1 Introduction

We construct our model by using differential equations to anticipate the dynamics of social group change and its long term behavior, with as few factors as possible. The most important assumption we make is that social group change relies on homophily, the tendency to make friends with people of similar traits. We let the traits in individuals be binary, so for a single trait, the individual either has the trait, or has the opposite trait. Building off of the two mechanisms that are adaptation and social selection behind the phenomenon of homophily in Smirnov and Thurner, we define two parameters $a$: the probability of people who would adapt and change their behavior (trait) to fit in a group and $s$: the probability of people who would not change their behavior (trait) and look for groups with the same traits. The two parameters here are determined by the nature of the trait which we call $t^+$, if the trait $t^+$ gains popularity for people in general, more people with the opposite trait $t^-$ would adapt to the trait $t^+$ instead of looking for people with the same trait $t^-$. So, $a$ would be larger than $s$. Similarly, if the trait $t^+$ is not received as a popular trait to have, $s$ would be larger than $a$. Since $a$ and $s$ are dependent solely on the nature of the trait, they are constant in every group in the set of people we are analyzing. Since an increase in $a$ leads to a decrease in $s$ and vice versa, it is reasonable to assume that $a + s = 1$. We will start with a simple linear model.

2 Methods

2.1 Two Groups, Single Trait

Define $N$ as the total population, $N_1$ and $N_2$ as the population of the two groups $A_1$ and $A_2$ such that $N_1 + N_2 = N$, $p_1$ and $p_2$ as the percentage of people in each group with the dominant trait, which is defined as the trait in a group which most people have. Only people in a group without the dominant trait are subject to adaptation or selection. If we assume the groups are homogeneous, namely, everyone has the same trait, then everyone will end up in the same group. So, it is reasonable to assume that the dominant traits of $A_1$ and $A_2$ are opposite to each other. Then, we can first make the table that illustrates the population flow for a specific group depending on their members’ traits and priority on which of two mechanisms they are choosing.

<table>
<thead>
<tr>
<th>Priority</th>
<th>People With Dominant Trait</th>
<th>Without Dominant Trait</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adaptation</td>
<td>Stay</td>
<td>Stay</td>
</tr>
<tr>
<td>Selection</td>
<td>Stay</td>
<td>Leave</td>
</tr>
</tbody>
</table>

and then write the system linear equations

$$\dot{N}_1 = (1 - s)(1 - p_2)N_2 - s(1 - p_1)N_1$$
$$\dot{N}_2 = s(1 - p_1)N_1 - (1 - s)(1 - p_2)N_2$$

The reason for the coefficient $s$ of $(1 - p_1)N_1$ is that $1 - p_1$ percent of the group $A_1$ is leaving their own group for group $A_2$ due to the impact of selection. The reason for the coefficient $1 - s = a$ of $(1 - p_2)N_2$ is that $1 - p_2$ percent of the group $A_2$ are leaving their own group for group $A_2$ due to the impact of adaptation. We can solve for the fixed points. The obvious one
is \((N_1^*, N_2^*) = (0, 0)\) but does not satisfy the condition that \(N_1 + N_2 = N\). The correct one is obtained by using the same condition \(N_1 + N_2 = N\).

\[
N_1^* = \frac{(1 - p_2)(1 - s)N}{(1 - p_2)(1 - s) + s(1 - p_1)}
\]

\[
N_2^* = \frac{s(1 - p_1)N}{(1 - p_2)(1 - s) + s(1 - p_1)}
\]

We can easily verify that \(N_1^*\) and \(N_2^*\) stay between 0 and \(N\), and they sum to be \(N\). When \((N_1, N_2)\) is above the line \(N_2 = \frac{s(1-p_1)}{(1-s)(1-p_2)}N_1\) that is increasing, \(\dot{N}_1 > 0\) and \(\dot{N}_2 < 0\). When \((N_1, N_2)\) is below the line, \(\dot{N}_1 < 0\) and \(\dot{N}_2 > 0\). So, \((N_1, N_2)\) is going to converge to this line, and we will have a stable fixed point uniquely determined by \(N_1 + N_2 = N\). Thus, in the long run the system is going to stabilize to the stable fixed point \((N_1^*, N_2^*)\).

### 2.2 Additional Flow with Outside

In this case, the total population \(N\) still contains the two groups as in 2.1, and also some individuals not affiliated with any of the two groups. Call the dominant trait in group \(A_1\) \(t^+\). We define \(p_3\) as the percentage of \(t^+\) in people with no affiliation, and \(k\) as the attracting probability of people with no affiliation to join \(A_1\) with dominant trait \(t^+\). Then, \(1 - k\) is the attracting probability to join \(A_2\), and \(k\) is a constant in the system. We can write a system of more complicated differential equations, but they are still linear.

\[
\dot{N}_1 = -sk(1 - p_1)N_1 - s(1 - k)(1 - p_1)N_1 + k(1 - s)(1 - p_2)N_2 + kp_3(N - N_1 - N_2)
\]

\[
= -s(1 - p_1) + kp_3)N_1 + k(1 - s)(1 - p_2) - kp_3)N_2 + kp_3N
\]

\[
\dot{N}_2 = -(1 - s)(1 - k)(1 - p_2)N_2 - k(1 - s)(1 - p_2)N_2 + sk(1 - p_1)N_1 + k(1 - p_3)(N - N_1 - N_2)
\]

\[
= -((1 - s)(1 - p_2) + k(1 - p_3)N_2 + (sk(1 - p_1) - k(1 - p_3))N_1 + k(1 - p_3)N
\]

Since the system is linear and all the parameters are constant, we can easily obtain the fixed point of the system, however complicated it is in expression. Instead of carrying out the cumbersome calculation of the fixed point, we are going to analyze the system numerically in terms of \(s\) and \(k\). We found that \(s\) has a more dominating impact on the location of the stable point. For a fixed \(s\), any dramatic change in \(k\) has little impact on the long term behavior. On the other hand, if we fix the value of \(k\) and let \(p_1\) and \(p_2\) not too close to 1, when \(s = 0.5\), namely, when \(t^+\) and \(t^-\) are equally popular, \(N_1^* = N_2^*\) and they are near half of the population. When \(s > 0.5\), namely, selection prevails due to the unpopularity of \(t^+\) which is the dominant trait in \(A_1\), \(N_1^* < N_2^*\) generally. Similarly, if \(s < 0.5\), \(N_1^* > N_2^*\) generally. However, if for example the starting \(p_1\) is too close to one, \(N_1\) is going to be close to \(N\), having approximately as much impact as \(s\) on the long term behavior. Thus, the initial percentage of the dominant trait in the group, the popularity of the trait have the most impact on the long term behavior, while having individuals outside the groups have little impact.

### 2.3 More Traits

When the system has more than 1 trait, we can approximate that system by picking out the trait with the highest \(a_i\), namely, the most popular one. The remaining traits are going to have relatively smaller impact on the system compared to the one chosen, and we can use what we have established in 2.2 to analyze the long term behavior.