

Monte Carlo simulation of the rise and the fall of languages

Christian Schulze and Dietrich Stauffer

Institute for Theoretical Physics, Cologne University D-50923 Köln, Euroland

e-mail: stauffer@thp.uni-koeln.de

Abstract: Similar to biological evolution and speciation we define a language through a string of 8 or 16 bits. The parent gives its language to its children, apart from a random mutation from zero to one or from one to zero; initially all bits are zero. The Verhulst deaths are taken as proportional to the total number of people, while in addition languages spoken by many people are preferred over small languages. For a fixed population size, a sharp phase transition is observed: For low mutation rates, one language contains nearly all people; for high mutation rates, no language dominates and the size distribution of languages is roughly log-normal as for present human languages. A simple scaling law is valid.

Keywords: Sociophysics, phase transition, bit-strings, scaling

1 Introduction

Human languages are grouped into families, like the Indo-European languages, which may all have arisen from one common original language. For example, ancient Latin split into Portuguese, Spanish, French, Italian, Romanian and other languages during the last two millenia. On the other hand, many of the present languages are spoken only by a relatively small number of people and are in danger of extinction [1, 2]. In this way languages are similar to biological species. We thus try to simulate languages using methods similar to the modelling of speciation [3, 4].

A language for us can be a human language (including Fortran, ...), a sign language, a system of bird songs, a human alphabet, or any other system of communication. We simulate it by a string of 8, 16 or 30 bits and define languages as different if they differ in at least one bit. The position of the bit in the string plays no role, in contrast to the Penna ageing model from which program elements are taken [5].

2 Model

We start with one person, i.e. $N(t = 0) = 1$, speaking language zero (all bits are zero). Then at each iteration t all $N(t)$ living people are subject to a Verhulst death, i.e. they die with probability $N(t)/K$ where K in biology is often called the carrying capacity and incorporates the limitations of food and space. Each survivor produces one offspring at each iteration which uses the same bitstring apart from one random mutation (bit changed from 0 to 1 or from 1 to 0) which happens with a probability p per person (or $p/8$ per bit if the language has 8 bits). Usually, all bit-strings are assumed to be equally fit, in contrast to typical biological models [3, 4].

Also at each iteration, each individual can switch from its present language to another randomly selected one, with probability

$$(2N(t)/K)(1 - x^2)$$

where x is the fraction of all people speaking the present language of that individual. The first factor, which approaches unity for long times, ensures that at the beginning with a low population density there is not yet much competition between languages, while in the later stationary high population the less spoken languages are in danger of extinction. The exponent two takes into account that normally two people communicate with each other; thus the survival probability of a language is proportional to the square of the number of people speaking it.

(The final population is $K/2$ and not K since we determine the Verhulst probability $y = N(t-1)/K$ at the beginning of iteration t and leave it at that value for the whole iteration. The Verhulst deaths thus reduce the population by a factor $1 - y$, and if each of the survivors has b offspring, the population is multiplied by another factor $1 + b$. For a stationary population, these two factors have to cancel: $(1 - y)(1 + b) = 1$, giving $y = b/(1 + b) = 1/2$ for our choice $b = 1$.)

3 Results

For an eventual stationary population of ten million at $t = 1000$, as a function of increasing mutation rate p , a sharp transition was observed between a dominance regime at low and a smooth distribution at high mutation rates p , Fig.1:

i) For low p , one language, usually the one with all bits zero, contains nearly all individuals, and the mutant languages differing from the dominant one by one bit only contain most of the rest. This behaviour is hardly realistic except for alphabets.

ii) For high mutation rates p , on the other hand, no language contains a large fraction of the population, and the distribution of language sizes (measured as the number of people speaking it) is roughly log-normal with higher statistics for small languages. This result agrees well with reality [2].

In Fig.1, part a shows the drastic difference between dominance (+) and smooth distribution (\times , stars), part b the slow approach to a symmetric log-normal distribution with increasing mutation rate. (We bin the number of people speaking one language into powers of two, lumping together all languages spoken by 33 to 64 people, for example.)

In the dominance regime i) of low p , the number $L(t)$ of languages first increases from unity towards about 10^2 and then decreases again to about a dozen (not counting languages with less than 10 speakers). In the smooth regime ii) of high p the number L of languages first increases and then reaches a plateau, which may even equal the maximal number $M = 2^8$ or $M = 2^{16}$ for 8 or 16 bits, respectively.

Also for a fixed mutation rate as a function of the final population $K/2$ we see a change from the dominance regime at low populations to a smooth distribution at high populations, Fig.2. For very large populations a rather narrow distribution of language sizes develops, i.e. the whole population is distributed about equally among the surviving languages. Fig.3 shows for an intermediate population a power law on the small-size side of the histogram, and a parabola-like curve, meaning a log-normal distribution in this log-log plot, for large language sizes.

A simple scaling law, seen in Fig.4, predicts the behaviour of the number L of languages as a function of the maximum possible number M of languages and the final population $N_\infty \simeq K/2$:

$$L/M = f(M/N_\infty) \quad .$$

The scaling function $f(z)$ equals unity for small z and decays as $1/z$ for large z . This means that for a population much larger than the possible number of languages, each language possibility is realized, while in the opposite limit each small group of individuals speaks its own language. Therefore we expect this simple scaling law to be valid also for longer bit-strings than the 8 and

16 bits simulated here. (32 bits allow for 4096 Mega languages, requiring too much computer memory in our program; 30 bits still worked.)

We also modified the model to take into account the influence of a “superior” language on another, like the many words of French origin in the German language. With some probability q , at the moment of a mutation the new value of a bit is not the opposite of the old value (as done above) but is the value of the corresponding bit in the superior language. We define as superior language the bit-string having one everywhere except for a zero in the left-most position, i.e. 127 for 8 and 32767 for 16 bits. The larger q is (in the smooth regime of large $p = 0.48$ per individual), the higher is the fraction of samples ending with the superior language as the largest one. About half of the samples have the superior language as the numerically strongest one if $q \simeq 0.02$ for 8 and 0.2 for 16 bits. If for 16 bits we take 127 instead of 32767 as the superior language, the results do not change much. (These probabilities hold for 10 million people and are appreciably larger, 0.05 and 0.34, for one million.)

4 Discussion

Our model is more microscopic than the previous ones known to us [6, 7] in that individuals are born, give birth, and die, instead of being lumped together into one differential equation. It also is more realistic since we allow for numerous languages instead of only two. For the latter choice, we would have to reduce our bit-string to a single bit, with $M = 2$ and thus $M/N \ll 1$, corresponding to the left part of Fig.4. There we observe $L = M$, that means both languages survive. In [6] only one language survived since one was assumed to be superior compared to the other. We, on the other hand, regarded all languages as intrinsically equally fit, except for the last paragraph.

We thank P.M.C. de Oliveira for suggesting to simulate languages, and the Julich supercomputer center for JUMP time.

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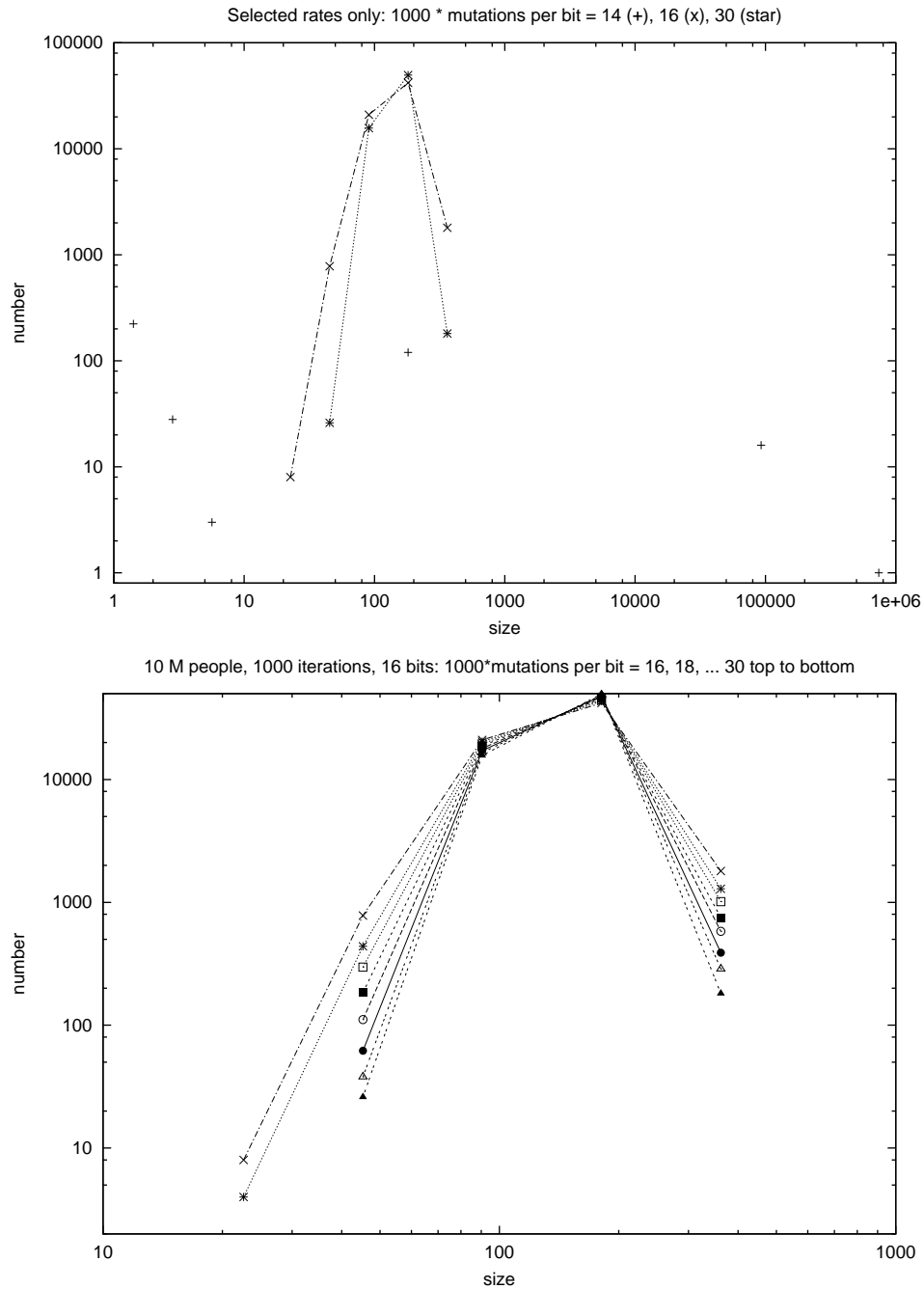


Figure 1: Histograms of language sizes for 16 bits, one sample only of $K/2 = 10$ million people, mutations per bit = 0.014 (+), 0.016 (x), 0.030 (stars) in part a and 0.016 to 0.030 in steps of 0.002 in part b.

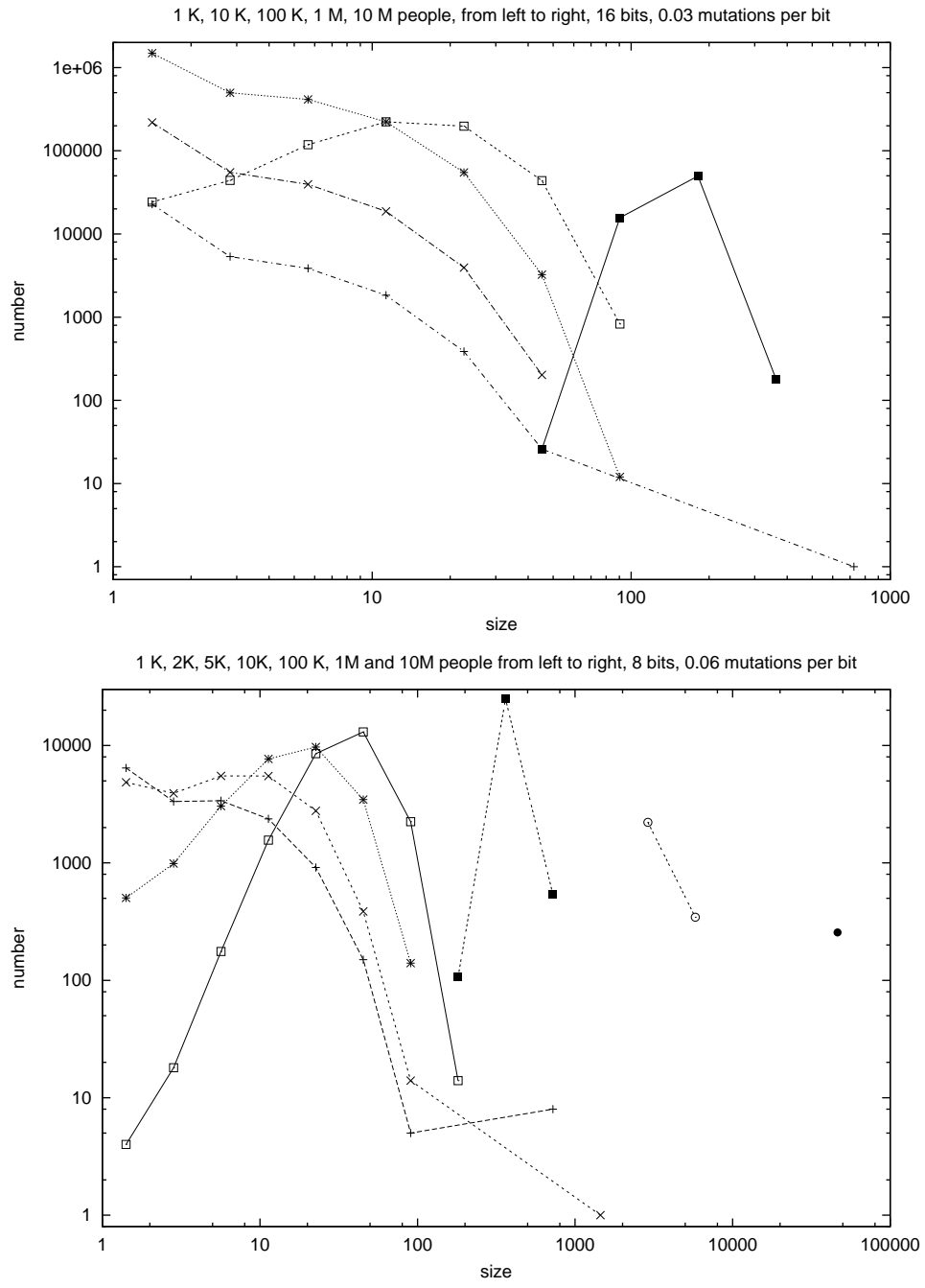


Figure 2: Histograms of language sizes for 16 bits (part a) and 8 bits (part b), with same mutation rate 0.48 per individual, for different population sizes, summed over up to 100 samples.

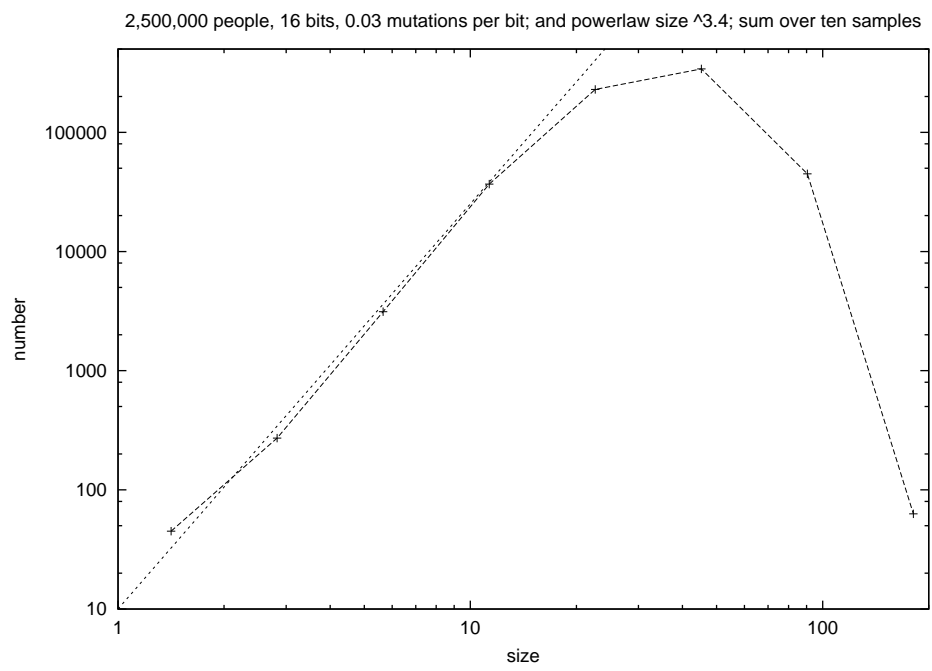


Figure 3: Roughly log-normal size distribution, with higher values for small sizes described by a power law.

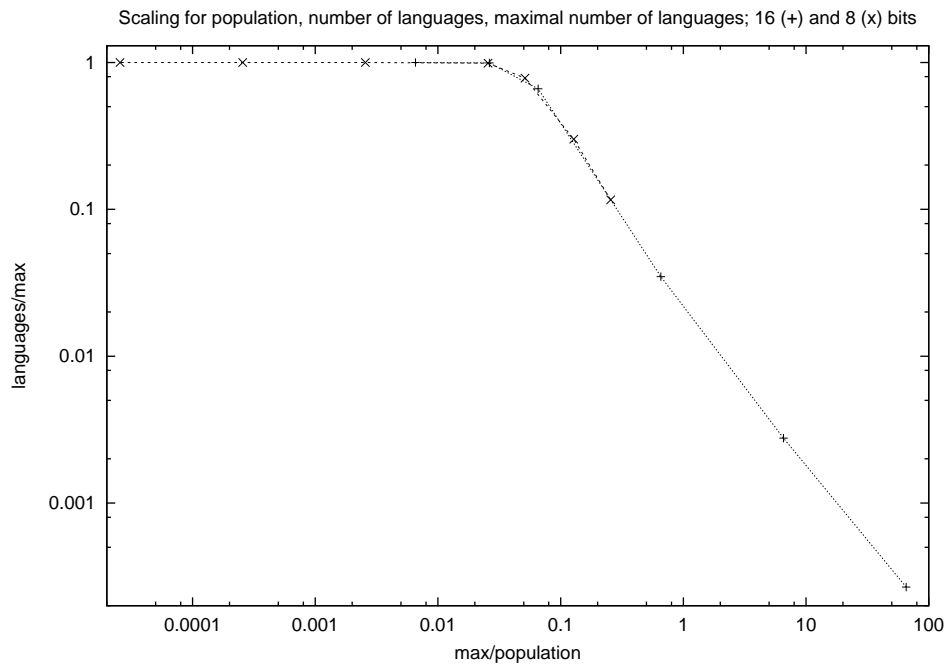


Figure 4: Scaling test: Symbols for 8 bits (\times) and 16 bits ($+$) follow the same scaling function f if plotted as L/M versus M/N_∞ . Runs with 30 bits and 10 or 100 million people fit in reasonably near the lower right corner (not shown).