Fixation Times for Language Evolution in Social Networks

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1. Introduction

Biological and cultural evolution both play a role in understanding evolution of language, but their interaction is complicated by their great difference in speed (Kirby & Hurford, 1997). This has led to debate on what could have evolved biologically (Baronchelli et al., 2013; Christiansen & Chater, 2008; De Boer & Thompson, 2018) with many of the arguments based on computational and mathematical analyses. However, no formal model to predict the speed of cultural evolution appears to exist. Here, we provide a mathematical tool to help understand how and when cultural evolution operates more quickly than biological evolution. The speed of biological evolution can be quantified mathematically by equations based on diffusion (Kimura, 1980), and these have been applied to language evolution (e. g. De Boer et al., 2020). For cultural evolution the must be modified, because it can occur in social networks with a heavy-tailed neighborhood distribution: some individuals are disproportionally influential (Amaral et al., 2000; Onnela et al., 2007). This means that the ordinary diffusion equations used in biology become fractional diffusion equations (Metzler & Klafter, 2000)

2. Method and Result

In analogy to biological evolution, a fixed-size population (that does not change biologically) is modeled where two cultural variants compete. Conditional fixation time ϑ (the number of interactions for a variant to take over the population, when it does so) then follows the following fractional differential equation:

$$\frac{c}{N^\alpha} \cdot \left[(p^\alpha(1-p) + p(1-p)^\alpha)_{RZ}D_x^\alpha\vartheta(p) \right.$$
$$\left. -\tan\frac{\pi\alpha}{2} \cdot (p^\alpha(1-p) - p(1-p)^\alpha)\,_FD_1^\alpha\vartheta(p) \right] = -p \tag{1}$$

with boundary conditions $\vartheta(0) = \vartheta(1) = 0$. The fixation time in absolute time (generations, not interactions) is then $\tau(p) = \vartheta(p)/(p \cdot N)$. N is the population size, p the proportion of the variant at the start, $1 < \alpha < 2$ is the parameter of the power law distribution that determines the heavy-tailedness of the neighborhood
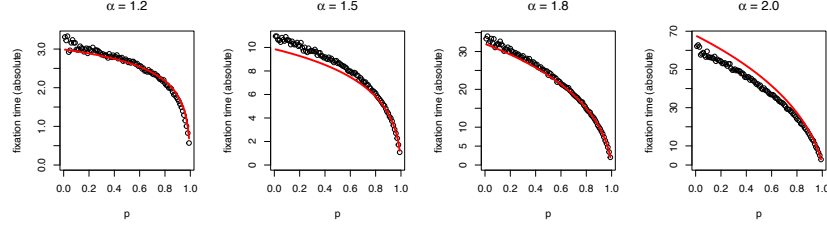
Figure 1. Fixation times (in arbitrary units of time) for culturally evolving populations with *N*=100 on social networks with differently distributed neighborhood sizes. Red lines represent solutions of the diffusion equation, and dots represent direct simulation. The leftmost graph corresponds to the most heavy-tailed distribution, while the rightmost graph corresponds to normally distributed neighborhood sizes (biological evolution). Vertical scales have different ranges to highlight the differences in curve shape.

distribution (the lower α, the more heavy-tailed) and c is a constant that depends on the precise shape of the neighborhood distribution. The operators $_{RZ}D_x^\alpha$ and $_FD_1^\alpha$ are *fractional derivatives* that generalize the second and first derivative, respectively (Herrmann, 2014, eqs 5.71 and 5.80). The first line of eq. 1 behaves similarly to ordinary diffusion (as in biological evolution). The second line introduces a drift away from the middle, which speeds up fixation.

Results of solving this equation and of directly simulating the evolutionary process are shown in Fig. 1. The correspondence between the model and the simulations is not perfect, but the diffusion model is a reasonable approximation. Importantly, fixation time is faster on the more heavy-tailed social networks, and because the curves are initially flatter, fixation time is less dependent on the initial prevalence of a culturally transmitted item in these cases.

3. Discussion and conclusion

Equation (1) has to the best of our knowledge not been described before, although similar systems have been studied (Carro et al., 2016). It allows us to estimate the time it takes for culture – formed by a population of agents interacting in a social network – to change; in the context of language evolution for instance for linguistic innovations to spread. The equation allows us to link properties of the social network (its size and the heavy-tailedness of its neighborhood distribution) and the initial frequency of a variant to the time it takes for this variant to spread. At the moment, the equation can only model drift, not selection (cultural variants do not differ in fitness), but the results from Fig. 1 suggest that even in this case cultural changes can spread rapidly, and their spread depends less strongly on their initial prevalence than in biological evolution. The form of the equation allows us to link it with the rich existing literature on fractional diffusion (Metzler & Klafter, 2000). Much remains to be done: extending the equation to differences in fitness, for instance, but also determining realistic values for α. Literature on *modern* social networks exists (Onnela et al., 2007), but it is an open question whether (pre-)historic cultural networks had the same structure.

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