b) = \frac{\Gamma(C)}{\prod_{i=1}^K \Gamma(c_i)} \prod_{i=1}^{K+n_b} x_i^{c_i}, \tag{6}$$

with  $C = \sum_{i=1}^N c_i$ . With this likelihood, distributions that closely predict the empirically observed distribution  $c_i$  are more likely than those which predict distributions far from the observed ones.

We are interested in how well  $M_b$  can predict the observed counts. Formally, we want a model such  $P(M_b \mid c, \alpha)$  is high—the probability of the model given the counts is large. By Bayes rule, and the independence of  $M_b$  and  $\alpha$ , we have that

$$\begin{aligned} P(M_b \mid c, \alpha) &\propto P(M_b)P(c \mid M_b, \alpha) \\ &= P(M_b) \int P(c \mid x, M_b)P(x \mid M_b, \alpha)dx. \end{aligned} \tag{7}$$

<sup>13</sup>This is a simplification for our purposes, but this same class of model will work with different prior expectations for each  $x_i$ .

Here we will consider the priors  $P(M_b) \propto 1$ , meaning that we are equally likely to think that each  $M_b$  is true a priori; this assumption can be altered if one is willing to keep track of the  $P(M_b)$  below. Using this, (5) and (6) above, this gives that

$$P(M_b | c, \alpha) \propto \frac{\Gamma(C)}{\prod_{i=1}^K \Gamma(c_i)} \cdot \frac{\Gamma((K + n_b) \cdot \alpha)}{\Gamma(\alpha)^{K+n_b}} \cdot \int \prod_{i=1}^{K+n_b} x_i^{c_i + \alpha - 1} dx \quad (8)$$

Here, the integral is a special form, a type-1 Dirichlet integral, and can be evaluated analytically to yield,

$$\begin{aligned} P(M_b | c, \alpha) &\propto \frac{\Gamma(C)}{\prod_{i=1}^K \Gamma(c_i)} \cdot \frac{\Gamma((K + n_b) \cdot \alpha)}{\Gamma(\alpha)^{K+n_b}} \cdot \frac{\Gamma(\alpha)^{n_b} \prod_{i=1}^K \Gamma(c_i + \alpha)}{\Gamma(C + (K + n_b) \cdot \alpha)} \\ &= \frac{\Gamma(C)}{\Gamma(\alpha)^K} \cdot \frac{\Gamma((K + n_b) \cdot \alpha)}{\Gamma(C + (K + n_b) \cdot \alpha)} \cdot \prod_{i=1}^K \frac{\Gamma(c_i + \alpha)}{\Gamma(c_i)}. \end{aligned} \quad (9)$$

Since this equation is only proportional to the posterior probability  $P(M_b | c, \alpha)$ , we must normalize it to get actual posterior probabilities. In this step, the first and last terms, which do not depend on  $n_b$  (the model) will cancel, giving

$$P(M_b | c, \alpha) = \frac{\frac{\Gamma((K+n_b)\cdot\alpha)}{\Gamma(C+(K+n_b)\cdot\alpha)}}{\sum_{b'} \frac{\Gamma((K+n_{b'})\cdot\alpha)}{\Gamma(C+(K+n_{b'})\cdot\alpha)}} \quad (10)$$

Notice that the denominator sum runs over all  $b'$ , but the term depends only on the number of 1s in  $b'$ ,  $n_{b'}$ . This means that we can group together similar elements in the denominator and rather than have an exponential sum over all binary strings of length  $N - K$ , we can have a smaller (and more numerically stable) sum:

$$P(M_b | c, \alpha) = \frac{\frac{\Gamma((K+n_b)\cdot\alpha)}{\Gamma(C+(K+n_b)\cdot\alpha)}}{\sum_{j=0}^{N-K} \binom{N-K}{j} \frac{\Gamma((K+j)\cdot\alpha)}{\Gamma(C+(K+j)\cdot\alpha)}}. \quad (11)$$

This equation, though not mathematically trivial, can easily be computed for any reasonable number of features.

Note that when  $\alpha = 1$  and  $K = N - 1$ , Equation (11) can be simplified significantly. In this case of two hypotheses, it is easier to work with the log posterior odds, or the Bayes factor (Jeffreys, 1961),

$$\log \frac{P(c | M_0, \alpha = 1)}{P(c | M_1, \alpha = 1)} = \log \frac{\frac{\Gamma(K)}{\Gamma(C+K)}}{\frac{\Gamma(K+1)}{\Gamma(C+K+1)}} = \log \frac{C + K}{K}. \quad (12)$$

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