**Replication of Kalick & Hamilton’s (1986) Agent-Based Model of Human Date Choice**

**Introduction**

A substantial breadth of early social psychological research focused on uncovering the methods with which humans seek and initiate romantic relationships. In particular, much of this literature sought to establish the role of physical attractiveness in this process – giving rise to theories such as the matching hypothesis (Walster et al., 1966), which suggests that individuals seek partners with comparable social desirability to themselves. This hypothesis has been used to explain observations of positive assortative mating, wherein romantic partners are more similar in their characteristics than would otherwise be expected by chance (Schwartz, 2013). A key study from Kalick and Hamilton (1986) examined these ideas, computationally, through the implementation and testing of agent-based models to simulate plausible methods of date choice in humans, and thereby guide this line of theorising with demonstrable evidence. Specifically, the agent-based models developed by Kalick and Hamilton (1986) presented the choosing of romantic partners as a process rooted in logic of the matching hypothesis – with individuals seeking partners of equal physical attractiveness to themselves – and as a process of finding the most attractive partner possible.

These models were thoroughly outlined in a recent paper from Grow (2021), who examined how different manipulations of the parameters within these models can flexibly reflect date choice in populations of various characteristics. In a similar fashion to Grow’s thorough explanation and testing of the equations and procedures comprising these computational social psychology theories, we replicated Kalick and Hamilton’s original models of similarity-based and attractiveness-based date choice, and conducted a brief test to compare the respective results with those established from other replications of the models, as well as with the outcomes that could be expected in real life social dynamics.

**Method**

As described in Grow’s (2021) report, Kalick and Hamilton’s (1986) ABMs both began with the generation of two groups, with the individuals of each group being randomly assigned a physical attractiveness score from a uniform distribution of values ranging 1 to 10. In order to replicate this step for our model, we initialised two vectors of uniformly-distributed random values, ranging 1:10, to represent the “agents” and “suitors” that would be paired as prospective couples through the algorithm. The original model then used another uniform distribution to randomly pair individual members from each group for a ‘date’, in each individual would probabilistically decide whether or not to couple with their counterpart. For this stage, we similarly used a uniform distribution to randomly select one agent and one suitor for a date and implemented the same probabilistic equations used in the original models. For the matching hypothesis ABM (similarity-based date choice), this equation was:

*P = or P =*

Where *Ai* is the attractiveness score of the selected agent, *Aj* is the attractiveness score of the selectedsuitor, and *P* is the probability of coupling. This meant that each individual, on each date, based their decision of whether to couple or not couple with their allocated counterpart on the basis of the similarity/difference between their respective attractiveness scores.

For the attractiveness-based date choice ABM, this equation was:

*P = or P =*

This meant that each individual, on each date, based their decision of whether to couple or not couple with their allocated counterpart on the basis of that counterpart’s attractiveness score.

Additionally, in both models, a correction was applied to each calculated coupling probability, according to the number of dates that each individual had been on already. This equation was:

*P = (P)(51 – d)/50*

This was implemented in order to simulate the ‘settling’ process by which individuals become less stringent about coupling as the number of unsuccessful dates they go on increases.

These date choice decision rule equations, set by Kalick and Hamilton’s models, were all implemented into our ABM function script.

Based on these rules, then, the individuals of each date determined whether or not to couple with their counterpart. If the collective probability calculations of both individuals determined that they were both willing to match, they consequently formed a relationship and were removed from the dating pool. If an individual ‘decided’ not to match, the pairing would be dissolved and a new random pair would be selected for a date. In our implementation, successful dates were processed by storing the attractiveness values representing each agent and suitor as a row in a “couples” matrix, then replacing their respective indices in the ”agents” and “suitors” vectors with empty spaces. For unsuccessful dates, the agent and suitor values were simply left in their respective vectors and no values were added to the couples matrix.

As with the original model, these steps were repeated until all agents and suitors were successfully coupled, and there were no individuals left in the dating pool.

Once the couples vector was filled, we were able to calculate the correlation between the attractiveness scores of the couples, to allow for the comparison of these coefficients with those obtained in the literature. This was achieved by applying the built-in MatLab function corrcoef(), to the couples vector, in our ABM script. By comparing and examining these correlations in the context of the existing literature, we sought to determine how each model fared as explanations for human date choice.

**Results**

From running each model simulation once, with 1000 agents and 1000 suitors (as specified in Grow’s (2021) report), we established an intra-couple attractiveness correlation of 0.6135 from the attractiveness choice rule model and an intra-couple attractiveness correlation of 0.6929 from the similarity choice rule model. Figures 1 and 2 (below) present these results.



Figure 1. Intra-couple attractiveness correlation determined from attractiveness-based date choice model.

Figure 2. Intra-couple attractiveness correlation determined from similarity-based date choice model.

The following script was then used to test the average intra-couple attractiveness correlations determined by each model:

% Run 50 simulations of attractiveness-based dating.

for iRunA = 1:50

correlationA(iRunA, 1) = runKalickHamilton(1000, 'attractiveness')

end

% Calculate mean couple correlation over 50 simulations.

meanCorrelationA = mean(correlationA)

% Run 50 simulations of attractiveness-based dating.

for iRunS = 1:50

correlationS(iRunS, 1) = runKalickHamilton(1000, 'similarity')

end

% Calculate mean couple correlation over 50 simulations.

meanCorrelationS = mean(correlationS)

The results from this script are presented in Table 1, below.

Table 1. Mean intra-couple attractiveness correlation, between 1000 couples, calculated from 50 runs of each of our models.

|  |  |
| --- | --- |
| Attractiveness | Similarity |
| **0.62** | **0.69** |

Table 2. Mean intra-couple attractiveness correlation, between 1000 couples, calculated from 50 runs of each of Kalick and Hamilton’s (1986) original models.

|  |  |
| --- | --- |
| Attractiveness | Similarity |
| **0.61** | **0.83** |

**Discussion**

The existing literature related to the phenomenon of assortative mating in humans (that is, the observed similarity that tends to occur between the attractiveness of members of a romantic couple) reports correlations of .42 (Feingold, 1981) and .53 (Citelli and Waid, 1980) between romantic partners, as well as correlations of .56 and .63 for serious daters and engaged or married couples (White, 1980; Kaznatcheev et al., 2010). Given this context, the results that we have established from this replication of Kalick and Hamilton’s ABMs demonstrate not only that our models were able to replicate a similar pattern of results to those established by the original models (presented in Table 2), but they also further substantiate the notion that assortative mating in humans can be more accurately explained by the attractiveness hypothesis model – which gives coefficients more reflective of the relationship observed between the attractiveness of romantic partners in real life.

While this short study offers an elementary contribution to the current understanding of human date choice and the phenomenon of assortative mating, consistent the other findings of the field, this modelling procedure also highlights further opportunities for learning more about this social psychological process. As highlighted by Grow (2021), for example, future research could involve the manipulation of parameters such as the distribution of attractiveness scores in the population, in order to achieve a more comprehensive explanation of the patterns observed between romantic couples.

**References**

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