



# A computer simulation to investigate the association between gene-based gifting and pair-bonding in early hominins

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## ABSTRACT

This article describes simulation research based on the Hamiltonian theory of gene-based altruism. It investigates the origin of semipermanent breeding bonds during hominin evolution. The research framework is based on a biologically detailed, ecologically situated, multi-agent microsimulation of emergent sociality. The research question tested is whether semipermanent breeding bonds (an emergent homoplastic social construct) might emerge among primate-like agents as the consequence of a mutation capable of supporting involuntary prosocial behavior. The research protocol compared several, single independent-variable longitudinal studies wherein hundreds of generations of autonomous, initially promiscuous, biologically detailed, hominin-like artificial life software agents were born, allowed to forage, reproduce, and die during experimental intervals lasting several simulated millennia. The temporal setting of the experiment was roughly contemporaneous with, or slightly after the time of, the *Pan-Homo* split. The simulation investigated what would happen if, within a population, a single gene for prosocial behavior (the independent variable in the experiment) was either switched on or switched-off. The null hypothesis predicted that, if the gene was switched off, then semipermanent breeding bonds (the dependent variable) would nonetheless emerge within the population. The results of the simulation rejected this null hypothesis, by showing that semipermanent breeding bonds would reliably emerge among the experimental populations but not among the control groups. Moreover, it was found that, across all experimental settings having constrained population numbers, the portion of each population having no prosocial trait would die out early, whereas the portion with the prosocial trait would survive. Large control populations had no discernible loss. The results of this research imply that, during the early stages of hominin evolution, there might have been a set of initially gene-based, altruistic excess forage-sharing social traits that contributed to the onset of morphological and additional complex social changes characteristic of this group. This work also demonstrates that modern computational technologies can extend our ability to test ‘what if’ hypotheses appropriate to the study of early hominin evolution.

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## 1. Introduction

Over fifty years ago, Hamilton (1963, 1964a, b) proposed a theory about gene-based altruism. This theory posited that if a prosocial mutation came into being, it might be passed on to succeeding generations as the result of explicitly non-cognitive, i.e., unconscious and non-reciprocal, reproductive social interaction. In the intervening fifty years, many researchers and theoreticians have considered the Hamiltonian argument. Often, they instantiated their models as agent-based simulations (e.g., Premo, 2006),

grounded them in game theory (e.g., Grund et al., 2013) and/or considered the argument using quantitative statistics (e.g., Gavrillets, 2012). Each time the argument was considered, the individual researchers had to decide if the hominin population under study needed to have some degree of cognitive capacity to support reciprocal prosocial interaction or if their respective research question could be nuanced such that the research could be run without modeling any explicit hominin cognitive attribute in support of prosocial behaviors. This meant researchers might miss the entire point of the initial Hamiltonian argument when they decided that their theoretical model should incorporate hominin cognitive support for prosocial behavior. The research reported in this paper deals with hominin populations having explicit biologically based

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prosocial behaviors, i.e., non-cognitive, non-reciprocal social interactions. In particular, it will be shown experimentally by means of computer simulation that a population could survive, evolve, and adapt on the basis of pure gene-based altruism.

Recent simulation research in the context of hominin evolution is perhaps best represented by the works of Premo (2006) and Gavrillets (2012). Premo (2006) provided a comprehensive simulation research experiment constructed as an agent-oriented simulation operating within a hybridized game-theoretical framework. His work demonstrated evidence of a strong correlation between gene-based altruism, species adaptive survival, and the distribution of forageables within a simulated environment. While Premo (2006) simulated hominin agents that enjoyed only asexual reproduction and 'lived' within an abstract simulation cycle uncoupled from real-world time, he also created two categories of agents whose simulated alleles expressed for phenotypic altruistic behavior. His first category of agent was one in which he installed a discrete set of cognitively nuanced social behaviors. His second agent category represented a non-cognitive hominin he referred to as a 'null' object. Premo's (2006) 'null' agents provided a control against which his more cognitively rich agents could be compared. These 'null' agents were similar to those in this paper, but only in an abstract sense, since the work reported here greatly narrows and extends the previous work by Premo (2006).

In the category of purely quantitative models, Gavrillets (2012) provided a powerful equation-based exploratory mechanism, based on an integrative computational process whose abstract product was evidence that individual, promiscuous hominins could transition to pair-bonded relationships. However, his research did not use an explicit articulation of time, i.e., his populations were neither born nor did they die, and there was no evolution. Simply, Gavrillets' (2012) model was not temporally coupled to the reproductive cycles of any hominin explicit biology, nor their needs to forage in order to survive. Ultimately, his research did not address the role that time and environment, as stochastic drivers of hominin behavior, must have played in hominin evolution. In contrast, in the present article the theory of gene-based altruism is tested using a highly detailed, temporally grounded, discrete-event, microsimulation technology called a spatial agent-based model (ABM; Grimm et al., 2010). This article describes that simulation research performed, the technology that was used, and discusses the results derived for the understanding of hominin origins and evolution.

### 1.1. Motivation

The original motivating challenge behind the simulation experiment described in this paper was to discover why reciprocal exogamy (a social behavior involving the intentional exchange of mating resources; Chapais, 2008) emerged among the higher primates in general and among *Homo* in particular. Based on this motivation, several non-critical hypotheses (listed in the next section) were formulated to help begin the process of operationalizing the problem space, so that its properties and mechanisms could be translated into computer code. However, the first problem was to find a way to sufficiently constrain the motivating challenge, while still producing plausible research whose experimental method could take advantage of a discrete-event simulation technology called ABM. What was required was to identify the set of necessary and sufficient causal mechanisms (biological, possibly cognitive, social, environmental, etc.) that: 1) could be translated into computer code; 2) would support emergent results, later identifiable as solutions directly related to the motivating challenge; and 3) would not provide any 'hard-coded' solutions in any sense. The descriptive name for the project software ('Clans') was selected based on the

notion that, if the research was successful, then one should expect to see extended family groups (or 'clans') self-organizing within each large and promiscuous experimental population. Logically, such evidence of clan-like social behavior would seem to be a necessary precondition to the emergence of reciprocal exogamy. Unfortunately, evidence of reciprocal exogamy never occurred during the experimental period, likely due to limitations of time and coding resources. However, when evidence of the self-organization of 'family-like' groups (more technically called evidence of semipermanent breeding bonds) began to emerge in the simulation, using only an independent variable gene for altruism, the work of Hamilton (1963, 1964a, b) came to mind. It is this part of the simulation experiment and its results that are described here.

### 1.2. Hypotheses

The central hypothesis operationalized for simulation in Clans was that prosocial, gene-based altruism should lead a simulated population of promiscuous hominin agents to develop emergent, semipermanent breeding bonds. The null hypothesis was that, if the same prosocial gene (for gene-based altruism) was withheld from an identical population, then semipermanent breeding bonds should still emerge. In contrast to the central hypothesis, and not implemented in Clans, were the original motivating challenges. These proposed that "reciprocal exogamy emerged because of innate drives for specific territoriality constrained by [...] bipedal mobility, social altruism and alliance, environmental and social circumscription, and sexually differentiated philopatry" (Rouly, 2015a:83). Philopatry, of course, refers to the tendency of community members of one sex to remain in collocation with conspecifics after sexual maturity is achieved, whereas the opposite sex members of the same community will typically engage in some degree of distal migration into unrelated social groups (Parish and de Waal, 2000). To assist in framing and operationalizing the central hypothesis (as instantiable computer code), two additional hypotheses were adopted: 1) a pristine environment is necessary for the identification of the fundamental principles of small-group social behavior, and 2) an environment having a sufficient absence of cultural confounds but also one having a sufficient fullness of socioenvironmental stimuli is required for a complete understanding of 'emergent' sociality. In this context, the word 'pristine' refers to a setting void of prescriptive culture, social assumption, or other human-constructed artifacts. These latter two 'framing' hypotheses led to the development of the artificial ecology inhabited by the Clans hominin agents.

### 1.3. The simulation technology

Initially, the simulation research had a single purpose: try to understand how *Pan*-like promiscuous individuals might transition into family-unit households and, much later, extended families and clans capable of practicing reciprocal exogamy. However, in hindsight, it seems that little empirical evidence exists about 'why' the Hominini transitioned from being presumably small groups of *Gorilla*-like polygynous and/or possibly *Pan*-like promiscuous individuals into family-units having stable breeding bonds, and much later extended families and clans. It seems reasonable to assume that the transition process was quite slow to develop into fuller social dominance among the early hominin species, even as *Ardipithecus*, *Australopithecus*, or even *Homo* emerged (Lovejoy, 1981; Chapais, 2008).

As a simulation technology, Clans is an example of the computational study of natural life called artificial life (ALife). As it will be shown in the next several paragraphs, ALife is only a few decades old. This science uses computer programs (simulations) to study an

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