Modeling Cultural Evolution on Social Networks using Fractional Diffusion

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1 Introduction

This work focuses on extending the diffusion approach to modelling cultural evolution on social networks. In this approach, developed for biological evolution by Kimura [6, 7], a finite population of usually fixed size is considered, in which two types of individuals exist, 'residents' and 'mutants'. The probabilistic spread of mutants is investigated. It approximates the discrete population with a continuum i.e., the mathematics allow for non-integer numbers of mutants. The resulting partial differential equations are easier to solve than the equations of the original discrete system [4, ch. 4] The equations are then solved for initial and final conditions with integer numbers of mutants and generally used to calculate the probability for a mutant to spread (fixation probability) and the time this takes (fixation time). The results match well with the exact discrete case even for small populations, and the match improves with increasing population size.

The diffusion equations developed for studying biological evolution assume that the number of mutants can only change with small jumps. This is related to the fact that any individual can only produce a limited number of offspring that survive until they can procreate themselves. More technically, the variance of the jump distribution is finite. This assumption is not necessarily warranted for cultural evolution. Because spread of cultural items (which will be referred to as memes from now on) happens on a social network, the number of 'offspring' of a given meme depends on the connectivity of the social network: an agent with many connections can propagate its memes more effectively than an agent with few connections. It turns out that the connectivity of human social networks, especially modern ones, follows a heavy-tailed distribution [1, 9]. This not only means that some agents have a lot more connections than most, but more importantly, that the distribution of the connectivity and therefore the potential jumps in the number of agents who know a certain meme, does not have finite variance*. This makes it necessary to use *fractional* diffusion equations for studying cultural evolution. Here, ongoing work on modifying the diffusion approach so that it can deal with jump distributions that do not have finite variance. We briefly present the necessary mathematical equations as well as numerical and simulation results to verify the diffusion models.

*Obviously, real social networks consisting of a finite number of agents have finite variance, as the maximum neighborhood size is the size of the network. However, in the diffusion approach a continuity limit is taken, in which infinite variance may occur. In practice this does not cause a large discrepancy between the diffusion model and the simulations, as illustrated by the results.

2 Methods

We aim to derive approximate diffusion equations and test these; therefore it is not only necessary to derive the appropriate equations, but also to solve these numerically and to compare them with a less efficient but conceptually simpler direct simulation. Analytically, it has been found that the probability $W_F(p)$ of ending up in a given final state F when starting with an initial proportion of mutant memes p is given by:

$$\mathscr{D}_p^{\alpha} W_F(p) = 0 \tag{1}$$

with boundary conditions $W_F(0) = 0$ and $W_F(1) = 1$ (i.e. the probability of ending up in the final state F is zero if there are no mutants, and if one starts with a population consisting exclusively of mutants, the final state F is already reached. The linear operator $\mathscr{D}_p^{\alpha}$ is discussed in more detail below. The parameter $1 < \alpha < 2$ determines how heavy the tails of the neighborhood distribution are. Interestingly, it turns out that the *exact shape* of the neighborhood distribution does not influence the diffusion equations, only its *asymptotic* (i.e. tail) behavior. In the context of complex networks, this may mean that the precise connectivity of the network is less important than the distribution of neighborhood sizes. The conditional fixation time $\theta_F(p)$ (i.e. the time to reach final state F, given that F is reached) is given by:

$$\mathscr{D}_p^{\alpha} \theta_F(p) = -W_F(p) \tag{2}$$

with boundary conditions $\theta_F(0) = 0$ and $\theta_F(1) = 0$. The linear operator $\mathscr{D}_p^{\alpha}$ turns out to be as follows:

$$\begin{aligned} &\mathscr{D}_p^{\alpha} f(p,t) \equiv \\ C \cdot N^{-\alpha} &\left[p^{\alpha}(1-p) \int_{-\infty}^{0} \frac{f(p+\rho,t) - f(p,t)}{|\rho|^{\alpha+1}} d\rho + \right. \\ &\left. (1-p)^{\alpha} p \int_{0}^{\infty} \frac{f(p+\rho,t) - f(p,t)}{|\rho|^{\alpha+1}} d\rho \right] \end{aligned} \tag{3}$$

where C is a numerical constant determined by the precise shape of the neighborhood distribution, and N is the network size. This operator has, to the best of out knowledge not yet been described in the literature, but is closely related to the Riesz and Feller fractional derivatives [5].

As the fractional differential equations cannot generally be solved analytically, they have been solved numerically using a Galerkin approach [3]. We have also implemented a direct implementation of the underlying random walks, which works by selecting random individuals, and their (random) neighborhoods, and copying the selected agent's meme to its neighbors. This was repeated until the population reaches fixation.

3 Results

The solution to the fixation probability as defined by equation 1 turns out to be $W_F(p) = p$ as can be verified by substituting it in the linear operator 3, but it can also be derived from a more intuitive argument. Because in cultural evolution without mutation/innovation (as modeled here), every meme must derive from a meme in the original

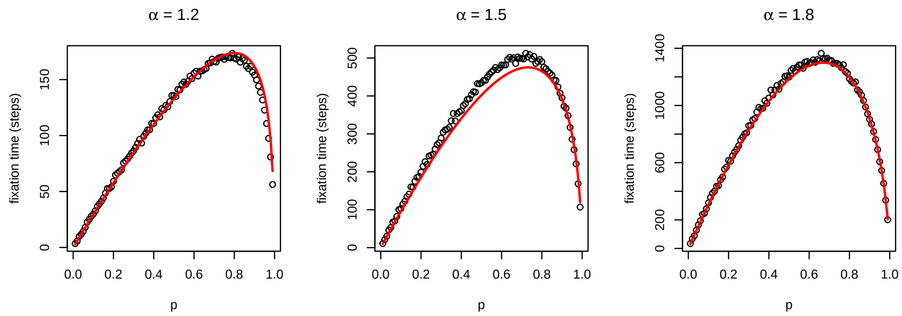

Fig. 1. Conditional fixation times for social networks with three different values for α. The circles indicate the results of the the direct simulation of the random walk and are the mean over 10000 runs. The red line indicates the value predicted by the numerical approximation of the fractional diffusion equations.

population, the probability of a meme going to fixation *must* be proportional to the proportion of that meme in the original population

There is no known analytical solution to the fixation time, but the results from the numerical approximation and the direct simulation are given in Fig. 1. It can be observed that the diffusion model closely models the direct simulation. It can also be observed that the fixation times are lower when α is lower. This is as expected, because for lower α, agents will have a higher probability to have extremely large neighborhoods. A final, but more subtle effect is that conditional fixation time initially tends to rise less steeply with increasing p when α is lower. This means that for small initial proportions of a mutant meme, the mutant meme will spread even more quickly than would be expected from the above-mentioned heavy-tailedness of the neighborhood when α is low.

4 Conclusion and Future Work

These initial results are promising in the sense that it appears possible to represent cultural evolution on social networks with fractional diffusion equations. Although the linear operator of equation 3 may look daunting, it can be interpreted in terms of more well-studied fractional derivatives such as the Riesz and Feller derivatives [5, §5.4], and thus the mathematical machinery of fractional calculus can be brought to bear on the problem of understanding cultural evolution on social networks. Still, a number of issues remain open. A technical problem is the derivation of the precise value of the numerical constant C from the distribution of jump sizes. Its value should follow from the precise shape of the jump distribution, but at the moment the analytically derived constant is off by approximately $\alpha^{\frac{1}{2}}$. At the moment our working hypothesis is that this is due to a difficulty approximating the underlying discrete neighborhood size distribution by a continuous equivalent in the derivation of equation 3. Also, the equations so far cannot account for differences in ‘fitness’ between different memes. In biological evolution, fitness differences play an important role, and this may also be the case in cultural evolution. There are models to account for diffusion and drift (selection) in systems where large jumps may occur [8, §4] and it is expected that eq. 3 can be modified analogously. A more fundamental issue is that there are a number of simplifying assumptions in the model that may be less valid for cultural evolution than for biological evolution and these should be critically evaluated. First of all, the binary representation of memes is very simple, and may not be valid for all types of cultural evolution. Second, the diffusion approximation implicitly assumes that agents may have different neighborhoods at different time steps (i.e. the social network may change). It may be that the diffusion approximation works less well when the social network remains fixed. Finally, an effort should be made to check whether the dynamics predicted by the fractional diffusion equations is actually observed in real-life instances of the spread of cultural items on social networks.

Summary. This abstract presents a first investigation of how to model cultural evolution on social networks using fractional diffusion equations. Social networks are characterised by heavy-tailed neighborhood distributions, and this implies that cultural evolution on a social network cannot be modeled using the ordinary diffusion equations that have been used successfully to study biological evolution. The abstract presents a number of results that show a) that the fractional diffusion approach works and b) what the qualitative effects of the heavy tails of the neighborhood distribution is on the time it takes for memes to spread on a social network – in particular that more heavy-tailed distributions result in disproportionally faster spread of memes. It ends by discussing a number of shortcomings of the present model and avenues for future research.

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