

# Grammar Structure and the Dynamics of Language Evolution

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**Abstract.** The complexity, variation, and change of languages make evident the importance of representation and learning in the acquisition and evolution of language. For example, analytic studies of simple language in unstructured populations have shown complex dynamics, depending on the fidelity of language transmission. In this study we extend these analysis of evolutionary dynamics to include grammars inspired by the principles and parameters paradigm. In particular, the space of languages is structured so that some pairs of languages are more similar than others, and mutations tend to change languages to nearby variants. We found that coherence emerges with lower learning fidelity than predicted by earlier work with an unstructured language space.

## 1 Introduction

The evolutionary dynamics of language provides insight into the factors allowing subpopulations to converge on common or similar languages. The problem has a more general significance for robotics and artificial life as a clear and empirically supported platform for the study of how coherent behavior can emerge in a population of distributed adaptive agents.

Of particular interest from the perspective of evolutionary dynamics are insights into the means and value of conserving linguistic diversity. The practical importance of linguistic diversity has attracted some attention [23, 21], though perhaps not as much as biological diversity. Recent studies that have applied a biological perspective to the evolution of linguistic convergence and diversity have shown promising results [7, 8, 22, 17, 11, 20, 15]. Most such studies that apply a biological perspective to language evolution have been based on very simple languages arbitrarily related to each one another. We believe these studies may be enriched by a more realistic description of language.

Language models based on the Chomskian paradigm [1, 2] view language as an aspect of individual psychology. There has been some debate about the extent to which the underlying representation of languages are inherited or learned and how language impacts fitness. Pinker and Bloom, for example, suggest that a

language instinct constrained by universal grammar sets the stage for language acquisition which then contributes to individual fitness [19, 18]. Hauser, Chomsky and Fitch argue more recently that while certain perceptual and articulatory abilities may have been selected for, it remains unclear how the most fundamental aspects of human language emerged [9, 6]. All parties agree that linguistically relevant properties are to some extent learned through cultural transmission and change through time. How this might occur has been the subject of many analytic and simulation studies [15, 16, 20, 11, 22].

As an organism is determined in part by its genome, language is determined in part by a lexicon of generators which in turn determine its phonology, semantics, morphology and syntax; these properties may evolve [10, 13]. Both the genome and at least part of language is inherited with variation, and therefore potentially a target for natural selection. These similarities have lead some researchers to adopt a quasi-species model [5, 4] for describing the dynamics of language evolution [17, 12]. In their model, grammars are mutationally equidistance from each other with arbitrarily assigned similarity. It seems, however, that the kind of changes language actually undergoes is much smaller than what this model seems to predict – the language of a child is, more or less, the same as that of its linguistic community. This suggests an approach according to with the languages most accessible to the current one via mutation are also very similar to it.

In this paper, we study how certain properties of the space of possible languages and learning mechanisms impact language change. We introduce a regularity in the language space by viewing the locus of language transmission as a series of learned parameters and calculating the similarity between languages as the proportion of parameters that agree. We explore the effect of this simple regularity on the dynamics of language evolution primarily through simulations. These simulations go beyond previous analytic studies of simple models, and we find that structure has a significant impact on stability results.

## 2 Methods

Consider a fully-connected finite population of  $N$  individuals, each of whom possesses a language which is encoded as a sequence of  $l$  linguistic ‘components’

Symbol	Parameters	value(s)
$N$	population size	500
$f_0$	base fitness	$10^{-3}$
$l$	Number of language parameters	1, 2, 3, or 6
$d$	Number of values per each parameter	64, 8, 4, or 2
$n$	Number of possible grammars	$64(= d^l)$
	Number of time steps	100,000

**Table 1.** Parameters used in the simulations.

or ‘parameters’. Each parameter can take only a limited number  $d$  of values. For example, a language  $L$  with 10 parameters each taking 3 values (A,B,C) can be represented by a linear sequence like AABABCBABA. (This string is not an example of a statement from the language, but rather a represents the language itself.) Such a representation is in the spirit of Chomsky’s “principles and parameters” approach to language[15]. To allay a potential source of confusion: parameters, as we use them here, correspond to whatever the relevant differences are between language *at the level of description relevant to transmission*. This will correspond to parameters in the Chomskian sense just in case these latter parameters are appropriately relevant to linguistic transmission. We are throughout assuming that whatever is being transmitted can be usefully viewed (at least to a first approximation) as a finite sequence of finite-valued parameters.

Representing a language as a sequence, we define the language similarity between individual  $i$  and  $j$ , denoted  $a_{ij}$ , as the proportion of parameters on which the two individuals agree. For example, the language similarity between an individual  $i$  whose language is represented as AAA and an individual  $j$  whose language is represented as ABA is  $2/3$  and  $a_{ij} = a_{ji}$ .

The fitness of an individual has two parts: the base fitness, denoted  $f_0$ , and a *linguistic merit* proportional to the probability of that the individual being able to successfully communicate with another, selected at random from his neighbors. A linguistic merit of an individual is proportional to the sum of language similarity between the individual and others it is in linguistic contact with (which is the entire population for this model). The overall fitness of an individual,  $f_i$ , is described as the following, as in [16]:

$$f_i = f_0 + \frac{1}{2} \sum_{j=1}^N (a_{ij} + a_{ji}) = f_0 + \sum_{j=1}^N a_{ij} \quad (1)$$

noting that  $a_{ij} = a_{ji}$  according to our definition of similarity.

At each time step, an individual is chosen to reproduce randomly and independently with a probability according to relative fitness. Reproduction can be thought of either as the individual producing an offspring which inherits the parent’s language and replaces another in the population, or another individual changing its language to match the “teacher’s” language. We will use the former terminology.

The offspring learns the parent’s language with a certain *learning fidelity*,  $q$ . This learning fidelity is properly a function of the specifics of the learning method the child uses and the complexity of the language, often modeled with a probability distribution over the possible transition from each language  $L_i$  to each other (possibly different)  $L_j$ . But in the present setting we use the first order approximation that the only incorrect/imperfect learning is a single parameter change per reproductive event. We refer to this constraint as *gradual learning*. The rationale behind this approach is that learning errors do not typically result in the learner acquiring a radically different language. This single parameter change constraint on incorrect/incomplete learning is analogous to only allowing single point mutations to the linear sequence representation of the language. As

such, it defines the “sequence space” [4] through which the population moves during the evolutionary process.

We study language change in an ideal population using a simulation, using the following algorithm. Initially each individual in the population  $P$  starts with a randomly chosen language from set of all possible languages.

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for each individual  $i \in P$ 
  compute fitness  $f_i$  of  $i$ 
end for
do until number of updates is met
  select an individual  $i \in P$ 
  select a second random individual  $j$  from the population
  replace individual  $j$  with an offspring  $k$  of individual  $i$ 
    if the offspring is mutant( mutation rate =  $\mu$ )
      change a random parameter of  $L_k$ 
    else
       $L_k = L_i$ 
    end if
  update fitness of the individual  $j$ 
end do

```

We measure the *dominant* language frequency directly at each time step by counting the number of individuals speaking each language. The dominant language at any given time is simply the language that is most frequent at that time, and will typically change over time unless the population has strongly converged.

The linguistic coherence of the population, denoted  $\phi$ , is defined as follows:

$$\phi = \frac{1}{N} \sum_{i=1}^N \sum_{j=1}^N a_{ij} \quad (2)$$

Counting the actual number of languages that exist in the population may disguise the degree of variation when some of the languages disproportionately dominate. Consequently, we used an analogue to the effective number of alleles in a population, which we will refer to as the effective number of languages in the population,  $n_e$  [3]:

$$n_e = \left( \sum_{i=1}^N p_i^2 \right)^{-1} \quad (3)$$

where  $p_i$  is the frequency of each language.

Table 1 shows the parameter settings for the experimental setup. We used a population size  $N$  of 500, a base fitness  $f_0$  of 0.001, and we let the number of different possible languages  $n$  be 64. Each language in a set can be represented as a linear sequence of length  $l$  with elements drawn from a set of  $d$  possible values. For set A, the similarity between languages that are not the same is set to a constant value  $a$  equal to 0.5. For all other sets,  $a_{ij}$  is the Hamming distance divided by sequence length as described above. The reproduction cycle repeated

for 100,000 times to make each run long enough to reach an equilibrium. Twenty replica runs, varying only the random number generator seed, were done at each  $q$  between 0.5 and 1 at 0.02 intervals.

For the fully-connected topology given a uniform similarity  $a$  between  $n$  different grammars, and the learning fidelity of  $q$ , three equilibrium solutions for grammar frequency were derived by Komarova *et. al.*[12]:

$$X_0 = 1/n \quad (4)$$

$$X_{\pm} = ((a-1)(1+(n-2)q) \mp \sqrt{D})(2(a-1)(n-1))^{-1} \quad (5)$$

where

$$D = 4[1 + a(n-2) + f_0(n-1)](1-q)(n-1)(a-1) + (1-a)^2[1 + (n-2)q]^2$$

Below a certain learning fidelity of  $q_1$ , only the symmetric solution  $X_0$  exists and no single language dominates. Solving for  $q$  when  $D = 0$  determines the critical leaning fidelity threshold  $q_1$ , which corresponds to the *error threshold* in molecular evolution.

$$q_1 = \frac{1}{(1-a)(n-2)^2} \left[ 4 + 2(n-1)^{\frac{3}{2}} \sqrt{(1+f_0)[1+a(n-2)+f_0(n-1)]} - 2f_0(n-1)^2 - 3n - a(2n^2 - 7n + 6) \right] \quad (6)$$

When  $q_1 < q < q_2$  for a specific  $q_2$ , both the symmetric  $X_{\pm}$  and asymmetric  $X_0$  solutions exist and are stable. For  $q > q_2$  however, only the asymmetric solution where one language dominates the population is stable. This  $q_2$  value is the point where  $X_0 = X_-$ , giving:

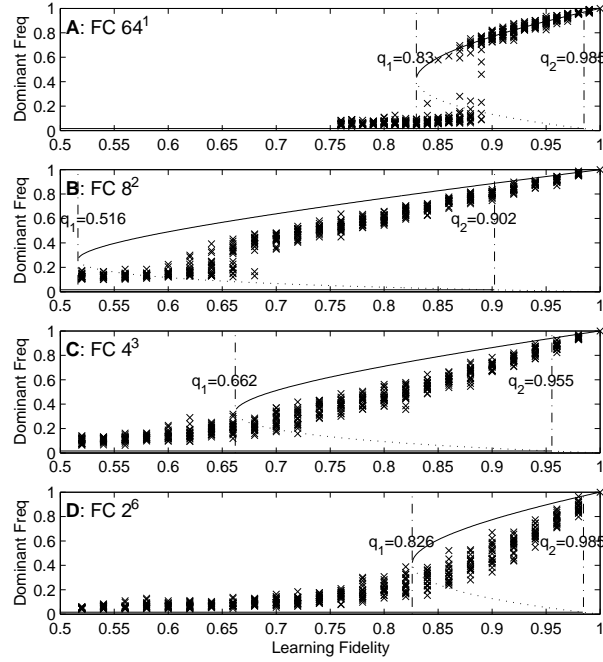
$$q_2 = (n^2(f_0 + a) + (n+1)(1-a)) (n^2(f_0 + a) + 2n(1-a))^{-1} \quad (7)$$

Komarova *et. al.* provide much more detail and proofs[12].

By introducing a regularity in language, we effectively change the transition matrix of  $a_{ij}$ . To compare our findings with the analytical result, we use the

Setting	l	d	n(=d <sup>l</sup> )	$\bar{a}$	$q_1$	$q_2$
A	1	64	64	0.500	0.830	0.985
B	2	8	64	0.111	0.516	0.902
C	3	4	64	0.238	0.662	0.955
D	6	2	64	0.492	0.826	0.985

**Table 2.** System settings, average language similarity ( $\bar{a}$ ),  $q_1$  and  $q_2$ . When  $l = 1$ , we use  $a = 0.5$ . A: one component with 64 options, B: two components with 8 options, C: three components with 4 options, D: 6 components with 2 options. Each setup has exactly the same number of possible languages.



**Fig. 1.** The dominant( $\times$ ) language frequency after 100,000 time steps overlaid with symmetric (horizontal line) and asymmetric (curved line) solutions for  $a$ (or  $\bar{a}$ ),  $n = 64$ ,  $f_0 = 0.001$ . Each point is an independent replica.  $d^l$  shown at the top left corner of each graph.

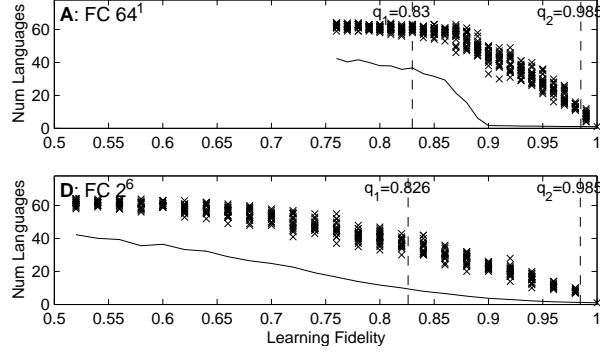
average language similarity  $\bar{a}$  for calculating  $q_1$  and  $q_2$ , where  $\bar{a}$  is calculated using the equation below:

$$\bar{a} = \frac{1}{n-1} \left( \sum_{k=1}^{l-1} \frac{l-k}{l} (d-1)^k \binom{n}{k} \right) \quad (8)$$

We consider 4 settings A-D, varying in the “amount of structure.” The four cases are listed in Table 2 together with the calculated  $\bar{a}$  for each case.

### 3 Results

We plot the experimental and analytic results for comparison in Figure 1. The empirical results for the uniform similarity of  $a = 0.5$  between two different languages closely follows the expectation from the analytic results arrived at by Komarova *et. al.*[12] as shown in Figure 1 A, which we have previously described in detail[14].



**Fig. 2.** The number of languages( $\times$ ) and the average effective number of languages( $—$ ).

The results of the multi-component languages (Figure 1 B, C and D) do not show the clear transition from symmetric to asymmetric solution. The trend is considerably smoother, with nothing but an increased variance in results at the point of the phase transition for parameter sets C and D. Parameter set B shows a region where both symmetric and asymmetric solutions appear stable for  $q$  values between 0.6 and 0.7, but it is notable that the empirical asymmetric dominant abundance is significantly below the analytical expectation for this set as well as C and D.

Since the setup A and D have similar  $\bar{a}$  values ( $\bar{a}_A \simeq \bar{a}_D$ ), they provide a better example of what difference the multi-parameter language brings to the language evolution scenario. Figure 2 compares the number of languages and the effective number of languages ( $n_e$ ), calculated using the equation (3). In the single-parameter language case A, all the possible languages exist in the population in the region where  $q < q_{1A}$ . On the other hand, the 6-parameter case D has only half of the all possible languages at  $q = q_{1D}$ .

Figure 1 A shows that if the learning fidelity is greater than 0.9, one language dominates in the population. That trend is illustrated clearly by the average effective number of languages in Figure 2 A. There are still over half of all possible languages remaining in the population at  $q = 0.9$ . This number overestimates the true variation in the population when some languages disproportionately dominate while most are at very low frequency. Incomplete/incorrect learning provides a constant influx of variants, but these variants do not propagate to any appreciable frequency due to their inferior fitness. The effective number of languages  $n_e$  for the set A at  $q = 0.9$  is close to 1 ( $n_e = 1.68$ ), which indicates that the population has converged to one language, and the rest of languages exist a very low frequency .

In contrast, Figure 2 D shows a gradual decline in number of languages as learning fidelity increases. For this set, the number of languages in the population starts decreasing noticeably for  $q$  values above 0.55, and the effective number of languages  $n_e$  decreases over the entire range. However, at  $q$  values above 0.9, set

D shows a higher  $n_e$  value (3.75 at  $q = 0.9$ ) than set A, indicating that there are more relatively high abundance languages in set D despite the fact that the total number of languages is lower.

In set A, all possible languages are a single step away in sequence space; in other words, all possible languages are reachable by a single incorrect/incomplete learning event. In set D, however, only a small subset of possible languages are producible as single step variants from the dominant language. These single-step variants of the dominant account for the majority of non-dominant languages in the population. Additionally, these variants have a high fitness relative  $\bar{a}$ , and a higher equilibrium frequency in mutation-selection balance.

## 4 Discussion

For the set of single-component languages, our empirical results closely match the analytic results produced by Komarova *et al.* In an unstructured language space, high fidelity learner-driven change, such as the sort exhibited by human languages, can only occur just above the critical error threshold  $q_1$ , near the bifurcation point.

These simulations show that substantial levels of linguistic coherence can be achieved with lower learning fidelity if structure is introduced. All four settings explored here have language spaces of exactly the same size, and yet the structured language sets allow fairly stable asymmetric solutions even with quite low learning fidelity and show a much more gradual approach to coherence.

We conclude that a simple regularity combined with gradual learning can dramatically reduce the number of languages that exist in the population, even in regions where analytic results indicate that only symmetric solutions will be stable. Gradual learning used in this experiment seems a more realistic approximation to reality than the “memoryless” learning used in previous work. The qualitatively different dynamics with respect to the critical learning fidelity suggests that convergence to a set of closely related languages is significantly easier than previously thought.

These results are in keeping with the expectations of a quasi-species interpretation. Gradual learning maps the grammars into a sequence space where some grammars have fewer mutational (incomplete/incorrect learning) steps from others. Calculating the similarity between grammars which determines fitness as one minus Hamming distance divided by sequence length ensures that grammars that are close in the sequence space have similar fitness values. This produces a smooth fitness landscape.

The upshot of this smooth fitness landscape is that selection operates on the quasi-species formed by the dominant grammar and its close variants. At learning fidelity values below  $q_1$ , the population converges not to a single dominant grammar with all other grammars equally represented, but instead to a family of similar grammars. The fidelity of this family is higher than the nominal learning fidelity because a sizable proportion of incomplete/incorrect learning events among members of the quasi-species result in other members of the quasi-species.



At still lower  $q$  values, that family of grammars (the quasi-species) spreads farther out in sequence space, until at some point it includes all possible grammars and is identical to the symmetric analytical solution provided by Nowak and Komarova's model [17, 12].

For learning fidelity values higher than  $q_1$ , we note that a structured grammar space weakens the selection against the minor variants of the dominant grammar in comparison to unstructured or single component grammar models. This effect causes the population to display a dominant abundance below the analytical model's expectations because the close variants of the dominant have a higher equilibrium abundance in mutation-selection balance.

We conjecture natural languages can be viewed as belonging to a highly structured set at some level of description relevant to a theory of learning and cultural transmission, even if this structure is not reducible to a simple sequence representation. As such, the qualitatively different dynamics explored here are important to understanding how human language evolves through time. Additionally, in technological applications where agents learn from each other and it is desirable for the overall system to converge, these results may provide a guide to designing properties of the language or state representation depending on the degree of convergence desired. If it is sufficient that agents of the system just mostly agree, i.e. converge to close variants of a dominant grammar, then a structured state space may provide a way to achieve faster convergence at higher mutation values. However, if absolute convergence is required, the state space must be designed such that minor variants are strongly selected against, producing a sharp fitness peak. This constraint also implies that a critical mutation/learning fidelity threshold exists.

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## References

1. N. Chomsky. *Aspects of the Theory of Syntax*. MIT Press, Cambridge, MA, 1965.
2. N. Chomsky. *Rules and Representations*. Basil Blackwell, London, 1980.
3. J. F. Crow and M. Kimura. *An Introduction to Population Genetics Theory*. Harper & Row Publishers, New York, Evanston and London, 1970.
4. M. Eigen, J. McCaskill, and P. Schuster. The molecular quasi-species. *Adv. Chem. Phys.*, 75:149–263, 1989.
5. M. Eigen and P. Schuster. *The hypercycle: A principle of natural self-organization*. Springer Verlag: Berlin, 1979.

6. W. T. Fitch, M. D. Hauser, and N. Chomsky. The evolution of the language faculty: Clarifications and implications. *Cognition*, Forthcoming, 2005.
7. T. Hashimoto and T. Ikegami. *Evaluation of symbolic grammar systems*. Springer-Verlag:Berlin, 1995.
8. T. Hashimoto and T. Ikegami. Emergence of net-grammar in communicating agents. *BioSystems*, 38:1–14, 1996.
9. M. D. Hauser, N. Chomsky, and W. T. Fitch. The faculty of language: what it is, who has it, and how did it evolve? *Science*, 298:1569–1579, 2002.
10. B. Joseph. Historical linguistics. In M. Aronoff and J. Rees-Miller, editors, *The Handbook of Linguistics*. Blackwell, Oxford, 2000.
11. S. Kirby. Spontaneous evolution of linguistic structure: an iterated learning model of the emergence of regularity and irregularity. *IEEE Transactions on Evolutionary Computation*, 5(2):102–110, 2001.
12. N. L. Komarova, P. Niyogi, and M. A. Nowak. Evolutionary dynamics of grammar acquisition. *Journal of Theoretical Biology*, 209(1):43–59, 2001.
13. S. M. Lamb and E. D. Mitchell. *Sprung from a Common Source: Investigations into the Prehistory of Languages*. Stanford University Press, Stanford, California, 1991.
14. Y. Lee, T. C. Collier, E. P. Stabler, and C. E. Taylor. The role of population structure in language evolution. In *The 10th International Conference on Artificial Life and Robotics*, Beppu, Oita, Japan, 2005.
15. P. Niyogi. *The Computational Nature of Language Learning and Evolution*. MIT Press, Cambridge, Massachusetts, 2003. <http://people.cs.uchicago.edu/~niyogi/Book.html>.
16. M. A. Nowak, N. Komarova, and P. Niyogi. Computational and evolutionary aspects of language. *Nature*, 417:611–617, 2002.
17. M. A. Nowak, N. L. Komarova, and P. Niyogi. Evolution of universal grammar. *Science*, 291:114–118, 2001.
18. S. Pinker. *The Language Instinct*. Penguin, London, 1994.
19. S. Pinker and P. Bloom. Natural language and natural selection. *Behavioral and Brain Sciences*, 13:707–784, 1990.
20. K. Smith, H. Brighton, and S. Kirby. Complex systems in language evolution: the cultural emergence of compositional structure. *Advances in Complex Systems*, 6(4):537–558, 12 2003.
21. Staff. Endangered languages: Babel runs backwards. *Economist*, 374(8407), January 2005.
22. L. Steels. Self-organizing vocabularies. In C. Langton and T. Shimohara, editors, *Artificial Life V*, pages 179–184, Nara, Japan, 1996.
23. W. J. Sutherland. Parallel extinction risk and global distribution of languages and species. *Nature*, 423:276–279, 2003.