

Computer simulation of language competition by physicists

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Abstract:

Computer simulation of languages is an old subject, but since the paper of Abrams and Strogatz (2003) several physics groups independently took up this field. We shortly review their work and bring more details on our own simulations.

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1 Introduction

Human languages distinguish us from other animals, but also birds or ants have systems of communication. Also, humans have invented alphabets and other formalized forms of writings. In principle the methods to be described here could be applied also to these other forms of communication, but mostly we are interested here in the presently about 10^4 different human languages on this planet[1]. We leave it to linguists to distinguish languages from dialects or language families; when we mention "language" readers may read dialect or family instead.

Everyday language contains thousands of words for different aspects of life, and with the special words of science, medicine, . . . we get much more. For the same concept of everyday life, each different language in general has a different word, and thus the number of possible languages is enormous and difficult to simulate. Things become easier if we look only at grammar; do we order (subject, object, verb) or (subject, verb, object) or . . .? Briscoe [2] mentioned about 30 independent binary grammatical choices, which leads to a manageable $2^{30} \simeq 10^9$ possible languages, which can be symbolized by a string of $\ell = 30$ bits. Thus many of the simulations described here use bit-strings with $\ell = 8, 16 \dots 64$.

The present situation is not in equilibrium; about every ten days a human language dies out, and in Brazil already more than half of the indigenous languages have vanished as a result of the European conquest. On the other hand, Latin has split in the last two millennia into several languages, from

Portuguese to Romanian, and many experts believe that Latin and the other Indo-European languages spoken 600 years ago from Iceland to Bengal (and now also in the Americas, Australia, Africa) have originated from the people who invented agriculture in the Konya plane of Turkey, 10^4 years ago. Thus similar to biology, also languages can become extinct or speciate into several daughter languages.

In contrast to biology, humans do not eat humans of other languages as regular food, and thus one does not have a complex ecosystem of predators eating prey as in biology. Instead, languages are meant for communication, and thus there is a tendency of only one language dominating in one region, like German in Germany etc. Will globalisation lead to all of us speaking one language in the distant future? For physics research, that situation has already arrived many years ago. If we follow the Bible, then at the beginning Adam and Eve spoke one language only, and only with the destruction of the Tower of Babel different languages originated.

Thus in the history mankind we may have had first a rise, and later a decay, in the number of different languages spoken. In Papua New Guinea [3] there are now 10^3 languages, each spoken by about 10^3 people; can this situation survive if television and mobile phones become more widespread there?

While we cannot answer these questions, we can at least simulate such "survival of the fittest" among languages, in a way similar but not identical to biology. We will not emphasize here the longer history of computer simulations of how children learn a language [4], see also [5], or how mankind developed the very first language out of ape sounds[6]. Instead we talk about the competition between different languages for adults. And we will emphasize the "agent-based" models simulating individuals, analogous to Monte Carlo and Molecular Dynamics for spins and molecules

The second section deals with differential equations (a method we regard as outdated), followed by agent-based simulations with few languages in section 3 and with many languages in section 4. Further results from the two many-language models are given in the appendix.

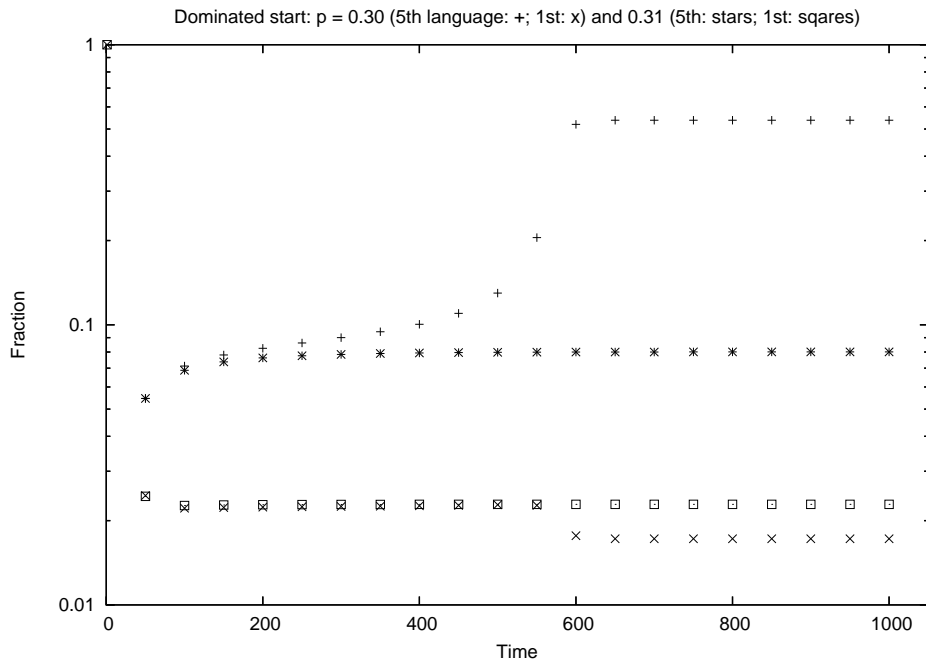


Figure 1: Development of one dominating language, or lack of such dominance, for the model of Nowak et al [4], with random matrix elements. We start from the dominance of another language. The different symbols correspond to two suitably selected languages and two slightly different mutation rates $p \simeq 0.3$. From [8].

2 Differential equations

Already Nettle [7] suggested a very simple differential equation to see how the number L of languages changes with time:

$$dL/dt = 70/t - L/20$$

Here the time unit is thousand years. (Actually L is the number of different language groups, and time is discrete). The second term on the RHS means a loss of five percent per millennium; the first term indicates the formation of new languages which became more difficult when the population became higher since then the higher demand for communication reduced the chances of new languages to develop. The aim was to explain why the recently

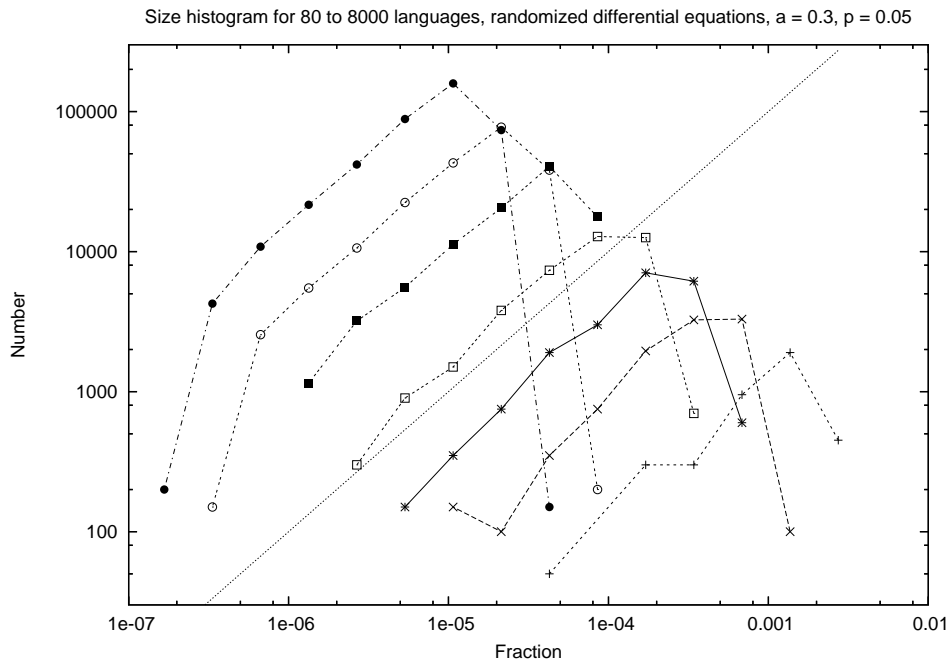


Figure 2: Size histogram, ignoring the dominating language, for the model of Nowak et al [4] with random matrix elements. The number of simulated languages varies from 80 on the right to its real value 8000 on the left; The straight line has slope 1 in this log-log plot. From [8].

populated Americas have a higher language diversity than Africa and Eurasia with their older human population. For long times, this differential equation means that L decays exponentially towards zero.

Nowak et al [4] use

$$dx_j/dt = \left(\sum_i f_i Q_{ij} x_i \right) - \phi x_j$$

for the fraction x_j of a population speaking language $j = 1, 2, 3 \dots L$. (Actually they apply this equation to the learning of languages or grammars by children; the interpretation for competition between adult languages is ours.) Here the fitness $f_i = \sum_j F_{ij} x_j$ of language i is determined by the degree F_{ij} to which a speaker of language i is understood by people speaking language j . The average fitness is $\phi = \sum_i f_i x_i$ and is subtracted to keep the sum

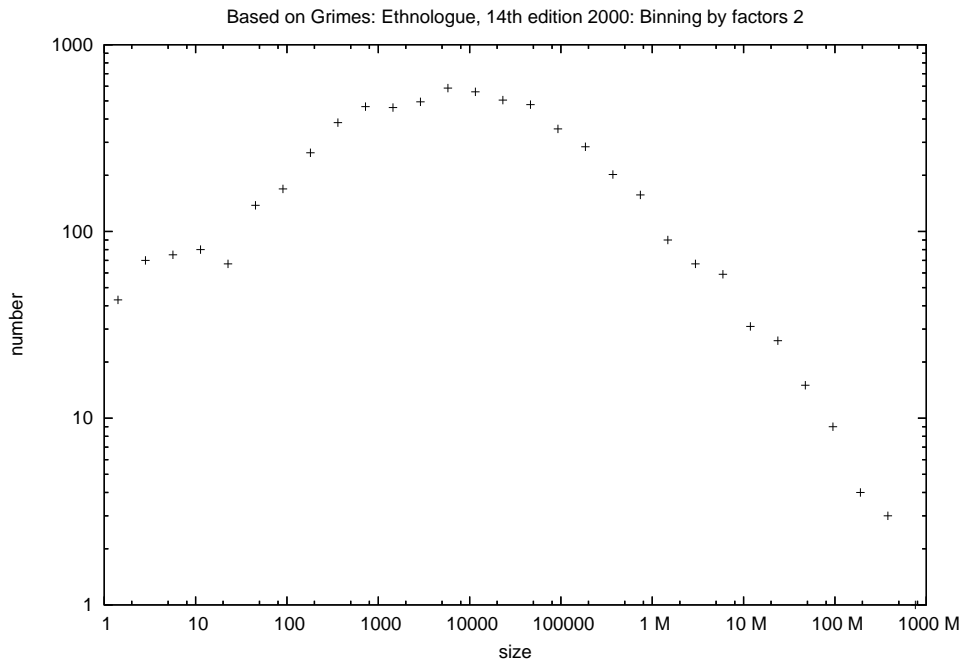


Figure 3: Size histogram for human languages, from [1]. We bin language sizes by factors of two, just as in Fig.2: Thus the leftmost point corresponds to size = 1, the second sums sizes 2 and 3, the third sums sizes 4 to 7, etc.

over all fractions x_j independent of time. The probability that children from i -speaking parents later speak language j is Q_{ij} .

For a large number L of languages, there are numerous free parameters in the matrices Q_{ij} and F_{ij} . With most of them the same one finds a sharp phase transition [4] as a function of mutation rates Q_{ij} . If one starts with only one language, then at low mutation rates most of the people still speak this language and only a minority has switched to other languages. For increasing mutation rates, suddenly the system jumps from this dominance of one language to a fragmentation state where all languages are spoken equally often. If, in turn, we start from such a fragmented state then it stays fragmented at high mutation rates. With decreasing mutation rates it suddenly jumps to the dominance of one language (numerically, one then has to give this one language a very slight advantage). The two jumps do not occur at the same mutation rate but show hysteresis: Starting with dominance and

increasing the mutation rate allows dominance for higher mutation rates then when we start with fragmentation and decrease the mutation rate.

Qualitatively these properties remain if the many matrix elements are selected randomly instead of being the same [8] except that the hysteresis has become very small. Fig.1 shows the case where we start with dominance and looks similar to the case where we start with fragmentation. The time development for two of the 30 simulated languages is shown for two slightly different mutation rates, and we see how for the lower mutation rate but not for the higher rate one of the two languages starts to dominate, at the expense of the other.

These 30 languages are more mathematical exercises, but Fig.2 applies these methods to up to $L = 8000$ languages, using two 8000×8000 random matrices F and Q . We show the size distribution of languages, where the size is the fraction of people speaking this language. On this log-log plot we see roughly parabolas, shifting to the left with increasing number L of languages. These parabolas correspond to log-normal distributions, roughly as observed empirically in Fig.3.

(Similar to Komarova [4] we assume the average F to be 0.3 except for $F_{ii} = 1$ and the average Q to be $p/(L - 1)$ except $Q_{ii} = 1 - p$; the actual values are selected randomly between zero and twice their average.)

There are two problems in this comparison of Figures 2 and 3: In these simulations, the (logarithmic) range over which the language sizes vary is quite small and does not change with increasing L . And the real distribution is unsymmetric, having higher values for small languages [9] than the log-normal distribution; this enhancement is missing in the simulation of Fig.2. Finally, we cheated: Fig.2 was taken in the dominance regime and the dominating language was ignored in the statistics.

Much more attractive for physicists was the one-page paper of Abrams and Strogatz [10] which was within weeks followed by a poster of Patriarca and Leppanen [11]. This pair of papers then triggered apparently independent research in Spain [12], Greece [13], Germany [14], Argentina [15] and at two different places in Brazil [16, 17], all on language competition.

The Abrams-Strogatz differential equation for the competition of a language Y with higher social status $1 - s$ against another language X with lower social status s is

$$dx/dt = (1 - x)x^a s - x(1 - x)^a(1 - s)$$

where $a \simeq 1.3$ and $0 < s \leq 1/2$. Here x is the fraction in the population

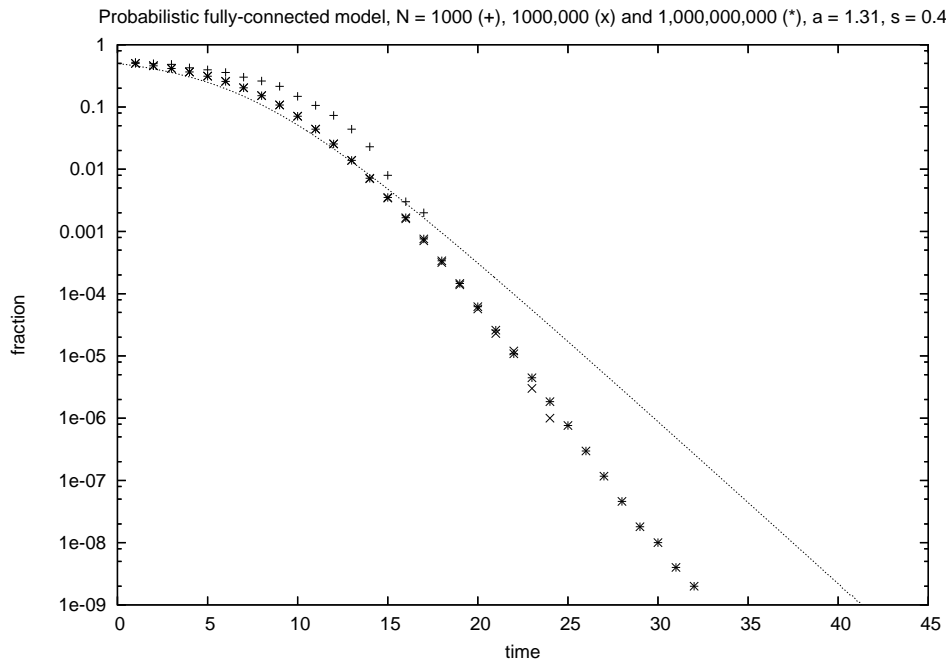


Figure 4: Exponential decay for the language with lower status, consisting initially of half the population. The symbols give Monte Carlo simulations where each individual is influenced by the whole population N , while the like is the result of the differential equation of Abrams and Strogatz. $a = 1.31$, $s = 0.4$, $N = 10^3, 10^6, 10^9$.

speaking language X with lower social status s while the fraction $1 - x$ speaks language Y. Figure 4 with no status difference, $s = 1/2$, shows as intended that language to win which is initially in the majority; the other language dies out. For $x(t = 0) < 1/2$ the language Y wins and for $x(t = 0) > 1/2$ the language X wins. This is highly plausible: If we would immigrate to Brazil where in most places most of the people speak Portuguese, then also we would have to learn Portuguese, not because of status but because of numbers. If the initial minority language has the higher status, as happened 500 years ago when Portuguese ships landed in Brazil, then it may win at the end, thanks to guns, writing, and other status aspects, as is the case in Brazil. Figures for unequal status are published in [8].

The Finnish group [11] generalized this simple differential equation to

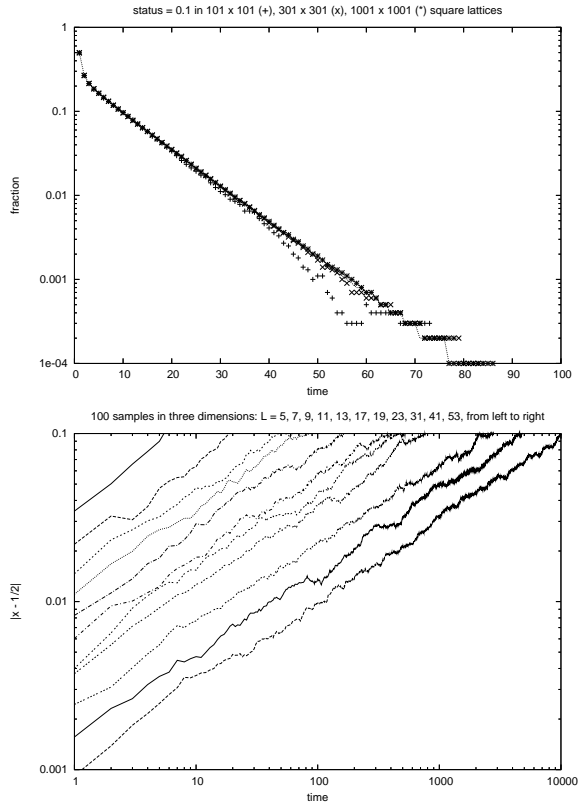


Figure 5: Part a: As for Fig.4 but on a 101×101 , 301×301 , 1001×1001 square lattices with $a = 1.31$, $s = 0.1$. Part b: Three-dimensional lattices, at the symmetry point $x(t = 0) = s = 1/2$, $a = 1$. After a long time, the concentration moves towards zero or one.

a square lattice, where it became a partial differential equation including a Laplacian $\nabla^2 x(\mathbf{r})$. Then having in one part of the lattice a higher status for X compared to Y, and in the other part the opposite status relation, they showed that the languages X and Y can coexist besides each other, with a narrow interface in between. This reminds us of Canal Street in New Orleans which in earlier times separated the French quarter from the English speaking part. We will later return to such geographical coexistence also without status differences, arising merely from an initial separation into an X part and a Y part [14, 18].

If we set $a = 1$ the simple logistic Verhulst equation results [19],

$$dx/dt = (2s - 1)(1 - x)x$$

which was applied to languages [20] already before Abrams and Strogatz. This case was generalized to two Verhulst equations [15] describing the two populations of people speaking languages X and Y. Now as in Lotka-Volterra equations for predators eating prey, both populations can coexist with each other in some parameter range, which in the usual Abrams-Strogatz model is possible only for $x(t = 0) = s = 1/2$.

The competition of two languages is changed if some people become bilingual, that means they learn to speak the other language which was not their mother tongue [12]. This was applied to Gallego versus Castellano in Spain; of course, some may regard Castellano spoken in Madrid as the proper Spanish, and Gallego as its dialect spoken in Galicia. As citizens of the Prussian occupied Westbank of the Rhine River, we know that publicly going into such details before liberation may be dangerous. A language is a dialect with an army and a navy behind it.

Of course, all these differential equations are dangerous approximations, just as mean field theory for critical phenomena in statistical physics is dangerous. We know since 80 years that the one-dimensional Ising model has a positive Curie temperature T_c in the mean-field approximation, while in reality $T_c = 0$. Thus do the Abrams-Strogatz results remain correct if we deal with individuals which randomly change from one language to the other, with probabilities corresponding to the original differential equation?

In general, the answer is yes [21]: As long as not both s and the initial concentration $x(t = 0)$ are $1/2$, one language still dies out, and it does so exponentially. This holds for the case of everybody influencing everybody, Fig.4, as well as for a square lattice where everybody is influenced only by its four lattice neighbours, Fig.5. The line in Fig.4 is the solution of the differential equation and agrees qualitatively with the Monte Carlo results represented by the separate symbols for various total constant populations N . Only for a completely symmetric start, $s = x(t = 0) = 1/2$, when the differential equation gives an equilibrium (stable for $a < 1$ and unstable for $a > 1$), the microscopic Monte Carlo simulation gives one or the other language dying out, while the differential equation then predicts both to always comprise half of the population each. More details are given in [21].

Finally we mention the model of [3] which also does not deal with individuals but avoids differential equations.

3 Microscopic models

Here we deal with the more modern methods of language simulations, based on individuals instead of on overall concentrations. Such methods are applied in physics since half a century and are called agent-based in some fields outside physics. First we review two models for only two (or a few) languages, then in much greater detail the two models for many languages.

3.1 Few languages

The model of Kosmidis et al [13] for mixing two languages X and Y uses bit-strings of length 20; each bit can be 0 (representing a word or grammatical aspect which is not learned) or 1 (an element which this individual has learned). If someone speaks language X perfectly and language Y not at all, the bit-string for this person is 11111111110000000000 while 00000000001111111111 corresponds to a perfect Y-speaker. People can become perfectly bilingual, having all 20 bits at 1, but this is rare. This model is particularly simple to explain the generation of a mixture language Z out of the two original languages X and Y. One merely has to take about ten bits equal to one and distribute them randomly among the 20 bit positions. This may then correspond to the creation of Shakespeare's English out of the Germanic language spoken by the Anglo-Saxons and the French spoken by the Normannic conquerors of the year 1066.

Biological ageing was included in the model of Schwammle [16], using the well-established Penna model [22, 19, 8] of mutation accumulation. Two languages X and Y are modelled. Individuals learn to speak from father and mother (and thus may become bilingual) and move on a square lattice in search of emptier regions. Bit-strings are used also here, but only for the ageing part to store genetic diseases; the two languages have no internal structure here. A bilingual person surrounded by neighbours speaking mostly language X forgets with some probability the language Y, and vice versa. The model allows for the coexistence of the two languages, each in a different region of the lattice, as in [11] but without giving one language a higher status than the other.

In his later model [16], that author allows for up to 16 languages. Again the structure of languages is ignored. Only young people can learn languages from others, and sometimes they learn a new language by themselves. As a function of the "mutation" probability to learn independently a new lan-

guage, the model gives dominance of one language for small mutation rates, and fragmentation of the population into many languages for high mutation rates, with a sharp phase transition separating these two possibilities, e.g. at a mutation rate near $1/4$. This phase transition is similar to that found by [4] as reviewed above.

3.2 Many languages

To explain the existence of the 10^4 present human languages, we need different models [17, 14] which we review now.

3.2.1 Colonization

After the first human beings came to the American continent by crossing the Bering street several ten thousand years ago, presumably they first all spoke one language. Then they moved southward from Alaska and separated into different tribes which slowly evolved different languages. This first colonization was modeled by Viviane de Oliveira and collaborators [17] by what we call the Viviane model .

Languages have no internal structure but are labelled by integers 1,2,3 ... Human population starts at the centre site of a square lattice with language 1, and from then on humans move to empty neighbour sites of already populated areas. Each site can carry a population of up to about 10^2 people, selected randomly. The size or fitness of a language is the number of people speaking it. On every new site, the population selects as its own language that of a populated neighbour site, with a probability proportional to the fitness of the neighbouring language. In addition, the language can mutate into a new language with a probability α/size . To prevent this mutation rate to become too small, this denominator is replaced in their later simulations by some maximum $\simeq 10^3$, if the actual language size is larger than this cut-off value. The simulation stops when all lattice sites have been populated. A complete Fortran program is listed in [14](d).

For a mutation coefficient $\alpha = 0.256$ the simulated language sizes in the Viviane model can reach the thousand millions of Chinese [14](d), but the shape differs from Fig.3 and corresponds more to two power laws than to one roughly log-normal parabola. In contrast to other models [4, 16, 14] there is no sharp phase transition between the dominance of one language and the fragmentation into numerous languages. [14](d).

This Brazilian group [23] earlier had claimed that the language size distribution follows two power laws, both indicating a decay of the number of languages with increasing language size. This fit, however, applies only to the large-size tail and not for small sizes where the power law would indicate an unrealistic divergence. Fig.3 in contrast shows there a very small number, with less than 10^2 of the 10^4 languages spoken by only one person [9]. The cumulative number of languages spoken by at least s people thus should be quite flat for small s instead of diverging with a power law for $s \rightarrow 0$, as fitted in [23]. A log-normal distribution gives a much better overall fit and is for large sizes not necessarily worse than the two power laws of [23].

Further results from the Viviane model are given in our appendix.

3.2.2 Bit-string model

Our own model uses bit-strings as in [13, 16] but for different purposes. Each different bit-string represents a different language though one may also define slightly different bit-strings as representing different dialects of the same language. Lengths ℓ of 8 to 64 bits have been simulated, and the results for 16 bits differed little from those of longer strings, while 8 bits behaved differently.

We used three different probabilities p , q , r though most properties can be also obtained from the special cases $q = 0$, $r = 1$. When a new individual is born its language is mutated with probability p compared to that of the mother. One of the ℓ bits is selected randomly and reverted, which means a zero bit becomes one and a one bit becomes zero. This p is the mutation probability per bit-string; the probability per bit is therefore p/ℓ .

When q is not zero, then the above mutation process is modified. With probability $1 - q$ it happens randomly as above, and with probability q the new value of the bit is obtained not by reverting it but by taking over the corresponding bit value of a randomly selected individual from the whole population. This transfer probability q thus describes the effect that one language can learn concepts from other languages. Many words of higher civilization in the German language came from French, while French beers sometimes have German names.

Thus far the simulations are similar to biology with vertical (p) and horizontal (q) gene transfer. Specific human thinking enters into the third probability $(1 - x^2)r$ (also $(1 - x)^2$ instead of $1 - x^2$ was used) to give up the own language and to switch to the language of another randomly selected

person. Here x is the fraction of people speaking the old language, and thus this probability to abandon the old language is particularly high for small languages. The new language is selected by a random process, but since it is that of a randomly selected person and not a randomly selected language, most likely the new language is one of the major languages in the population. In this way we simulate the same trend towards dominating language which was already modelled by Abrams and Strogatz, as described above in the example of our emigration to Brazil. This flight from small to large languages, through the parameter r , distinguishes the language competition from biological competition between species in an ecosystem, and takes into account human consideration of the utility of the language.

The population size is kept from going to infinity by a Verhulst death probability proportional to the actual population size. Thus if we start with one person, the population will grow until it reaches the carrying capacity given by the reciprocal proportionality factor. More practical is an initial population which is already about equal to the final equilibrium population. With the latter choice one can start with either everybody talking the same language, or everybody talking a randomly selected language. A complete Fortran program for the simple case $q = 0$, $r = 1$ is listed in [8].

Compared to the Viviane model explained above, our model is more complicated since it has three probabilities p, q, r instead of only one coefficient α . However, one can set $q = 0$, $r = 1$ in our model and then has the same number of free parameters. The Viviane model simulates the flight from small to large languages by a mutation probability inversely proportional to the size of the languages while we separate the mutations (independent of language size) from the flight probability $(1 - x^2)r$. Moreover, we simulate a continuous competition of languages while the Viviane model simulates the unique historical event of a human population spreading over a continent where no humans lived before.

The results of our model are reported in [8, 14]. Most important is the sharp phase transition, for increasing mutation rate p at fixed q and r , between dominance at small and fragmentation at large p . For dominance, at least three quarters of the population speak one language, and most of the others speak a variant differing by only one bit from that language. For fragmentation, on the other hand, the population spreads over all possible languages. If we start with dominance, the phase transition to fragmentation was already described in the biblical story of the Tower of Babel. If we start with fragmentation, we get dominance for long enough times and

small enough mutation rates, if we use $(1-x)^2$ instead of $1-x^2$ for the flight probability. Fig.6 shows the phase diagram for $\ell = 8$ and 16 if we start from fragmentation. In Fig.7, particularly long simulations for $\ell = 64$ and one million people show how an initial dominance decays into fragmentation.

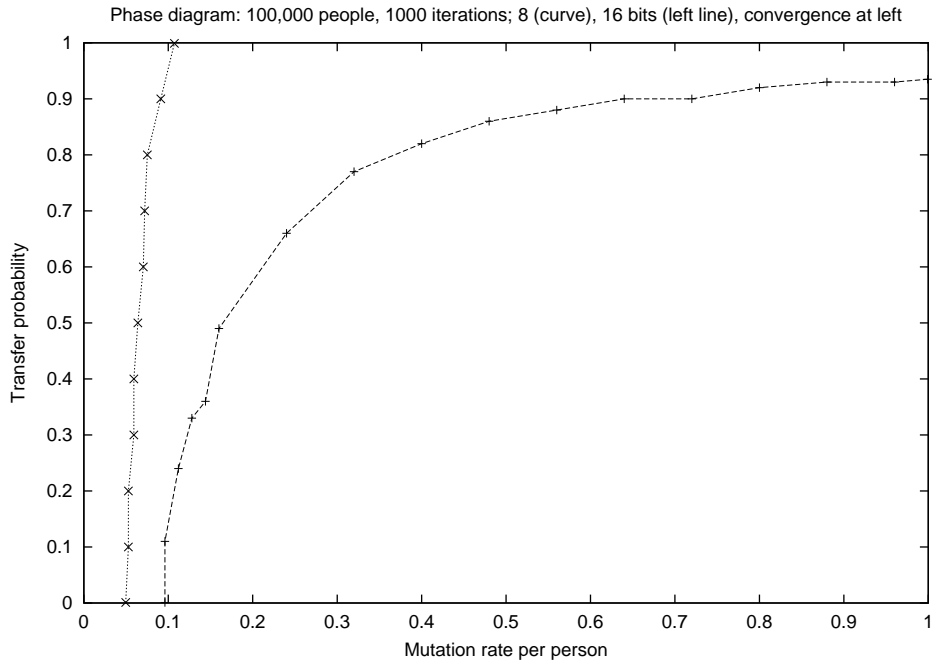


Figure 6: Phase diagram for dominance in the upper left part and fragmentation in the lower right part. The higher the mutation rate p and the lower the transfer rate q is the more fragmented is the population into many different languages. We start with an equilibrium distribution of 100,000 languages, each speaking a randomly selected language. The curve corresponds to $\ell = 8$ bits, the nearly straight line to $\ell = 16$; $r = 1$ in both cases. From [14].

Tesileanu and Meyer-Ortmanns [18] introduced into this model the Hamming distance as a measure of dissimilarity between languages. This Hamming distance counts the number of different bits in a position-by-position comparison of two bit-strings. Thus the $\ell = 4$ strings 0101 and 1010 have a Hamming distance of four. This distance can be normalized to lie between zero and one, through division by ℓ . Fig.8 shows this normalized Hamming distance for both the two largest languages and the average over all possible

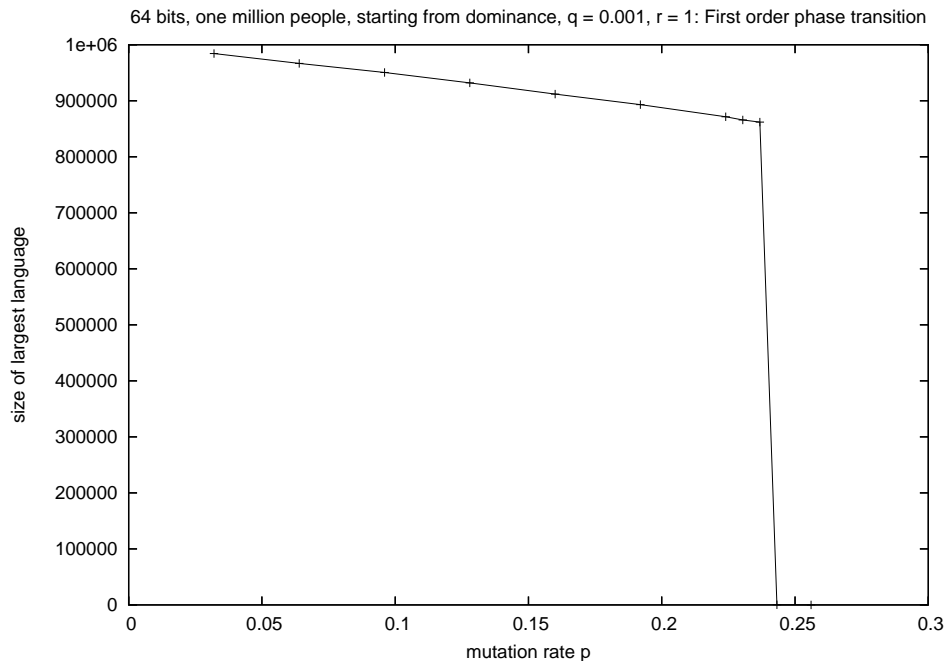


Figure 7: Phase transition from dominance to fragmentation for one million people and 64 bits, i.e. much more possible languages than people. We show the size of the most-often spoken language after 300 iterations; it jumps from 10^6 to 10^2 .

pairs. Not much difference is seen except that the one for the single pair fluctuates much stronger than the average over all pairs. And for dominance the difference is very small while for fragmentation is it nearly 1/2. Thus for fragmented populations, the various languages are nearly uncorrelated, and half their bits agree accidentally while the other half disagrees. For dominance, the minor languages are mostly one-bit mutants of the dominating language. Fig.8, like Fig.7 before, shows a clear first-order phase transition, that means a sharp jump. Thus far we were not able to modify this model such that it gives a second-order transition where the fraction of people speaking the largest language goes continuously to zero at a sharp critical point. Such a modification might give a more realistic distribution of language sizes.

The time dependence of the size of the largest cluster, if we start with fragmentation, suggests a complicated nucleation process. Originally all lan-

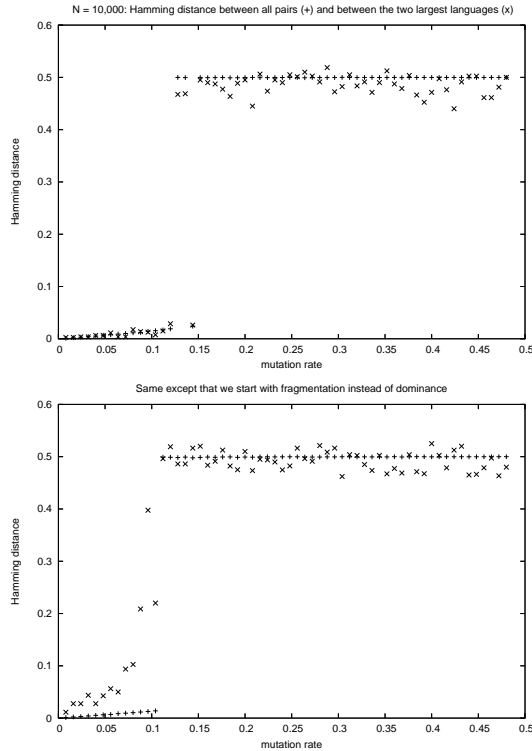


Figure 8: Difference between languages, as measured by the normalized Hamming distance = fraction of different bits. We show both the average distance between all pairs and that between the two largest languages, for 10,000 people and $q = 0$. The top part starts with dominance, the bottom part with fragmentation. From F.W.S. Lima, priv. comm.

languages are about equal in size, and then due to random fluctuations one language happens to be somewhat more equal than the others. This language then wins over, first slowly, then rapidly. The time needed for one language to win increases about logarithmically when the population increases from 10^3 to 10^8 . Thus for an infinite population, as simulated by deterministic differential equations of the Nowak et al style [4], the emergence of dominance out of a fragmented population might never happen in our model.

First-order phase transitions like those in Figs. 7 and 8 are usually accompanied by hysteresis, like when undercooled liquid water is to crystallize into ice. Thus we should get different positions of the effective transition (for

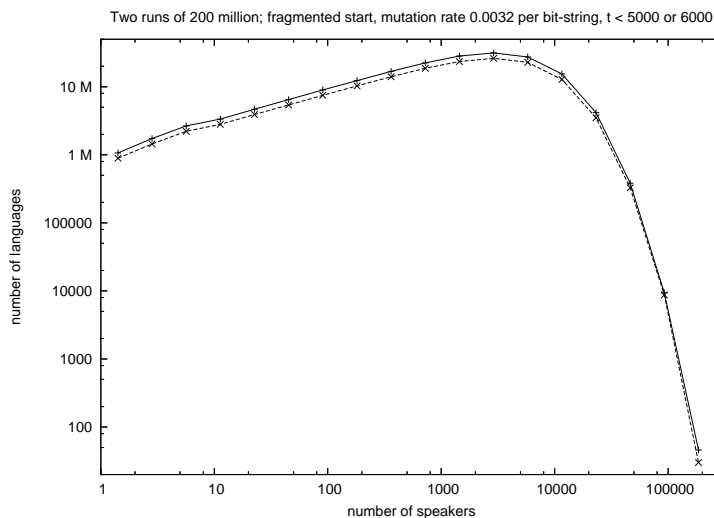


Figure 9: Size distribution far from equilibrium during the phase transition from fragmentation to dominance, $\ell = 16$, $q = 0$. Additional smoothening by random multiplications was applied [24].

fixed population size and fixed observation time) depending on whether we start from dominance or fragmentation. This is shown in [14](b), using in both cases $(1 - x)^2$ for the flight probability.

The language size distribution shows the desired shape of a slightly asymmetric parabola on the log-log plot (log-normal distribution) but the actual language sizes are far too small compared with reality. This is not due to lack of computer power but comes from the sharp first-order transition, Figs.7 and 8. Either one language dominates as if 80 percent of the world speaks Chinese. Or all 2^ℓ languages are equivalent apart from fluctuations and thus each is spoken only by a small population. If the first-order transition would be changed into a second-order one, the results for mutation rates slightly below the critical point might be better.

An alternative was suggested by linguist Wichmann [24]: The present language distribution is not in equilibrium. If we assume that parts of the world are on one side and parts on the other side of the phase transition from dominance to fragmentation (or from fragmentation to dominance), then the above equilibrium results are not good. Instead, we show in Fig. 9 two runs for a non-equilibrium situation of about 5000 iterations at very low mutation

rate, starting from fragmentation. The results are averaged over the second half of the simulation with the time adjusted such that the phase transition of fig.11 happened during that second half. Now the language sizes vary over five orders of magnitude, much better than before. (If we start from dominance the size distribution is similar but more symmetric [24].)

4 Conclusion

The last few years have seen the development of a variety of different approaches to simulate the competition between existing languages of adult humans. Each model has its advantages and disadvantages.

If we follow the tradition of physics, that theories should explain precise experimental data, then the size histogram of the 10^4 human languages, Fig.3, seems to be best candidate. Empirically it is based on Grimes [1] and was analyzed e.g. by [9, 1, 3, 23]. In order to simulate this language size distribution, we need models for 10^4 different languages, and only two of them have been published thus far, the Viviane model and our model [14, 17].

Future work with these models could look at the similarities and differences between the languages (bit-strings), as started in [18] and Fig.8, or the geography of languages and their dialects [25], as started in [17].

We thank our coauthors [24, 21] for collaboration.

5 Appendix

This appendix brings some more results for many languages, first on the Viviane model [17] and then on our model [14].

5.1 Viviane colonization model

For the model of [17], one can look at the history how languages split from a mother languages, and later produced more daughter languages. In contrast to linguistic field research, which looks only at the last few thousand years, computer simulations can store and analyze the whole history since the beginning. [14](d) shows for a small 64×64 lattice, how one language split into daughters, etc, very similar to biological speciation trees. For clarity we omitted numerous languages which had no "children". For larger lattices we

found that even for many thousand languages a few steps suffice on average to reach from any of the languages in this tree the oldest ancestor language on the top of the tree. Other tree simulations were published in [26].

Often a conquering population imposes its language to the native population. Perhaps in Europe, before the arrival of Indo-European farmers, the Cro Magnon people spoke a language family of which the Basque language is the only present survivor. Better documented, though not necessarily more true, is the story of the single Gallic village in today's France which resisted the Roman conquest two millennia ago, thanks to the efforts of Asterix and Obelix (helped by doping). In the Viviane model, where people may adopt the language of their neighbours, such a single resistance center can influence many other sites during the later spread of languages. indeed a rather large fraction of the total population is influenced by Asterix, particularly for large mutation rates [14](d). In physics, such simulation of the influence of a single "error" are called "damage spreading".

5.2 Our bit-string model

While the Viviane model always happens on a lattice, for our model the lattice is optional. If we want to study the geographical coexistence of two languages in adjacent regions, then of course a lattice is needed [14](b). Now on every lattice site live many people. Without any difference in status, as opposed to [11], on one side one language dominates and on the other side the other language, if initially each region was occupied only by speakers of its own language. Also in the transition region the other $2^\ell - 2$ languages play no major role. The situation in this figure may correspond to New Orleans a long time ago, where Canal Street separated the French quarter from the newer English settlement. These methods could be applied to dialectometry, as documented for France by Goebel [25].

Bit-strings allow only $Q = 2$ choices per position, but the lattice model was also generalized to $Q = 3$ and 5 choices. Surprisingly, the phase transition curve [14](d) between dominance for low and fragmentation for high mutation rates was independent of this number Q of choices. Only when ℓ was changed, the different transition curves were obtained.

If we want to apply the lattice model to geography we want compact geographical language regions to emerge from a fragmented start. Then not only the transfer of language elements but also the flight to another language needs to be restricted to lattice neighbours, i.e. people learn new

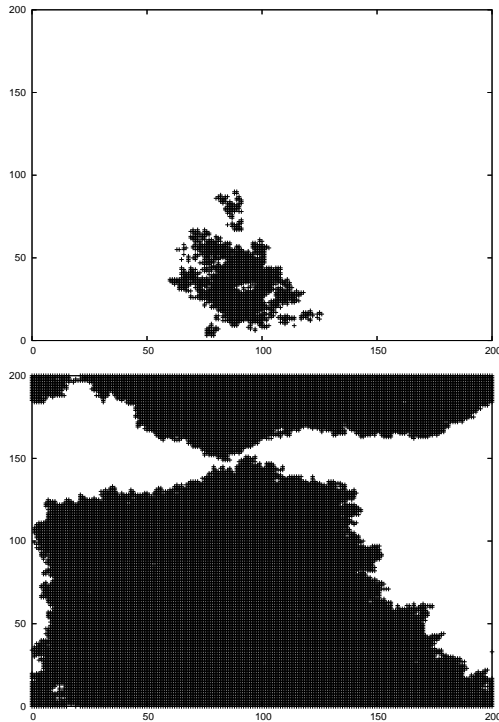


Figure 10: Domain formation if flight and transfer happen only to/from a language learned from a lattice neighbour. We mark the sites where the largest language is spoken, after 240 and 450 iterations. For $t \geq 514$ nearly everybody speaks this language. ($L = 200$, $p = 0.016$, $q = 0.9$, $r = 1$, $\ell = 16$, $Q = 2$, periodic boundary conditions).

elements or a new language only from one of the four nearest neighbours, randomly selected. Fig.10 shows how one language, accidentally the largest at intermediate times, grows until it covers nearly the whole lattice.

One may look, without lattice, on the history of people speaking one randomly selected language in an initially fragmented population. Because of mutations, after a long enough time everybody has moved at least once to another language. But since the number $L = 2^\ell$ of possible languages is finite, some people move back to their original language, like emigrants whose offspring later return to their old country. Thus after 50 iterations to give an equilibrium, we mark all those speaking language zero. Their offspring carries that mark also, even if they mutate their language, and we count at

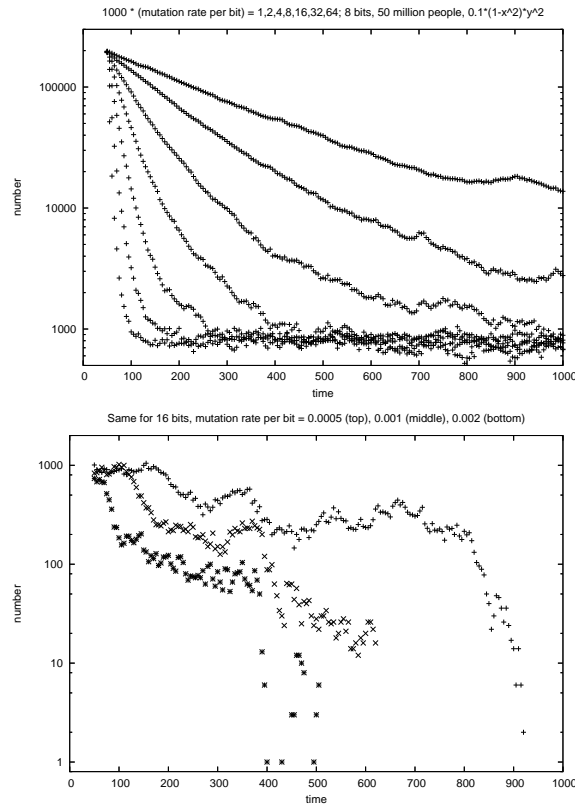


Figure 11: Decay of population originally speaking one particular language for $\ell = 8$ (top) and 16 (bottom).

each time step the number of marked people speaking language zero.

Then we see a rapid decrease of that number; to slow down the decay we modified the flight probability to $0.1(1 - x^2)y^2$ where y is the fraction for the language which the individual from fraction x considers to switch to. Then a slower decay as in Fig.11 results, faster for higher mutation rates. For $\ell = 8$ bits we see nicely the random background of less than thousand people (from 50 million) who returned to the language zero of their ancestors; for $\ell = 16$ both the initial and the final number of zero speakers are much smaller since the 50 million can now distribute among 65536 instead of only 256 possible languages.

Human languages can be grouped into families, like the Indo-European family of 10^2 different languages. To simulate language families we need

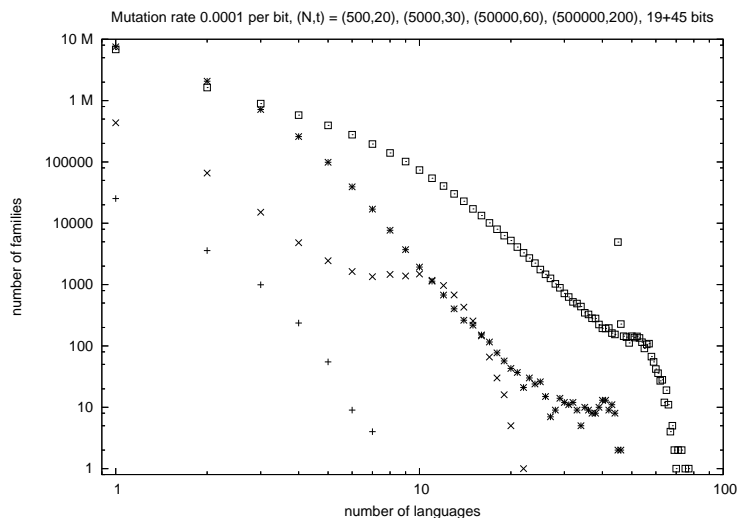


Figure 12: Distribution of the number of languages in a language family, from sums over 100 or 10 independent simulations at various population sizes, $p = 0.0064$. The observation time increases slightly with increasing population size. From ongoing work with S. Wichmann and F.W.S. Lima.

a criterion which bit-strings belong into one family. Thus we worked with $\ell = 64$ bits and assumed, following Wichmann, that the leading 19 bits determine the family and the remaining 45 bits the different languages within one family. The numbers 2^{19} and 2^{45} of possible families and languages are so large that our computer simulations with less than a million people do not notice their finite size. Indeed, the results in Fig.12 for 500, 5000, 50,000 and 500,000 people are roughly independent of population size and show a mostly monotonically decaying probability distribution function for the number of languages within one family. Empirical observations were published e.g. by Wichmann [1].

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